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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN HOMEOSTASIS AND ADAPTATION

(57) Abstract: Isolated nucleic acid molecules, designated HA nucleic acid molecules, which encode novel HA proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing HA nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated HA proteins, mutated HA proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of HA genes in this organism.

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS
INVOLVED IN HOMEOSTASIS AND ADAPTATION**

Related Applications

5 This application claims priority to prior filed U.S. Provisional Patent Application
Serial No. 60/141031, filed June 25, 1999. This application also claims priority to prior
filed German Patent Application No. 19931636.8, filed July 8, 1999, German Patent
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10 9, 1999, German Patent Application No. 19932128.0, filed July 9, 1999, German Patent
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Application No. 19941391.6, filed August 31, 1999, and German Patent Application No.
25 19942088.2, filed September 3, 1999. The entire contents of all of the aforementioned
applications are hereby expressly incorporated herein by this reference.

Background of the Invention

30 Certain products and by-products of naturally-occurring metabolic processes in
cells have utility in a wide array of industries, including the food, feed, cosmetics, and
pharmaceutical industries. These molecules, collectively termed 'fine chemicals',
include organic acids, both proteinogenic and non-proteinogenic amino acids,

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nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful
5 organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

10

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C.*
15 *glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as homeostasis and adaptation (HA) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in
20 industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The HA nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the HA nucleic acids of the
25 invention, or modification of the sequence of the HA nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The HA nucleic acids of the invention may also be used to identify an organism
30 as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C.*

glutamicum genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The HA nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The HA proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the maintenance of homeostasis in *C. glutamicum*, or in the ability of this microorganism to adapt to different environmental conditions. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an HA protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by engineering enzymes which modify or degrade aromatic or aliphatic compounds such that these enzymes are increased or decreased in activity or number, it may be possible to modulate the production of one or more fine chemicals which are the modification or degradation products of these compounds. Similarly, enzymes involved in the metabolism of inorganic compounds provide key molecules (*e.g.* phosphorous,

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sulfur, and nitrogen molecules) for the biosynthesis of such fine chemicals as amino acids, vitamins, and nucleic acids. By altering the activity or number of these enzymes in *C. glutamicum*, it may be possible to increase the conversion of these inorganic compounds (or to use alternate inorganic compounds) to thus permit improved rates of incorporation of inorganic atoms into these fine chemicals. Genetic engineering of *C. glutamicum* enzymes involved in general cellular processes may also directly improve fine chemical production, since many of these enzymes directly modify fine chemicals (e.g., amino acids) or the enzymes which are involved in fine chemical synthesis or secretion. Modulation of the activity or number of cellular proteases may also have a direct effect on fine chemical production, since many proteases may degrade fine chemicals or enzymes involved in fine chemical production or breakdown.

Further, the aforementioned enzymes which participate in aromatic/aliphatic compound modification or degradation, general biocatalysis, inorganic compound metabolism or proteolysis are each themselves fine chemicals, desirable for their activity in various *in vitro* industrial applications. By altering the number of copies of the gene for one or more of these enzymes in *C. glutamicum* it may be possible to increase the number of these proteins produced by the cell, thereby increasing the potential yield or efficiency of production of these proteins from large-scale *C. glutamicum* or related bacterial cultures.

The alteration of an HA protein of the invention may also indirectly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by modulating the activity and/or number of those proteins involved in the construction or rearrangement of the cell wall, it may be possible to modify the structure of the cell wall itself such that the cell is able to better withstand the mechanical and other stresses present during large-scale fermentative culture. Also, large-scale growth of *C. glutamicum* requires significant cell wall production. Modulation of the activity or number of cell wall biosynthetic or degradative enzymes may allow more rapid rates of cell wall biosynthesis, which in turn may permit increased growth rates of this microorganism in culture and thereby increase the number of cells producing the desired fine chemical.

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By modifying the HA enzymes of the invention, one may also indirectly impact the yield, production, or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, many of the general enzymes in *C. glutamicum* may have a significant impact on global cellular processes (e.g., regulatory processes) which in turn have a significant effect on fine chemical metabolism. Similarly, proteases, enzymes which modify or degrade possibly toxic aromatic or aliphatic compounds, and enzymes which promote the metabolism of inorganic compounds all serve to increase the viability of *C. glutamicum*. The proteases aid in the selective removal of misfolded or misregulated proteins, such as those that might occur under the relatively stressful environmental conditions encountered during large-scale fermentor culture. By altering these proteins, it may be possible to further enhance this activity and to improve the viability of *C. glutamicum* in culture. The aromatic/aliphatic modification or degradation proteins not only serve to detoxify these waste compounds (which may be encountered as impurities in culture medium or as waste products from cells themselves), but also to permit the cells to utilize alternate carbon sources if the optimal carbon source is limiting in the culture. By increasing their number and/or activity, the survival of *C. glutamicum* cells in culture may be enhanced. The inorganic metabolism proteins of the invention supply the cell with inorganic molecules required for all protein and nucleotide (among others) synthesis, and thus are critical for the overall viability of the cell. An increase in the number of viable cells producing one or more desired fine chemicals in large-scale culture should result in a concomitant increase in the yield, production, and/or efficiency of production of the fine chemical in the culture.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as HA proteins, which are capable of, for example, performing a function involved in the maintenance of homeostasis in *C. glutamicum*, or of participating in the ability of this microorganism to adapt to different environmental conditions. Nucleic acid molecules encoding an HA protein are referred to herein as HA nucleic acid molecules. In a preferred embodiment, an HA protein participates in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or possesses a *C. glutamicum* enzymatic or proteolytic activity. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an HA protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of HA-
5 encoding nucleic acids (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the
10 isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,
15 SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred HA proteins of the present invention also preferably possess at least one of the HA activities described herein.

20 In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein
25 or portion thereof maintains an HA activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%,
30 preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from

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those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (e.g., an HA fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (e.g., a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (i.e., the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (e.g., a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* HA protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, e.g., recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an HA protein by culturing the host cell in a suitable medium. The HA protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an HA gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated HA sequence as a transgene. In another embodiment, an endogenous HA gene within the genome of the

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microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered HA gene. In another embodiment, an endogenous or introduced HA gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional HA protein. In still
5 another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an HA gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the HA gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being
10 particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of
15 one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 440) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated HA protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the
20 isolated HA protein or portion thereof can participate in the maintenance of homeostasis in *C. glutamicum*, or can perform a function involved in the adaptation of this microorganism to different environmental conditions. In another preferred embodiment, the isolated HA protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the
25 Sequence Listing) such that the protein or portion thereof maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions.

The invention also provides an isolated preparation of an HA protein. In preferred embodiments, the HA protein comprises an amino acid sequence of the
30 invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention

(*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%,
5 and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated HA protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered
10 SEQ ID NO: of the Sequence Listing) and is able to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated HA protein can comprise an amino acid sequence
15 which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred
20 that the preferred forms of HA proteins also have one or more of the HA bioactivities described herein.

The HA polypeptide, or a biologically active portion thereof, can be operatively linked to a non-HA polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the HA protein alone. In other
25 preferred embodiments, this fusion protein participates in the maintenance of homeostasis in *C. glutamicum*, or performs a function involved in the adaptation of this microorganism to different environmental conditions. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

30 In another aspect, the invention provides methods for screening molecules which modulate the activity of an HA protein, either by interacting with the protein itself or a

substrate or binding partner of the HA protein, or by modulating the transcription or translation of an HA nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an HA nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an HA nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates HA protein activity or HA nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* processes involved in cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or enzymatic or proteolytic activities. The agent which modulates HA protein activity can be an agent which stimulates HA protein activity or HA nucleic acid expression. Examples of agents which stimulate HA protein activity or HA nucleic acid expression include small molecules, active HA proteins, and nucleic acids encoding HA proteins that have been introduced into the cell. Examples of agents which inhibit HA activity or expression include small molecules and antisense HA nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant HA gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment,

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said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

5 The present invention provides HA nucleic acid and protein molecules which are involved in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or that have a *C. glutamicum* enzymatic or proteolytic activity. The molecules of the invention may be utilized in the modulation of production of fine chemicals from
10 microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of activity of a protein involved in the production of a fine chemical (*e.g.*, an enzyme) has a direct impact on the yield, production, and/or efficiency of production of a fine chemical from the modified *C. glutamicum*), or an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of
15 the desired compound (*e.g.*, where modulation of the activity or number of copies of a *C. glutamicum* aromatic or aliphatic modification or degradation protein results in an increase in the viability of *C. glutamicum* cells, which in turn permits increased production in a large-scale culture setting). Aspects of the invention are further explicated below.

20

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include
25 organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty
30 acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of

Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

10

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

20 Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

30 Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical

industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed

from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

5 Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in
10 terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p.
15 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules
20 which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have
25 significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal
30 functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to

occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (*e.g.*, pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthanol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been

identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the *nifS* class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

25 C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules

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which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability
5 of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson,
10 R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine
15 and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for
20 several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

25 The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*,
30 Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from

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ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Maintenance of Homeostasis in *C. glutamicum* and Environmental Adaptation

The metabolic and other biochemical processes by which cells function are sensitive to environmental conditions such as temperature, pressure, solute concentration, and availability of oxygen. When one or more such environmental condition is perturbed or altered in a fashion that is incompatible with the normal functioning of these cellular processes, the cell must act to maintain an intracellular environment which will permit them to occur despite the hostile extracellular environment. Gram positive bacterial cells, such as *C. glutamicum* cells, have a number of mechanisms by which internal homeostasis may be maintained despite unfavorable

extracellular conditions. These include a cell wall, proteins which are able to degrade possibly toxic aromatic and aliphatic compounds, mechanisms of proteolysis whereby misfolded or misregulated proteins may be rapidly destroyed, and catalysts which permit intracellular reactions to occur which would not normally take place under the

5 conditions optimal for bacterial growth.

Aside from merely surviving in a hostile environment, bacterial cells (*e.g.* *C. glutamicum* cells) are also frequently able to adapt such that they are able to take advantage of such conditions. For example, cells in an environment lacking desired carbon sources may be able to adapt to growth on a less-suitable carbon source. Also,

10 cells may be able to utilize less desirable inorganic compounds when the commonly utilized ones are unavailable. *C. glutamicum* cells possess a number of genes which permit them to adapt to utilize inorganic and organic molecules which they would normally not encounter under optimal growth conditions as nutrients and precursors for metabolism. Aspects of cellular processes involved in homeostasis and adaptation are

15 further explicated below.

A. Modification and Degradation of Aromatic and Aliphatic Compounds

Bacterial cells are routinely exposed to a variety of aromatic and aliphatic compounds in nature. Aromatic compounds are organic molecules having a cyclic ring

20 structure, while aliphatic compounds are organic molecules having open chain structures rather than ring structures. Such compounds may arise as by-products of industrial processes (*e.g.*, benzene or toluene), but may also be produced by certain microorganisms (*e.g.*, alcohols). Many of these compounds are toxic to cells, particularly the aromatic compounds, which are highly reactive due to the high-energy ring structure. Thus, certain

25 bacteria have developed mechanisms by which they are able to modify or degrade these compounds such that they are no longer hazardous to the cell. Cells may possess enzymes that are able to, for example, hydroxylate, isomerize, or methylate aromatic or aliphatic compounds such that they are either rendered less toxic, or such that the modified form is able to be processed by standard cellular waste and degradation pathways. Also, cells may

30 possess enzymes which are able to specifically degrade one or more such potentially hazardous substance, thereby protecting the cell. Principles and examples of these types of modification and degradation processes in bacteria are described in several publications,

e.g., Sahm, H. (1999) "Procaryotes in Industrial Production" in Lengeler, J.W. *et al.*, eds. *Biology of the Procaryotes*, Thieme Verlag: Stuttgart; and Schlegel, H.G. (1992) *Allgemeine Mikrobiologie*, Thieme: Stuttgart).

Aside from simply inactivating hazardous aromatic or aliphatic compounds, many
5 bacteria have evolved to be able to utilize these compounds as carbon sources for continued
metabolism when the preferred carbon sources of the cell are not available. For example,
Pseudomonas strains able to utilize toluene, benzene, and 1,10-dichlorodecane as carbon
sources are known (Chang, B.V. *et al.* (1997) *Chemosphere* 35(12): 2807-2815; Wischnak,
C. *et al.* (1998) *Appl. Environ. Microbiol.* 64(9): 3507-3511; Churchill, S.A. *et al.* (1999)
10 *Appl. Environ. Microbiol.* 65(2): 549-552). There are similar examples from many other
bacterial species which are known in the art.

The ability of certain bacteria to modify or degrade aromatic and aliphatic
compounds has begun to be exploited. Petroleum is a complex mixture of chemicals which
includes aliphatic molecules and aromatic compounds. By applying bacteria having the
15 ability to degrade or modify these toxic compounds to an oil spill, for example, it is possible
to eliminate much of the environmental damage with high efficiency and low cost (see, for
example, Smith, M.R. (1990) "The biodegradation of aromatic hydrocarbons by bacteria"
Biodegradation 1(2-3): 191-206; and Suyama, T. *et al.* (1998) "Bacterial isolates degrading
aliphatic polycarbonates," *FEMS Microbiol. Lett.* 161(2): 255-261).

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B. Metabolism of Inorganic Compounds

Cells (*e.g.*, bacterial cells) contain large quantities of different molecules, such as
water, inorganic ions, and organic substances (*e.g.*, proteins, sugars, and other
macromolecules). The bulk of the mass of a typical cell consists of only 4 types of atoms:
25 carbon, oxygen, hydrogen, and nitrogen. Although they represent a smaller percentage of
the content of a cell, inorganic substances are equally as important to the proper functioning
of the cell. Such molecules include phosphorous, sulfur, calcium, magnesium, iron, zinc,
manganese, copper, molybdenum, tungsten, and cobalt. Many of these compounds are
critical for the construction of important molecules, such as nucleotides (phosphorous) and
30 amino acids (nitrogen and sulfur). Others of these inorganic ions serve as cofactors for
enzymic reactions or contribute to osmotic pressure. All such molecules must be taken up
by the bacterium from the surrounding environment.

For each of these inorganic compounds it is desirable for the bacterium to take up the form which can be most readily used by the standard metabolic machinery of the cell. However, the bacterium may encounter environments in which these preferred forms are not readily available. In order to survive under these circumstances, it is important for bacteria to have additional biochemical mechanisms which are able to convert less metabolically active but readily available forms of these inorganic compounds to ones which may be used in cellular metabolism. Bacteria frequently possess a number of genes encoding enzymes for this purpose, which are not expressed unless the desired inorganic species are not available. Thus, these genes for the metabolism of various inorganic compounds serve as another tool which bacteria may use to adapt to suboptimal environmental conditions.

After carbon, the most important element in the cell is nitrogen. A typical bacterial cell contains between 12-15% nitrogen. It is a constituent of amino acids and nucleotides, as well as many other important molecules in the cell. Further, nitrogen may serve as a substitute for oxygen as a terminal electron acceptor in energy metabolism. Good sources of nitrogen include many organic and inorganic compounds, such ammonia gas or ammonia salts (*e.g.*, NH_4Cl , $(\text{NH}_4)_2\text{SO}_4$, or NH_4OH), nitrates, urea, amino acids, or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract, etc. Ammonia nitrogen is fixed by the action of particular enzymes: glutamate dehydrogenase, glutamine synthase, and glutamine-2-oxoglutarate aminotransferase. The transfer of amino-nitrogen from one organic molecule to another is accomplished by the aminotransferases, a class of enzymes which transfer one amino group from an alpha-amino acid to an alpha-keto acid. Nitrate may be reduced via nitrate reductase, nitrite reductase, and further redox enzymes until it is converted to molecular nitrogen or ammonia, which may be readily utilized by the cell in standard metabolic pathways.

Phosphorous is typically found intracellularly in both organic and inorganic forms, and may be taken up by the cell in either of these forms as well, though most microorganisms preferentially take up inorganic phosphate. The conversion of organic phosphate to a form which the cell can utilize requires the action of phosphatases (*e.g.*, phytases, which hydrolyze phyate-yielding phosphate and inositol derivatives). Phosphate is a key element in the synthesis of nucleic acids, and also has a significant role in cellular energy metabolism (*e.g.*, in the synthesis of ATP, ADP, and AMP).

Sulfur is a requirement for the synthesis of amino acids (*e.g.*, methionine and cysteine), vitamins (*e.g.*, thiamine, biotin, and lipoic acid) and iron sulfur proteins. Bacteria obtain sulfur primarily from inorganic sulfate, though thiosulfate, sulfite, and sulfide are also commonly utilized. Under conditions where these compounds may not be readily
5 available, many bacteria express genes which enable them to utilize sulfonate compounds such as 2-aminosulfonate (taurine) (Kertesz, M.A. (1993) "Proteins induced by sulfate limitation in *Escherichia coli*, *Pseudomonas putida*, or *Staphylococcus aureus*." *J. Bacteriol.* 175: 1187-1190).

Other inorganic atoms, *e.g.*, metal or calcium ions, are also critical for the
10 viability of cells. Iron, for example, plays a key role in redox reactions and is a cofactor of iron-sulfur proteins, heme proteins, and cytochromes. The uptake of iron into bacterial cells may be accomplished by the action of siderophores, chelating agents which bind extracellular iron ions and translocate them to the interior of the cell. For reference on the metabolism of iron and other inorganic compounds, see: Lengeler *et al.*
15 (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart; Neidhardt, F.C. *et al.*, eds. *Escherichia coli* and *Salmonella*. ASM Press: Washington, D.C.; Sonenshein, A.L. *et al.*, eds. (1997) *Bacillus subtilis* and Other Gram-Positive Bacteria, ASM Press: Washington, D.C.; Voet, D. and Voet, J.G. (1992) *Biochemie*, VCH: Weinheim; Brock, T.D. and Madigan, M.T. (1991) *Biology of Microorganisms*, 6th ed. Prentice Hall:
20 Englewood Cliffs, p. 267-269; Rhodes, P.M. and Stanbury, P.F. *Applied Microbial Physiology – A Practical Approach*, Oxford Univ. Press: Oxford.

C. Enzymes and Proteolysis

The intracellular conditions for which bacteria such as *C. glutamicum* are
25 optimized are frequently not conditions under which many biochemical reactions would normally take place. In order to make such reactions proceed under physiological conditions, cells utilize enzymes. Enzymes are proteinaceous biological catalysts, spatially orienting reacting molecules or providing a specialized environment such that the energy barrier to a biochemical reaction is lowered. Different enzymes catalyze
30 different reactions, and each enzyme may be the subject of transcriptional, translational, or posttranslational regulation such that the reaction will only take place under appropriate conditions and at specified times. Enzymes may contribute to the

degradation (*e.g.*, the proteases), synthesis (*e.g.*, the synthases), or modification (*e.g.*, transferases or isomerases) of compounds, all of which enable the production of necessary compounds within the cell. This, in turn, contributes to the maintenance of cellular homeostasis.

5 However, the fact that enzymes are optimized for activity under the physiological conditions at which the bacterium is most viable means that when environmental conditions are perturbed, there is a significant possibility that enzyme activity will also be perturbed. For example, changes in temperature may result in aberrantly folded proteins, and the same is true for changes of pH – protein folding is
10 largely dependent on electrostatic and hydrophobic interactions of amino acids within the polypeptide chain, so any alteration to the charges on individual amino acids (as might be brought about by a change in cellular pH) may have a profound effect on the ability of the protein to correctly fold. Changes in temperature effectively change the amount of kinetic energy that the polypeptide molecule possesses, which affects the
15 ability of the polypeptide to settle into a correctly folded, energetically stable configuration. Misfolded proteins may be harmful to the cell for two reasons. First, the aberrantly folded protein may have a similarly aberrant activity, or no activity whatsoever. Second, misfolded proteins may lack the conformational regions necessary for proper regulation by other cellular systems and thus may continue to be active but in
20 an uncontrolled fashion.

 The cell has a mechanism by which misfolded enzymes and regulatory proteins may be rapidly destroyed before any damage occurs to the cell: proteolysis. Proteins such as those of the *la/lon* family and those of the *Clp* family specifically recognize and degrade misfolded proteins (see, *e.g.*, Sherman, M.Y., Goldberg, A.L. (1999) *EXS* 77:
25 57-78 and references therein and Porankiewicz J. (1999) *Molec. Microbiol.* 32(3): 449-58, and references therein; Neidhardt, F.C., *et al.* (1996) *E. coli* and *Salmonella*, ASM Press: Washington, D.C. and references therein; and Pritchard, G.G., and Coolbear, T. (1993) *FEMS Microbiol. Rev.* 12(1-3): 179-206 and references therein). These enzymes bind to misfolded or unfolded proteins and degrade them in an ATP-dependent manner.
30 Proteolysis thus serves as an important mechanism employed by the cell to prevent damage to normal cellular functions upon environmental changes, and it further permits

cells to survive under conditions and in environments which would otherwise be toxic due to misregulated and/or aberrant enzyme or regulatory activity.

Proteolysis also has important functions in the cell under optimal environmental conditions. Within normal metabolic processes, proteases aid in the hydrolysis of peptide bonds, in the catabolism of complex molecules to provide necessary degradation products, and in protein modification. Secreted proteases play an important role in the catabolism of external nutrients even prior to the entry of these compounds into the cell. Further, proteolytic activity itself may serve regulatory functions; sporulation in *B. subtilis* and cell cycle progression in *Caulobacter* spp. are known to be regulated by key proteolytic events in each of these species (Gottesman, S. (1999) *Curr. Opin. Microbiol.* 2(2): 142-147). Thus, proteolytic processes are key for cellular survival under both suboptimal and optimal environmental conditions, and contribute to the overall maintenance of homeostasis in cells.

15 D. Cell Wall Production and Rearrangements

While the biochemical machinery of the cell may be able to readily adapt to different and possibly unfavorable environments, cells still require a general mechanism by which they may be protected from the environment. For many bacteria, the cell wall affords such protection, and also plays roles in adhesion, cell growth and division, and transport of desired solutes and waste materials.

In order to function, cells require intracellular concentrations of metabolites and other molecules that are substantially higher than those of the surrounding media. Since these metabolites are largely prevented from leaving the cell due to the presence of the hydrophobic membrane, the tendency of the system is for water molecules to enter the cell from the external medium such that the interior concentrations of solutes match the exterior concentrations. Water molecules are readily able to cross the cellular membrane, and this membrane is not able to withstand the resulting swelling and pressure, which may lead to osmotic lysis of the cell. The rigidity of the cell wall greatly improves the ability of the cell to tolerate these pressures, and offers a further barrier to the unwanted diffusion of these metabolites and desired solutes from the cell. Similarly, the cell wall also serves to prevent unwanted material from entering the cell.

The cell wall also participates in a number of other cellular processes, such as adhesion and cell growth and division. Due to the fact that the cell wall completely surrounds the cell, any interaction of the cell with its surroundings must be mediated by the cell wall. Thus, the cell wall must participate in any adherence of the cell to other cells and
5 to desired surfaces. Further, the cell cannot grow or divide without concomitant changes in the cell wall. Since the protection that the wall affords requires its presence during growth, morphogenesis and multiplication, one of the key steps in cell division is cell wall synthesis within the cell such that a new cell divides from the old. Thus, frequently cell wall biosynthesis is regulated in tandem with cell growth and cell division (see, *e.g.*, Sonenshein,
10 A.L. et al, eds. (1993) *Bacillus subtilis* and Other Gram-Positive Bacteria, ASM: Washington, D.C.).

The structure of the cell wall varies between gram-positive and gram-negative bacteria. However, in both types, the fundamental structural unit of the wall remains similar: an overlapping lattice of two polysaccharides, N-acetyl glucosamine (NAG) and N-
15 acetyl muramic acid (NAM) which are cross-linked by amino acids (most commonly L-alanine, D-glutamate, diaminopimelic acid, and D-alanine), termed 'peptidoglycan'. The processes involved in the synthesis of the cell wall are known (see, *e.g.*, Michal, G., ed. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York).

20 In gram-negative bacteria, the inner cellular membrane is coated by a single-layered peptidoglycan (approximately 10 nm thick), termed the murein-sacculus. This peptidoglycan structure is very rigid, and its structure determines the shape of the organism. The outer surface of the murein-sacculus is covered with an outer membrane, containing porins and other membrane proteins, phospholipids, and lipopolysaccharides. To maintain a
25 tight association with the outer membrane, the gram-negative cell wall also has interspersed lipid molecules which serve to anchor it to the surrounding membrane.

In gram-positive bacteria, such as *Corynebacterium glutamicum*, the cytoplasmic membrane is covered by a multi-layered peptidoglycan, which ranges from 20-80 nm in thickness (see, *e.g.*, Lengeler *et al.* (1999) *Biology of Prokaryotes* Thieme Verlag: Stuttgart,
30 p. 913-918, p. 875-899, and p. 88-109 and references therein). The gram-positive cell wall also contains teichoic acid, a polymer of glycerol or ribitol linked through phosphate groups. Teichoic acid is also able to associate with amino acids, and forms covalent bonds with

muramic acid. Also present in the cell wall may be lipoteichoic acids and teichuronic acids. If present, cellular surface structures such as flagella or capsules will be anchored in this layer as well.

5 III. Elements and Methods of the Invention

 The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as HA nucleic acid and protein molecules, which participate in the maintenance of homeostasis in *C. glutamicum*, or which perform a function involved in the adaptation of this microorganism to different environmental
10 conditions. In one embodiment, the HA molecules participate in *C. glutamicum* cell wall biosynthesis or rearrangements, in the metabolism of inorganic compounds, in the modification or degradation of aromatic or aliphatic compounds, or have an enzymatic or proteolytic activity. In a preferred embodiment, the activity of the HA molecules of the present invention with regard to *C. glutamicum* cell wall biosynthesis or
15 rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or enzymatic or proteolytic activity has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the HA molecules of the invention are modulated in activity, such that the *C. glutamicum* cellular processes in which the HA molecules participate (*e.g.*, *C.*
20 *glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or enzymatic or proteolytic activity) are also altered in activity, resulting either directly or indirectly in a modulation of the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

25 The language, "HA protein" or "HA polypeptide" includes proteins which participate in a number of cellular processes related to *C. glutamicum* homeostasis or the ability of *C. glutamicum* cells to adapt to unfavorable environmental conditions. For example, an HA protein may be involved in *C. glutamicum* cell wall biosynthesis or rearrangements, in the metabolism of inorganic compounds in *C. glutamicum*, in the
30 modification or degradation of aromatic or aliphatic compounds in *C. glutamicum*, or have a *C. glutamicum* enzymatic or proteolytic activity. Examples of HA proteins include those encoded by the HA genes set forth in Table 1 and by the odd-numbered

SEQ ID NOs. The terms "HA gene" or "HA nucleic acid sequence" include nucleic acid sequences encoding an HA protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of HA genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The term "homeostasis" is art-recognized and includes all of the mechanisms utilized by a cell to maintain a constant intracellular environment despite the prevailing extracellular environmental conditions. A non-limiting example of such processes is the utilization of a cell wall to prevent osmotic lysis due to high intracellular solute concentrations. The term "adaptation" or "adaptation to an environmental condition" is art-recognized and includes mechanisms utilized by the cell to render the cell able to survive under nonpreferred environmental conditions (generally speaking, those environmental conditions in which one or more

5 favored nutrients are absent, or in which an environmental condition such as temperature, pH, osmolarity, oxygen percentage and the like fall outside of the optimal survival range of the cell). Many cells, including *C. glutamicum* cells, possess genes encoding proteins which are expressed under such environmental conditions and which permit continued growth in such suboptimal conditions.

In another embodiment, the HA molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an HA protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by engineering enzymes which modify or degrade aromatic or aliphatic compounds such that these enzymes are increased or decreased in activity or number, it may be possible to modulate the production of one or more fine chemicals which are the modification or degradation products of these compounds. Similarly, enzymes involved in the metabolism of inorganic compounds provide key molecules (*e.g.* phosphorous, sulfur, and nitrogen molecules) for the biosynthesis of such fine chemicals as amino acids, vitamins, and nucleic acids. By altering the activity or number of these enzymes in *C. glutamicum*, it may be possible to increase the conversion of these inorganic compounds (or to use alternate inorganic compounds) to thus permit improved rates of incorporation of inorganic atoms into these fine chemicals. Genetic engineering of *C. glutamicum* enzymes involved in general cellular processes may also directly improve fine chemical production, since many of these enzymes directly modify fine chemicals (*e.g.*, amino acids) or the enzymes which are involved in fine chemical synthesis or secretion. Modulation of the activity or number of cellular proteases may also have a direct effect on fine chemical production, since many proteases may degrade fine chemicals or enzymes involved in fine chemical production or breakdown.

Further, the aforementioned enzymes which participate in aromatic/aliphatic compound modification or degradation, general biocatalysis, inorganic compound metabolism or proteolysis are each themselves fine chemicals, desirable for their activity in various *in vitro* industrial applications. By altering the number of copies of the gene for one or more of these enzymes in *C. glutamicum* it may be possible to increase the

number of these proteins produced by the cell, thereby increasing the potential yield or efficiency of production of these proteins from large-scale *C. glutamicum* or related bacterial cultures.

The alteration of an HA protein of the invention may also indirectly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by modulating the activity and/or number of those proteins involved in the construction or rearrangement of the cell wall, it may be possible to modify the structure of the cell wall itself such that the cell is able to better withstand the mechanical and other stresses present during large-scale fermentative culture. Also, large-scale growth of *C. glutamicum* requires significant cell wall production. Modulation of the activity or number of cell wall biosynthetic or degradative enzymes may allow more rapid rates of cell wall biosynthesis, which in turn may permit increased growth rates of this microorganism in culture and thereby increase the number of cells producing the desired fine chemical.

By modifying the HA enzymes of the invention, one may also indirectly impact the yield, production, or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, many of the general enzymes in *C. glutamicum* may have a significant impact on global cellular processes (*e.g.*, regulatory processes) which in turn have a significant effect on fine chemical metabolism. Similarly, proteases, enzymes which modify or degrade possibly toxic aromatic or aliphatic compounds, and enzymes which promote the metabolism of inorganic compounds all serve to increase the viability of *C. glutamicum*. The proteases aid in the selective removal of misfolded or misregulated proteins, such as those that might occur under the relatively stressful environmental conditions encountered during large-scale fermentor culture. By altering these proteins, it may be possible to further enhance this activity and to improve the viability of *C. glutamicum* in culture. The aromatic/aliphatic modification or degradation proteins not only serve to detoxify these waste compounds (which may be encountered as impurities in culture medium or as waste products from cells themselves), but also to permit the cells to utilize alternate carbon sources if the optimal carbon source is limiting in the culture. By increasing their number and/or activity, the survival of *C. glutamicum* cells in culture may be enhanced. The inorganic metabolism

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proteins of the invention supply the cell with inorganic molecules required for all protein and nucleotide (among others) synthesis, and thus are critical for the overall viability of the cell. An increase in the number of viable cells producing one or more desired fine chemicals in large-scale culture should result in a concomitant increase in the yield,
5 production, and/or efficiency of production of the fine chemical in the culture.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* HA DNAs and the predicted amino acid sequences of the *C.*
10 *glutamicum* HA proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins that participate in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or
15 degradation of aromatic or aliphatic compounds, or that have a *C. glutamicum* enzymatic or proteolytic activity.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used
20 herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more
25 preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The HA protein or a biologically active portion or fragment thereof of the invention can participate in the maintenance of homeostasis in *C. glutamicum*, or can perform a function involved in the adaptation of this microorganism to different
30 environmental conditions, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections.

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode HA polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of HA-encoding nucleic acid (*e.g.*, HA DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated HA nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* HA DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis,

T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an HA nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* HA DNAs of the invention. This DNA comprises sequences encoding HA proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in nucleic acid sequences of the Sequence Listing

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA," "RXN," "RXS, or "RXC" followed by 5 digits (*i.e.*, RXA02458, RXN00249, RXS00153, or RXC00963).

5 Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences in of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by

10 their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02548 is set forth in SEQ ID NO:1, while the amino acid sequence which it

15 encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA02458, RXN00249, RXS00153, and RXC00963 are translations of the coding regions of the nucleotide sequences of nucleic

20 acid molecules RXA02458, RXN00249, RXS00153, and RXC00963, respectively. of the correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA,

25 RXN, RXS, or RXC designation. For example, SEQ ID NO:5, designated, as indicated on Table 1, as "F RXA00249", is an F-designated gene, as are SEQ ID NOs: 11, 15, and 33 (designated on Table 1 as "F RXA02264", "F RXA02274", and "F RXA00675", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not

30 intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is

significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an HA protein. The nucleotide sequences determined from the cloning of the HA genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning HA

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homologues in other cell types and organisms, as well as HA homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone HA homologues.

Probes based on the HA nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an HA protein, such as by measuring a level of an HA-encoding nucleic acid in a sample of cells, *e.g.*, detecting HA mRNA levels or determining whether a genomic HA gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is able to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. Proteins involved in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of

inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or that have a *C. glutamicum* enzymatic or proteolytic activity, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an HA protein"

- 5 contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of HA protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most
10 preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the HA nucleic acid molecules of the invention are preferably biologically active portions of one of the HA proteins. As used herein,
15 the term "biologically active portion of an HA protein" is intended to include a portion, *e.g.*, a domain/motif, of an HA protein that can participate in the maintenance of homeostasis in *C. glutamicum*, or that can perform a function involved in the adaptation of this microorganism to different environmental conditions, or has an activity as set forth in Table 1. To determine whether an HA protein or a biologically active portion
20 thereof can participate in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or has a *C. glutamicum* enzymatic or proteolytic activity, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

25 Additional nucleic acid fragments encoding biologically active portions of an HA protein can be prepared by isolating a portion of one of the amino acid sequences in of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the HA protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the
30 HA protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID

NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same HA protein as that encoded by the nucleotide sequences shown in of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid
5 sequence shown in the Sequence Listing (e.g., an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

10 It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the
15 invention which is greater than that of a sequence of the prior art (e.g., a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00471 (SEQ ID NO:293), a nucleotide sequence which is greater than and/or at least 41% identical to the
20 nucleotide sequence designated RXA00500 (SEQ ID NO:143), and a nucleotide sequence which is greater than and/or at least 35% identical to the nucleotide sequence designated RXA00502 (SEQ ID NO:147). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4
25 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%,
30 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%,

88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* HA nucleotide set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of HA proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the HA gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an HA protein, preferably a *C. glutamicum* HA protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the HA gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in HA that are the result of natural variation and that do not alter the functional activity of HA proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* HA DNA of the invention can be isolated based on their homology to the *C. glutamicum* HA nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are

hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* HA protein.

In addition to naturally-occurring variants of the HA sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded HA protein, without altering the functional ability of the HA protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the HA proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said HA protein, whereas an "essential" amino acid residue is required for HA protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having HA activity) may not be essential for activity and thus are likely to be amenable to alteration without altering HA activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding HA proteins that contain changes in amino acid residues that are not essential for HA activity. Such HA proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the HA activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of participating in the maintenance of homeostasis in *C. glutamicum*, or of performing a function involved in the adaptation of this microorganism to different environmental conditions, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid

molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences in, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an HA protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic

acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an HA protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an HA coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an HA activity described herein to identify mutants that retain HA activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding HA proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire HA coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an HA protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 3 (RXN00249) comprises nucleotides 1 to 957). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding HA. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding HA disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense

nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of HA mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of HA mRNA. For

5 example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of HA mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an

10 antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified

15 nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine,

20 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutosine, pseudouracil, queosine, 2-thiocytosine, 5-

25 methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from

30 the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an HA protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by
5 conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or
10 an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

15 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a
20 chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they
25 have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave HA mRNA transcripts to thereby inhibit translation of HA mRNA. A ribozyme having specificity for an HA-encoding nucleic acid can be designed based upon the nucleotide sequence of an HA DNA molecule disclosed herein (*i.e.*, SEQ ID
30 NO. 3 (RXN00249)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an HA-encoding mRNA. See, *e.g.*, Cech *et al.*

U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, HA mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

- 5 Alternatively, HA gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an HA nucleotide sequence (*e.g.*, an HA promoter and/or enhancers) to form triple helical structures that prevent transcription of an HA gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and
10 Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

- Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an HA protein (or a portion thereof). As
15 used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of
20 autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to
25 which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,
30 such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which are

5 operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory

10 sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and

15 those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *amy*, *SPO2*, λ -*P_R*- or λ *P_L*, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF α* , *AC*, *P-60*, *CYC1*,

20 *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or *ubiquitin*- or *phaseolin*-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors

25 of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, HA proteins, mutant forms of HA proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of HA proteins in prokaryotic or eukaryotic cells. For example, HA genes

30 can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel,

C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the HA protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin.

Recombinant HA protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89 ; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

- One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

- In another embodiment, the HA protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23,

pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. 5 (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the HA proteins of the invention can be expressed in insect cells 10 using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the HA proteins of the invention may be expressed in 15 unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for 20 plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in 25 mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both 30 prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed.*, Cold Spring

Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to HA mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene

expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) (1986).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an HA protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is

generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an HA protein or can be
5 introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an HA gene into which a deletion, addition or substitution
10 has been introduced to thereby alter, *e.g.*, functionally disrupt, the HA gene. Preferably, this HA gene is a *Corynebacterium glutamicum* HA gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous HA gene is functionally disrupted (*i.e.*, no longer
15 encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous HA gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous HA protein). In the homologous recombination vector, the altered portion
20 of the HA gene is flanked at its 5' and 3' ends by additional nucleic acid of the HA gene to allow for homologous recombination to occur between the exogenous HA gene carried by the vector and an endogenous HA gene in a microorganism. The additional flanking HA nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA
25 (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced HA gene has homologously recombined with the endogenous HA gene are selected, using art-known techniques.

30 In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an HA gene on a vector placing it under control of the lac

operon permits expression of the HA gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous HA gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced HA gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional HA protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an HA gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the HA gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described HA gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an HA protein. Accordingly, the invention further provides methods for producing HA proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an HA protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered HA protein) in a suitable medium until HA protein is produced. In another embodiment, the method further comprises isolating HA proteins from the medium or the host cell.

25 C. *Isolated HA Proteins*

Another aspect of the invention pertains to isolated HA proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized.

30 The language "substantially free of cellular material" includes preparations of HA protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language

"substantially free of cellular material" includes preparations of HA protein having less than about 30% (by dry weight) of non-HA protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-HA protein, still more preferably less than about 10% of non-HA protein, and most preferably less than about 5% non-HA protein. When the HA protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of HA protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of HA protein having less than about 30% (by dry weight) of chemical precursors or non-HA chemicals, more preferably less than about 20% chemical precursors or non-HA chemicals, still more preferably less than about 10% chemical precursors or non-HA chemicals, and most preferably less than about 5% chemical precursors or non-HA chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the HA protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* HA protein in a microorganism such as *C. glutamicum*.

An isolated HA protein or a portion thereof of the invention can participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. The portion of the protein is preferably a biologically active portion as described herein. In another

preferred embodiment, an HA protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the HA protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the HA protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred HA proteins of the present invention also preferably possess at least one of the HA activities described herein. For example, a preferred HA protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can participate in the maintenance of homeostasis in *C. glutamicum*, or can perform a function involved in the adaptation of this microorganism to different environmental conditions, or which has one or more of the activities set forth in Table 1.

In other embodiments, the HA protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the HA protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%,

69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which
5 has at least one of the HA activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains
10 to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an HA protein include peptides comprising amino acid sequences derived from the amino acid sequence of an HA protein, e.g., the amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing, the amino
15 acid sequence of a protein homologous to an HA protein, which include fewer amino acids than a full length HA protein or the full length protein which is homologous to an HA protein, and exhibit at least one activity of an HA protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with
20 at least one activity of an HA protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an HA protein include one or more selected domains/motifs or portions thereof having biological activity.

25 HA proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the HA protein is expressed in the host cell. The HA protein can then be isolated from the cells by an appropriate purification scheme using standard
30 protein purification techniques. Alternative to recombinant expression, an HA protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native HA protein can be isolated from cells (e.g., endothelial

cells), for example using an anti-HA antibody, which can be produced by standard techniques utilizing an HA protein or fragment thereof of this invention.

The invention also provides HA chimeric or fusion proteins. As used herein, an HA "chimeric protein" or "fusion protein" comprises an HA polypeptide operatively
5 linked to a non-HA polypeptide. An "HA polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an HA protein, whereas a "non-HA polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the HA protein, *e.g.*, a protein which is different from the HA protein and which is derived from the same or a different organism. Within the
10 fusion protein, the term "operatively linked" is intended to indicate that the HA polypeptide and the non-HA polypeptide are fused in-frame to each other. The non-HA polypeptide can be fused to the N-terminus or C-terminus of the HA polypeptide. For example, in one embodiment the fusion protein is a GST-HA fusion protein in which the HA sequences are fused to the C-terminus of the GST sequences. Such fusion proteins
15 can facilitate the purification of recombinant HA proteins. In another embodiment, the fusion protein is an HA protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an HA protein can be increased through use of a heterologous signal sequence.

Preferably, an HA chimeric or fusion protein of the invention is produced by
20 standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid
25 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric
30 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An HA-

encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the HA protein.

Homologues of the HA protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the HA protein. As used herein, the term "homologue" refers to a variant form of the HA protein which acts as an agonist or antagonist of the activity of the HA protein. An agonist of the HA protein can retain substantially the same, or a subset, of the biological activities of the HA protein. An antagonist of the HA protein can inhibit one or more of the activities of the naturally occurring form of the HA protein, by, for example, competitively binding to a downstream or upstream member of a biochemical cascade which includes the HA protein, by binding to a target molecule with which the HA protein interacts, such that no functional interaction is possible, or by binding directly to the HA protein and inhibiting its normal activity.

In an alternative embodiment, homologues of the HA protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the HA protein for HA protein agonist or antagonist activity. In one embodiment, a variegated library of HA variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of HA variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential HA sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of HA sequences therein. There are a variety of methods which can be used to produce libraries of potential HA homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential HA sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the HA protein coding can be used to generate a variegated population of HA fragments for screening and subsequent

selection of homologues of an HA protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an HA coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to
5 form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the HA protein.

10 Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of HA homologues. The most widely used techniques, which are amenable to high through-put
15 analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the
20 frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify HA homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated HA library, using methods well known in the art.

25

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of
30 genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of HA protein regions required for function; modulation of an HA protein activity; modulation of the

metabolism of one or more inorganic compounds; modulation of the modification or degradation of one or more aromatic or aliphatic compounds; modulation of cell wall synthesis or rearrangements; modulation of enzyme activity or proteolysis; and modulation of cellular production of a desired compound, such as a fine chemical.

- 5 The HA nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the
- 10 extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae*
- 15 is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in
- 20 these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.
- 25 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of
- 30 *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum*

are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The HA nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The processes involved in adaptation and the maintenance of homeostasis in which the molecules of the invention participate are utilized by a wide variety of species; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the HA nucleic acid molecules of the invention may result in the production of HA proteins having functional differences from the wild-type HA proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an HA protein, either by interacting with the protein itself or a substrate or binding partner of the HA protein, or by modulating the transcription or translation of an HA nucleic acid molecule of the invention. In such methods, a microorganism
5 expressing one or more HA proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the HA protein is assessed.

The modulation of activity or number of HA proteins involved in cell wall biosynthesis or rearrangements may impact the production, yield, and/or efficiency of
10 production of one or more fine chemicals from *C. glutamicum* cells. For example, by altering the activity of these proteins, it may be possible to modulate the structure or thickness of the cell wall. The cell wall serves in large measure as a protective device against osmotic lysis and external sources of injury; by modifying the cell wall it may be possible to increase the ability of *C. glutamicum* to withstand the mechanical and shear
15 force stresses encountered by this microorganism during large-scale fermentor culture. Further, each *C. glutamicum* cell is surrounded by a thick cell wall, and thus, a significant portion of the biomass present in large scale culture consists of cell wall. By increasing the rate at which the cell wall is synthesized or by activating cell wall synthesis (through genetic engineering of the HA cell wall proteins of the invention) it
20 may be possible to improve the growth rate of the microorganism. Similarly, by decreasing the activity or number of proteins involved in the degradation of cell wall or by decreasing the repression of cell wall biosynthesis, an overall increase in cell wall production may be achieved. An increase in the number of viable *C. glutamicum* cells (as may be accomplished by any of the foregoing described protein alterations) should
25 result in increased numbers of cells producing the desired fine chemical in large-scale fermentor culture, which should permit increased yields or efficiency of production of these compounds from the culture.

The modulation of activity or number of *C. glutamicum* HA proteins that participate in the modification or degradation of aromatic or aliphatic compounds may
30 also have direct or indirect impacts on the production of one or more fine chemicals from these cells. Certain aromatic or aliphatic modification or degradation products are desirable fine chemicals (e.g., organic acids or modified aromatic and aliphatic

compounds); thus, by modifying the enzymes which perform these modifications (e.g., hydroxylation, methylation, or isomerization) or degradation reactions, it may be possible to increase the yields of these desired compounds. Similarly, by decreasing the activity or number of proteins involved in pathways which further degrade the modified
5 or breakdown products of the aforementioned reactions it may be possible to improve the yields of these fine chemicals from *C. glutamicum* cells in culture.

These aromatic and aliphatic modification and degradative enzymes are themselves fine chemicals. In purified form, these enzymes may be used to degrade aromatic and aliphatic compounds (e.g., toxic chemicals such as petroleum products),
10 either for the bioremediation of polluted sites, for the engineered decomposition of wastes, or for the large-scale and economically feasible production of desired modified aromatic or aliphatic compounds or their breakdown products, some of which may be conveniently used as carbon or energy sources for other fine chemical-producing compounds in culture (see, e.g., Faber, K. (1995) Biotransformations in Organic
15 Chemistry, Springer: Berlin and references therein; and Roberts, S.M., ed. (1992-1996) Preparative Biotransformations, Wiley: Chichester, and references therein). By genetically altering these proteins such that their regulation by other cellular mechanisms is lessened or abolished, it may be possible to increase the overall number or activity of these proteins, thereby improving not only the yield of these fine chemicals
20 but also the activity of these harvested proteins.

The modification of these aromatic and aliphatic modifying and degradation enzymes may also have an indirect effect on the production of one or more fine chemical. Many aromatic and aliphatic compounds (such as those that may be encountered as impurities in culture media or as waste products from cellular
25 metabolism) are toxic to cells; by modifying and/or degrading these compounds such that they may be readily removed or destroyed, cellular viability should be increased. Further, these enzymes may modify or degrade these compounds in such a manner that the resulting products may enter the normal carbon metabolism pathways of the cell, thus rendering the cell able to use these compounds as alternate carbon or energy
30 sources. In large-scale culture situations, when there may be limiting amounts of optimal carbon sources, these enzymes provide a method by which cells may continue to grow and divide using aromatic or aliphatic compounds as nutrients. In either case, the

resulting increase in the number of *C. glutamicum* cells in the culture producing the desired fine chemical should in turn result in increased yields or efficiency of production of the fine chemical(s).

Modifications in activity or number of HA proteins involved in the metabolism of inorganic compounds may also directly or indirectly affect the production of one or more fine chemicals from *C. glutamicum* or related bacterial cultures. For example, many desirable fine chemicals, such as nucleic acids, amino acids, cofactors and vitamins (*e.g.*, thiamine, biotin, and lipoic acid) cannot be synthesized without inorganic molecules such as phosphorous, nitrate, sulfate, and iron. The inorganic metabolism proteins of the invention permit the cell to obtain these molecules from a variety of inorganic compounds and to divert them into various fine chemical biosynthetic pathways. Therefore, by increasing the activity or number of enzymes involved in the metabolism of these inorganic compounds, it may be possible to increase the supply of these possibly limiting inorganic molecules, thereby directly increasing the production or efficiency of production of various fine chemicals from *C. glutamicum* cells containing such altered proteins. Modification of the activity or number of inorganic metabolism enzymes of the invention may also render *C. glutamicum* able to better utilize limited inorganic compound supplies, or to utilize nonoptimal inorganic compounds to synthesize amino acids, vitamins, cofactors, or nucleic acids, all of which are necessary for continued growth and replication of the cell. By improving the viability of these cells in large-scale culture, the number of *C. glutamicum* cells producing one or more fine chemicals in the culture may also be increased, in turn increasing the yields or efficiency of production of one or more fine chemicals.

C. glutamicum enzymes for general processes are themselves desirable fine chemicals. The specific properties of enzymes (*i.e.*, regio- and stereospecificity, among others) make them useful catalysts for chemical reactions *in vitro*. Either whole *C. glutamicum* cells may be incubated with an appropriate substrate such that the desired product is produced by enzymes in the cell, or the desired enzymes may be overproduced and purified from *C. glutamicum* cultures (or those of a related bacterium) and subsequently utilized in *in vitro* reactions in an industrial setting (either in solution or immobilized on a suitable immobile phase). In either situation, the enzyme can either be a natural *C. glutamicum* protein, or it may be mutagenized to have an altered activity;

typical industrial uses for such enzymes include as catalysts in the chemical industry (e.g., for synthetic organic chemistry) as food additives, as feed components, for fruit processing, for leather preparation, in detergents, in analysis and medicine, and in the textile industry (see, e.g., Yamada, H. (1993) "Microbial reactions for the production of useful organic compounds," *Chimica* 47: 5-10; Roberts, S.M. (1998) Preparative biotransformations: the employment of enzymes and whole-cells in synthetic chemistry," *J. Chem. Soc. Perkin Trans. 1*: 157-169; Zaks, A. and Dodds, D.R. (1997) "Application of biocatalysis and biotransformations to the synthesis of pharmaceuticals," *DDT* 2: 513-531; Roberts, S.M. and Williamson, N.M. (1997) "The use of enzymes for the preparation of biologically active natural products and analogues in optically active form," *Curr. Organ. Chemistry* 1: 1-20; Faber, K. (1995) Biotransformations in Organic Chemistry, Springer: Berlin; Roberts, S.M., ed. (1992-96) Preparative Biotransformations, Wiley: Chichester; Cheetham, P.S.J. (1995) "The applications of enzymes in industry" in : Handbook of Enzyme Biotechnology, 3rd ed., Wiseman, A., ed., Ellis: Horwood, p. 419-552; and Ullmann's Encyclopedia of Industrial Chemistry (1987), vol. A9, Enzymes, p. 390-457). Thus, by increasing the activity or number of these enzymes, it may be possible to also increase the ability of the cell to convert supplied substrates to desired products, or to overproduce these enzymes for increased yields in large-scale culture. Further, by mutagenizing these proteins it may be possible to remove feedback inhibition or other repressive cellular regulatory controls such that greater numbers of these enzymes may be produced and activated by the cell, thereby leading to greater yields, production, or efficiency of production of these fine chemical proteins from large-scale cultures. Further, manipulation of these enzymes may alter the activity of one or more *C. glutamicum* metabolic pathways, such as those for the biosynthesis or secretion of one or more fine chemicals.

Mutagenesis of the proteolytic enzymes of the invention such that they are altered in activity or number may also directly or indirectly affect the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, by increasing the activity or number of these proteins, it may be possible to increase the ability of the bacterium to survive in large-scale culture, due to an increased ability of the cell to rapidly degrade proteins misfolded in response to the high temperatures, nonoptimal pH, and other stresses encountered during fermentor culture.

Increased numbers of cells in these cultures may result in increased yields or efficiency of production of one or more desired fine chemicals, due to the relatively larger number of cells producing these compounds in the culture. Also, *C. glutamicum* cells possess multiple cell-surface proteases which serve to break down external nutrients into
5 molecules which may be more readily incorporated by the cells as carbon/energy sources or nutrients of other kinds. An increase in activity or number of these enzymes may improve this turnover and increase the levels of available nutrients, thereby improving cell growth or production. Thus, modifications of the proteases of the invention may indirectly impact *C. glutamicum* fine chemical production.

10 A more direct impact on fine chemical production in response to the modification of one or more of the proteases of the invention may occur when these proteases are involved in the production or degradation of a desired fine chemical. By decreasing the activity of a protease which degrades a fine chemical or a protein involved in the synthesis of a fine chemical it may be possible to increase the levels of
15 that fine chemical (due to the decreased degradation or increased synthesis of the compound). Similarly, by increasing the activity of a protease which degrades a compound to result in a fine chemical or a protein involved in the degradation of a fine chemical, a similar result should be achieved: increased levels of the desired fine chemical from *C. glutamicum* cells containing these engineered proteins.

20 The aforementioned mutagenesis strategies for HA proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related
25 strains of bacteria expressing mutated HA nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally
30 occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

Table 1: Genes in the Application

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXA02548	GR00727	3	293	SULFATE ADENYLATE TRANSFERASE SUBUNIT 2 (EC 2.7.7.4)
3	4	RXN00249	VV0057	36825	35869	ADENYLYLSULFATE KINASE (EC 2.7.1.25)
5	6	F RXA00249	GR00037	8837	7884	ADENYLYLSULFATE KINASE (EC 2.7.1.25)
7	8	RXA01073	GR00300	1274	2104	NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
9	10	RXN02913	VV0020	8998	8513	UREASE BETA SUBUNIT (EC 3.5.1.5)
11	12	F RXA02264	GR00655	123	4	UREASE ALPHA SUBUNIT (EC 3.5.1.5)
13	14	RXN02274	VV0020	8509	6800	UREASE ALPHA SUBUNIT (EC 3.5.1.5)
15	16	F RXA02274	GR00656	3	1604	UREASE ALPHA SUBUNIT (EC 3.5.1.5)
17	18	RXA02265	GR00655	452	153	UREASE GAMMA SUBUNIT (EC 3.5.1.5)
19	20	RXA02278	GR00656	3420	4268	UREASE OPERON URED PROTEIN
21	22	RXA02275	GR00656	1632	2102	UREASE ACCESSORY PROTEIN UREE
23	24	RXA02276	GR00656	2105	2782	UREASE ACCESSORY PROTEIN UREF
25	26	RXA02277	GR00656	2802	3416	UREASE ACCESSORY PROTEIN UREG
27	28	RXA02603	GR00742	7742	8737	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
29	30	RXA01385	GR00406	5320	3440	PHENOL 2 MONOOXYGENASE (EC 1.14.13.7)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
31	32	RXN00675	VV0005	33258	34049	METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
33	34	F RXA00675	GR00178	2	484	METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
35	36	RXA01609	GR00449	2740	3612	METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
37	38	RXA01358	GR00393	5337	6857	ATP-DEPENDENT PROTEASE LA (EC 3.4.21.53)
39	40	RXA01458	GR00420	3225	2176	ATP-DEPENDENT PROTEASE LA (EC 3.4.21.53)
41	42	RXA01654	GR00459	986	1981	ATP-DEPENDENT PROTEASE LA (EC 3.4.21.53)
43	44	RXN01868	VV0127	9980	11905	(AL022121) putative alkaline serine protease [Mycobacterium tuberculosis]
45	46	F RXA01868	GR00534	1640	30	ZINC METALLOPROTEASE (EC 3.4.24.-)
47	48	F RXA01869	GR00534	1954	1652	ZINC METALLOPROTEASE (EC 3.4.24.-)
49	50	RXN03028	VV0008	41156	43930	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
51	52	F RXA02470	GR00715	2216	3196	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA

Urease

Proteolysis

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
53	54	F RXA02471	GR00715	3159	4991	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
55	56	RXA02630	GR00748	2654	1332	(AL021999) putative serine protease [Mycobacterium tuberculosis]
57	58	RXA02834	GR00823	3	497	ATPases with chaperone activity, ATP-dependent protease subunit
59	60	RXA00112	GR00016	3687	2497	PROBABLE PERIPLASMIC SERINE PROTEASE DO-LIKE PRECURSOR
61	62	RXA00566	GR00152	742	137	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (EC 3.4.21.92)
63	64	RXA00567	GR00152	1388	798	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (EC 3.4.21.92)
65	66	RXN03094	VV0057	1794	43	CLPB PROTEIN
67	68	F RXA01668	GR00464	2205	3920	CLPB PROTEIN
69	70	RXN01120	VV0182	5678	4401	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX
71	72	F RXA01120	GR00310	2349	1072	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX
73	74	RXA00744	GR00202	10722	9781	Periplasmic serine proteases
75	76	RXA00844	GR00228	3620	4453	Hypothetical Secretory Serine Protease (EC 3.4.21.-)
77	78	RXA02317	GR00324	862	5	ATP-dependent Zn proteases
79	80	RXA02644	GR00685	9664	9053	PEPTIDASE E (EC 3.4.-.-)
81	82	RXA01151	GR00751	767	117	XAA-PRO DIPEPTIDASE (EC 3.4.13.9)
83	84	RXN02820	VV0131	4799	6109	GAMMA-GLUTAMYL TRANSPEPTIDASE (EC 2.3.2.2)
85	86	F RXA02820	GR00801	1	507	GAMMA-GLUTAMYL TRANSPEPTIDASE (EC 2.3.2.2)
87	88	F RXA02000	GR00589	3430	3933	GAMMA-GLUTAMYL TRANSPEPTIDASE (EC 2.3.2.2)
89	90	RXN03178	VV0334	921	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
91	92	F RXA02859	GR10005	846	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
93	94	RXA00137	GR00022	738	1826	XAA-PRO AMINOPEPTIDASE (EC 3.4.11.9)
95	96	RXN00499	VV0086	8158	9438	PROLINE IMINOPEPTIDASE (EC 3.4.11.5)
97	98	F RXA00499	GR00125	3	959	PROLINE IMINOPEPTIDASE
99	100	RXN00877	VV0099	2221	3885	PEPTIDYL-DIPEPTIDASE DCP (EC 3.4.15.5)
101	102	F RXA00877	GR00242	3	1067	PEPTIDYL-DIPEPTIDASE DCP (EC 3.4.15.5)
103	104	RXN01014	VV0209	13328	10728	AMINOPEPTIDASE N (EC 3.4.11.2)
105	106	F RXA01014	GR00289	3	1580	AMINOPEPTIDASE N (EC 3.4.11.2)
107	108	F RXA01018	GR00290	2289	3152	AMINOPEPTIDASE N (EC 3.4.11.2)
109	110	RXA01147	GR00323	1353	94	VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.1)
111	112	RXN01161	GR00329	1253	117	XAA-PRO AMINOPEPTIDASE (EC 3.4.11.9)
113	114	RXN01181	VV0085	1	957	AMINOPEPTIDASE AI (EC 3.4.11.1)
115	116	F RXA01181	GR00337	1	957	AMINOPEPTIDASE
117	118	RXN01277	VV0009	32155	34158	PROLYL ENDOPEPTIDASE (EC 3.4.21.26)
119	120	F RXA01277	GR00368	1738	50	PROLYL ENDOPEPTIDASE (EC 3.4.21.26)
121	122	RXA01914	GR00548	125	550	AMINOPEPTIDASE
123	124	RXA02048	GR00624	207	1580	AMINOPEPTIDASE N (EC 3.4.11.2)
125	126	RXN00621	VV0135	5853	5071	PROTEASE II (EC 3.4.21.83)
127	128	F RXA00621	GR00163	4075	4857	PTRB periplasmic protease
129	130	RXN00622	VV0135	5150	3735	PROTEASE II (EC 3.4.21.83)
131	132	F RXA00622	GR00163	4778	6193	PTRB periplasmic protease
133	134	RXN00982	VV0149	7596	6091	(L42758) proteinase [Streptomyces lividans]
135	136	F RXA00977	GR00275	1647	2660	(L42758) proteinase [Streptomyces lividans]
137	138	F RXA00982	GR00276	5194	4949	(L42758) proteinase [Streptomyces lividans]
139	140	RXA00152	GR00023	7175	5880	HFLC PROTEIN (EC 3.4.-.-)
141	142	RXA02558	GR00731	4939	3965	HFLC PROTEIN (EC 3.4.-.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
143	144	RXA00500	GR00125	969	1643	O-SIALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57)
145	146	RXA00501	GR00125	1643	2149	O-SIALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57)
147	148	RXA00502	GR00125	2156	3187	O-SIALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
149	150	RXN02589	VV0098	16346	17110	Hypothetical Methyltransferase (EC 2.1.1.-)
151	152	F RXA02589	GR00741	13804	13040	Predicted S-adenosylmethionine-dependent methyltransferase
153	154	RXA00226	GR00032	26836	26012	SAM-dependent methyltransferases
155	156	RXN01885	VV0184	2004	2804	Hypothetical Methyltransferase (EC 2.1.1.-)
157	158	F RXA01885	GR00539	1589	2389	SAM-dependent methyltransferases
159	160	RXA02592	GR00741	18477	17707	SAM-dependent methyltransferases
161	162	RXN01795	VV0093	722	1318	MODIFICATION METHYLASE (EC 2.1.1.73)
163	164	F RXA01795	GR00507	706	1140	MODIFICATION METHYLASE (EC 2.1.1.73)
165	166	RXA01214	GR00351	1640	3130	LACCASE 1 PRECURSOR (EC 1.10.3.2)
167	168	RXA01250	GR00364	592	5	LACCASE 1 PRECURSOR (EC 1.10.3.2)
169	170	RXA02477	GR00715	10581	11201	CARBONIC ANHYDRASE (EC 4.2.1.1)
171	172	RXN00833	GR00225	374	6	THIOL PEROXIDASE (EC 1.11.1.-)
173	174	F RXA00833	GR00225	374	6	THIOL PEROXIDASE (EC 1.11.1.-)
175	176	RXA01224	GR00354	4186	5208	2-NITROPROPANE DIOXYGENASE (EC 1.13.11.32)
177	178	RXA01182	GR00337	1363	971	Hypothetical Oxidoreductase
179	180	RXA02531	GR00726	1226	1936	Hypothetical Oxidoreductase
181	182	RXN00689	VV0005	22416	20926	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (EC 1.2.1.8)
183	184	F RXA00689	GR00180	1401	775	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (EC 1.2.1.8)
185	186	RXN03128	VV0120	3	857	MORPHINE 6-DEHYDROGENASE (EC 1.1.1.218)
187	188	F RXA02192	GR00643	2	523	MORPHINE 6-DEHYDROGENASE (EC 1.1.1.218)
189	190	RXA02351	GR00679	132	1070	NITRILOTRIACETATE MONOOXYGENASE COMPONENT A (EC 1.14.13.-)
191	192	RXN00905	VV0238	8075	8875	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
193	194	F RXA00905	GR00247	2	694	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
195	196	RXA00906	GR00247	630	1133	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
197	198	RXA00907	GR00247	1143	1265	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
199	200	RXA02101	GR00631	3104	1842	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
201	202	RXN02565	VV0154	14299	13034	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
203	204	F RXA02565	GR00733	1	342	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
205	206	F RXA02567	GR00734	3	740	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
207	208	RXN03077	VV0043	1729	2913	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
209	210	F RXA02855	GR10002	1693	2877	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
211	212	RXA00026	GR00003	3657	5042	Hypothetical Amidohydrolase (EC 3.5.1.-)
213	214	RXA01971	GR00569	963	133	Hypothetical Metal-Dependent Hydrolase
215	216	RXA01802	GR00509	3461	4291	Predicted hydrolases (HAD superfamily)
217	218	RXN00866	VV0258	3557	4522	Predicted Zn-dependent hydrolases
219	220	F RXA00866	GR00236	3555	4499	Predicted Zn-dependent hydrolases
221	222	RXA02410	GR00703	792	127	Predicted Zn-dependent hydrolases

Enzymes in general

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
223	224	RXA00961	GR00267	2	433	SALICYLATE HYDROXYLASE (EC 1.14.13.1)
225	226	RXA00111	GR00016	930	1922	SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3)
227	228	RXA01932	GR00555	6479	5583	ACETYL-HYDROLASE (EC 3.1.1.-)
229	230	RXA02574	GR00739	833	1840	PUTATIVE SECRETED HYDROLASE
231	232	RXN00983	VV0231	1796	321	SIALIDASE PRECURSOR (EC 3.2.1.18)
233	234	F RXA00983	GR00278	1200	4	SIALIDASE PRECURSOR (EC 3.2.1.18)
235	236	RXA00984	GR00278	1716	1300	SIALIDASE PRECURSOR (EC 3.2.1.18)
237	238	RXN02513	VV0193	737	6	SIALIDASE PRECURSOR (EC 3.2.1.18)
239	240	F RXA02513	GR00722	93	824	SIALIDASE PRECURSOR (EC 3.2.1.18)
241	242	RXA00903	GR00246	637	5	Putative epimerase
243	244	RXA01224	GR00354	4186	5208	2-NITROPROPANE DIOXYGENASE (EC 1.13.11.32)
245	246	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
247	248	RXN02478	VV0119	7564	6350	SIALIDASE PRECURSOR (EC 3.2.1.18)
249	250	RXN00343	VV0125	1118	6	3-OXOSTEROID 1-DEHYDROGENASE (EC 1.3.99.4)
251	252	RXN01555	VV0135	29820	28861	3-OXOSTEROID 1-DEHYDROGENASE (EC 1.3.99.4)
253	254	RXN01166	VV0117	18142	16838	EXTRACELLULAR LIPASE PRECURSOR (EC 3.1.1.3)
255	256	RXN02001	VV0326	630	1787	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
257	258	RXN03145	VV0142	7561	7115	4-OXALOCOTONATE TAUTOMERASE (EC 5.3.2.-)
259	260	RXN01466	VV0019	7050	6091	ARYLESTERASE (EC 3.1.1.2)
261	262	RXN01145	VV0077	7538	6525	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
263	264	RXN03088	VV0052	3431	3817	Hypothetical Methyltransferase (EC 2.1.1.-)
265	266	RXN02952	VV0320	1032	1547	PUTATIVE REDUCTASE
267	268	RXN00513	VV0092	1573	653	CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE (EC 2.7.8.23)
269	270	RXN01152	VV0136	1740	907	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77)
271	272	RXN00787	VV0321	3736	5637	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
273	274	RXN01302	VV0148	2837	2385	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
275	276	F RXA01302	GR00376	370	5	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
277	278	RXN01308	VV0148	2406	4	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
279	280	F RXA01307	GR00377	686	6	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
281	282	F RXA01308	GR00378	1211	6	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
283	284	RXN01309	VV0158	1	801	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
285	286	F RXA01309	GR00379	719	51	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
287	288	RXA02017	GR00610	1731	1048	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)
289	290	RXA02018	GR00610	2788	1739	NITRATE REDUCTASE BETA CHAIN (EC 1.7.99.4)
291	292	RXA02016	GR00610	1036	260	NITRATE REDUCTASE GAMMA CHAIN (EC 1.7.99.4)
293	294	RXA00471	GR00119	2997	3886	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARL
295	296	RXA00133	GR00021	201	1013	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
297	298	RXA00650	GR00169	4017	3382	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP

N-metabolism

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
299	300	RXA01189	GR00339	2545	1937	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
301	302	RXA01607	GR00449	123	752	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
303	304	RXN00470	VV0086	27401	28669	NITRATE/NITRITE SENSOR PROTEIN NARX (EC 2.7.3.-)
305	306	F RXA00470	GR00119	1752	2951	NITRATE/NITRITE SENSOR PROTEIN NARX (EC 2.7.3.-)
307	308	RXA00756	GR00203	2932	1937	N UTILIZATION SUBSTANCE PROTEIN A
309	310	RXA00139	GR00022	2514	3224	N UTILIZATION SUBSTANCE PROTEIN B
311	312	RXA01303	GR00376	1724	390	NITRITE EXTRUSION PROTEIN
313	314	RXA01412	GR00412	620	417	NITROGEN FIXATION PROTEIN FIXI (PROBABLE E1-E2 TYPE CATION ATPASE) (EC 3.6.1.-)
315	316	RXA00773	GR00205	3208	4350	NITROGEN REGULATION PROTEIN NIFR3
317	318	RXA02746	GR00764	1	267	NITROGEN REGULATORY PROTEIN P-II
319	320	RXA02745	GR00763	15350	14472	MODULATION ATP-BINDING PROTEIN I
321	322	RXN00820	VV0054	19455	19817	MODULATION PROTEIN N
323	324	F RXA00820	GR00221	1007	1369	MODULATION PROTEIN N
325	326	RXA01059	GR00296	8782	9390	OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE (EC 1.-.-.-)
327	328	RXN01386	VV0008	39246	38317	NITRILASE REGULATOR
329	330	RXN00073	VV0154	2369	687	FERRDOXIN--NITRITE REDUCTASE (EC 1.7.7.1)
331	332	RXN03131	VV0127	276	4	RHIZOPINE CATABOLISM PROTEIN MOCC
333	334	RXS00153	VV0167	4195	4620	MODULATION PROTEIN

Urease

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code
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Phosphate and Phosphonate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
335	336	RXN01716	VV0319	3259	2774	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
337	338	RXN02972	VV0319	2763	2353	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
339	340	RXN00663	VV0142	10120	11493	PHOH PROTEIN HOMOLOG
341	342	RXN00778	VV0103	18126	19250	PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
343	344	RXN00250	VV0189	286	1032	DEDA PROTEIN - ALKALINE PHOSPHATASE LIKE PROTEIN

Sulfate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
345	346	RXA00072	GR00012	446	6	PHOSPHADENOSINE PHOSPHOSULFATE REDUCTASE (EC 1.8.99.4)
347	348	RXA00793	GR00211	1469	2644	SULFATE STARVATION-INDUCED PROTEIN 6
349	350	RXA01192	GR00342	161	733	SULFATE STARVATION-INDUCED PROTEIN 6

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
351	352	RXA00715	GR00188	2120	2914	THIOSULFATE SULFURTRANSFERASE (EC 2.8.1.1)
353	354	RXA01684	GR00463	1306	485	THIOSULFATE SULFURTRANSFERASE (EC 2.8.1.1)
355	356	RXN02334	VV0141	7939	7217	THIOSULFATE SULFURTRANSFERASE (EC 2.8.1.1)
357	358	F RXA02334	GR00672	2	355	THIOSULFATE SULFURTRANSFERASE (EC 2.8.1.1)

Fe-Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
359	360	RXN01499	VV0008	7034	3213	ENTEROBACTIN SYNTHETASE COMPONENT F
361	362	RXN01997	VV0084	33308	33793	FERRITIN

Mg Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
363	364	RXA01848	GR00524	1532	789	MAGNESIUM-CHELATASE SUBUNIT CHLI
365	366	RXN01849	VV0139	16415	17515	MAGNESIUM-CHELATASE SUBUNIT CHLI
367	368	F RXA01849	GR00524	2004	1555	MAGNESIUM-CHELATASE SUBUNIT CHLI
369	370	F RXA01691	GR00474	570	4	MAGNESIUM-CHELATASE SUBUNIT CHLI
371	372	RXN00665	VV0252	135	635	MG2+/CITRATE COMPLEX SECONDARY TRANSPORTER

Modification and degradation of aromatic compounds

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
373	374	RXN03026	VV0007	28635	28901	3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)
375	376	RXN02908	VV0025	8507	8247	O-SUCCINYLBENZOIC ACID-COA LIGASE (EC 6.2.1.26)
377	378	RXN03000	VV0235	570	4	SALICYLATE HYDROXYLASE (EC 1.14.13.1)
379	380	RXN03036	VV0014	671	6	PROTocatechuate 3,4-dioxygenase beta chain (EC 1.13.11.3)
381	382	RXN02974	VV0229	12631	12437	4-NITROPHENYLPHOSPHATASE (EC 3.1.3.41)
383	384	RXN00393	VV0025	7241	6348	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
385	386	RXN00948	VV0107	4266	5384	12-oxophylodienate reductase (EC 1.3.1.42)
387	388	RXN01923	VV0020	3384	4133	2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE HYDROLASE (EC 3.7.1.-)
389	390	RXN00398	VV0025	14633	13884	2-PYRONE-4,6-DICARBOXYLATE LACTONASE (EC 3.1.1.57)
391	392	RXN02813	VV0128	13120	14118	3-CARBOXY-CIS,CIS-MUCONATE CYCLOISOMERASE HOMOLOG (EC 5.5.1.2)
393	394	RXN00136	VV0134	13373	14467	3-DEHYDROQUINATE SYNTHASE (EC 4.6.1.3)
395	396	RXN02508	VV0007	26733	28586	3-DEHYDROSHIKIMATE DEHYDRATASE (EC 4.2.1.-)
397	398	RXN02839	VV0362	3	449	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
399	400	RXN00639	VV0128	7858	8712	CATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1)
401	402	RXN02530	VV0057	5469	6125	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8)
403	404	RXN00434	VV0112	12078	11212	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
405	406	RXN01619	VV0050	24649	23675	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
407	408	RXN01842	VV0234	1615	2532	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
409	410	RXN00641	VV0128	7440	5950	TOLUATE 1,2-DIOXYGENASE ALPHA SUBUNIT (EC 1.14.12.-)
411	412	RXN01993	VV0182	16	1143	VANILLATE DEMETHYLASE (EC 1.14.-)
413	414	RXN00658	VV0083	15705	16397	PHENOL 2-MONOXYGENASE (EC 1.14.13.7)
415	416	RXN00178	VV0174	14670	15554	hydroxyquinol 1,2-dioxygenase (EC 1.13.11.37)
417	418	RXN01461	VV0128	12414	13025	PROTocatechuate 3,4-dioxygenase ALPHA CHAIN (EC 1.13.11.3)
419	420	RXN01653	VV0321	12867	11407	DIBENZOTHIOPHENE DESULFURIZATION ENZYME A
421	422	RXN02053	VV0009	39448	40026	DRGA PROTEIN
423	424	RXN00177	VV0174	13589	14656	MALEYLACETATE REDUCTASE (EC 1.3.1.32)
425	426	RXC00963	VV0249	1816	2652	PROTEIN involved in degradation of aromatic compounds

Modification and degradation of aliphatic compounds

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
427	428	RXN00299	VV0176	43379	42402	ALKANAL MONOOXYGENASE ALPHA CHAIN (EC 1.14.14.3)
429	430	F RXA00299	GR00048	7376	6633	ALKANAL MONOOXYGENASE ALPHA CHAIN (EC 1.14.14.3)
431	432	RXA00332	GR00057	16086	15385	ALKANAL MONOOXYGENASE ALPHA CHAIN (EC 1.14.14.3)
433	434	RXA01838	GR00519	2	820	ALKANAL MONOOXYGENASE ALPHA CHAIN (EC 1.14.14.3)
435	436	RXA02643	GR00750	1603	560	ALKANAL MONOOXYGENASE ALPHA CHAIN (EC 1.14.14.3)
437	438	RXA01933	GR00555	6590	7192	2-HALOALKANOIC ACID DEHALOGENASE I (EC 3.8.1.2)
439	440	RXA02351	GR00679	132	1070	NITRILOTRIACETATE MONOOXYGENASE COMPONENT A (EC 1.14.13.-)

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminic acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	gluB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)			
	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651			
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 198723292-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 198723292-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)			Glucose-6-phosphate dehydrogenase		Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
E13655					
L01508	IlvA		Threonine dehydratase		Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15		3-deoxy-D-arabinoheptulosonate-7-phosphate synthase		Chen, C. et al. "The cloning and nucleotide sequence of <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC		Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomerase		Keilhauer, C. et al. "Isoleucine synthesis in <i>Corynebacterium glutamicum</i> : molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PisM		Phosphoenolpyruvate sugar phosphotransferase		Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the <i>Corynebacterium glutamicum</i> mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB		Malate synthase		Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126			Pyruvate kinase		Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA		Isocitrate lyase		
L35906	dxr		Diphtheria toxin repressor		Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dxrR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774			Prephenate dehydratase		Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA				Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE		Anthranilate synthase, 5' end		Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA		Tryptophan synthase, 3' end		Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

		Phosphoenolpyruvate carboxylase	
M25819			O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Koller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	accD; bmQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the bmQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock A TP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Ciancioffo, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pla-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-36 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4): 740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,'" <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)			
X90360	Promoter fragment F22		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37		Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	Ammonium transport system	amt	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	Glycine betaine transport system	betP	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649		orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	Lysine exporter protein; Lysine export regulator protein	lysE; lysG	Vrijic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Péter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicum proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site <i>Corynebacterium</i> 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

* A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRI	GECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx00026	1509	GB_RO:MMHC310M6	158405	AF109906	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.	Mus musculus	38,003	10-DEC-1998
		GB_HTG2:AC007029	119007	AC007029	Homo sapiens clone DJ0855F16, *** SEQUENCING IN PROGRESS	Homo sapiens	37,943	7-Apr-99
		GB_HTG2:AC007029	119007	AC007029	***, 1 unordered pieces.			
rx00072					Homo sapiens clone DJ0855F16, *** SEQUENCING IN PROGRESS	Homo sapiens	37,943	7-Apr-99
					***, 1 unordered pieces.			
rx00111	1116	GB_BA1:SAUSIGA	2748	M94370	Stigmatella aurantiaca sigma factor (sigA) gene, complete cds.	Stigmatella aurantiaca	40,435	16-Aug-94
		GB_BA1:SC5B8	28500	AL022374	Streptomyces coelicolor cosmid 5B8.	Streptomyces coelicolor	40,090	22-Apr-98
		GB_BA2:AE001767	9086	AE001767	Thermotoga maritima section 79 of 136 of the complete genome.	Thermotoga maritima	35,091	2-Jun-99
rx00112	1314	GB_EST35:AU075536	418	AU075536	AU075536 Rice shoot Oryza sativa cDNA clone S0028_2Z, mRNA sequence.	Oryza sativa	39,423	7-Jul-99
		GB_GSS9:AQ157585	647	AQ157585	nbxb0009B16r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0009B16r, genomic survey sequence.	Oryza sativa	40,867	12-Sep-98
		GB_GSS14:AQ510314	542	AQ510314	nbxb0095O05f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0095O05f, genomic survey sequence.	Oryza sativa	39,372	04-MAY-1999
rx00133	936	GB_BA1:SC2G5	38404	AL035478	Streptomyces coelicolor cosmid 2G5.	Streptomyces coelicolor	41,170	11-Jun-99
		GB_EST7:W64291	515	W64291	md98h12.1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:386087 5' similar to gb:L26528 Mus musculus Rab11b mRNA, complete cds (MOUSE); mRNA sequence.	Mus musculus	35,306	10-Jun-96
		GB_PR3:AC005624	39594	AC005624	Homo sapiens chromosome 19, cosmid R30017, complete sequence.	Homo sapiens	39,054	6-Sep-98
rx00137	1212	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase synthase (aroB) genes, complete cds, and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	99,867	04-MAY-1999
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	40,959	17-Jun-98
		GB_BA1:MT3DEHQ	3437	X59509	M.tuberculosis, genes for 3-dehydroquinase synthase and 3-dehydroquinase.	Mycobacterium tuberculosis	52,583	30-Jun-93
rx00139	834	GB_BA1:BLELONP	738	X99289	B.lactofermentum gene encoding elongation factor P.	Corynebacterium glutamicum	100,000	1-Nov-97
		GB_PL1:SPAC24C9	38666	Z98601	S.pombe chromosome I cosmid c24C9.	Schizosaccharomyces pombe	35,230	24-Feb-99
		GB_HTG1:CEY102A5_1110000	Z99711	Z99711	Caenorhabditis elegans chromosome V clone Y102A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	37,775	Z99711

Table 4 (continued)

rx00152	1419	GB_BA1:MTCV277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	58,500	17-Jun-98
		GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	Mycobacterium tuberculosis	38,913	03-DEC-1996
		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	64,009	26-MAR-1998
rx00226	948	GB_PR3:AC005756	43299	AC005756	Homo sapiens chromosome 19, fosmid 39347, complete sequence.	Homo sapiens	36,209	02-OCT-1998
		GB_GSS5:AQ818463	413	AQ818463	HS_5250_A2_B08_SP6E RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=826 Col=16 Row=C, genomic survey sequence.	Homo sapiens	37,288	26-Aug-99
		GB_GSS5:AQ782337	832	AQ782337	HS_3184_B1_H12_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=23 Row=P, genomic survey sequence.	Homo sapiens	35,917	2-Aug-99
rx00249	980	GB_BA2:AF035608	3614	AF035608	Pseudomonas aeruginosa ATP sulfurylase small subunit (cysD) and ATP sulfurylase GTP-binding subunit/APS kinase (cysN) genes, complete cds.	Pseudomonas aeruginosa	50,205	1-Jun-98
		GB_BA1:AB017641	17101	AB017641	Micromonospora griseorubida gene for polyketide synthase, complete cds.	Micromonospora griseorubida	40,266	2-Apr-99
		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	38,429	26-MAR-1998
rx00299	1101	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein Ynbw (yhbw) gene, partial cds.	Corynebacterium glutamicum	100,000	4-Jun-98
		GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	41,143	20-Nov-98
		GB_BA2:AF181035	5922	AF181035	Rhodobacter sphaeroides glycogen utilization operon, complete sequence.	Rhodobacter sphaeroides	36,701	7-Sep-99
rx00332	825	GB_BA1:CGTHRC	3120	X56037	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).	Corynebacterium glutamicum	37,730	17-Jun-97
		GB_PAT:109078	3146	I09078	Sequence 4 from Patent WO 8809819.	Unknown.	38,700	02-DEC-1994
		GB_PR3:HSJ333B15	73666	AL109954	Human DNA sequence from clone 333B15 on chromosome 20, complete sequence.	Homo sapiens	37,203	23-Nov-99
rx00470	1392	GB_PL2:DCPCNAM	865	X62977	D. carota mRNA for proliferating cell nuclear antigen (PCNA).	Daucus carota	37,914	30-Sep-99

Table 4 (continued)

	GB_PL2:AC006267	101644	AC006267	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5 cM, Arabidopsis thaliana complete sequence.	36,158	27-Apr-99
rxa00471 813	GB_BA1:TT10SARNA	721	Y15063	Thermus thermophilus 10Sa RNA gene.	39,494	18-Aug-98
	GB_BA1:SERERYAA	11219	M63676	S. erythraea first ORF of eryA gene, complete cds.	38,781	26-Apr-93
	GB_PAT:AR049367	11219	AR049367	Sequence 1 from patent US 5824513.	38,781	29-Sep-99
	GB_BA1:SERERYAA	11219	M63676	S. erythraea first ORF of eryA gene, complete cds.	38,205	26-Apr-93
rxa00499 1404	GB_PR4:AC007206	42732	AC007206	Homo sapiens chromosome 19, cosmid R27370, complete sequence.	34,982	4-Apr-99
	GB_EST26:A1344735	462	A1344735	qp05a10.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917114 3' similar to gb:M15800 T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN (HUMAN); mRNA sequence.	42,675	2-Feb-99
rxa00500 798	GB_PR4:AC006479	161837	AC006479	Homo sapiens clone DJ1051J04, complete sequence.	38,462	11-Nov-99
	GB_PR4:AC006111	190825	AC006111	Homo sapiens chromosome 16 clone RPC1-11_461A8, complete sequence.	40,736	3-Jul-99
	GB_HTG2:AF128834	196589	AF128834	Homo sapiens chromosome 8 clone BAC 57G24 map 8p12, *** SEQUENCING IN PROGRESS *** in unordered pieces.	34,062	28-Feb-99
	GB_HTG2:AF128834	196589	AF128834	Homo sapiens chromosome 8 clone BAC 57G24 map 8p12, *** SEQUENCING IN PROGRESS *** in unordered pieces.	34,062	28-Feb-99
rxa00501 630	GB_BA1:D86429	5925	D86429	Saccharopolyspora rectivirgula gene for beta-galactosidase, complete cds.	53,871	09-DEC-1998
	GB_HTG1:HS1099D15	1301	AL035456	Homo sapiens chromosome 20 clone RP5-1099D15, *** SEQUENCING IN PROGRESS *** in unordered pieces.	33,546	23-Nov-99
	GB_HTG1:HS1099D15	1301	AL035456	Homo sapiens chromosome 20 clone RP5-1099D15, *** SEQUENCING IN PROGRESS *** in unordered pieces.	33,546	23-Nov-99
rxa00502 1155	GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	34,783	01-MAR-1994
	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	34,900	01-MAR-1994
	GB_HTG1:HS179115	210672	Z84464	Homo sapiens chromosome 13 clone 179115, *** SEQUENCING IN PROGRESS *** in unordered pieces.	32,898	22-Jan-97
	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	37,011	17-Jun-98
rxa00566 729	GB_BA2:AF071885	2188	AF071885	Streptomyces coelicolor ATP-dependent Clp protease proteolytic subunit 1 (clpP1) and ATP-dependent Clp protease proteolytic subunit 2 (clpP2) genes, complete cds; and ATP-dependent Clp protease ATP-binding subunit ClpX (clpX) gene, partial cds.	62,963	29-Jun-99
	GB_BA2:AF013216	15742	AF013216	Myxococcus xanthus Dog (dog), isocitrate lyase (icl), Mls (mls), Ufo (ufo), fumarate hydratase (fhy), and proteosome major subunit (clpP) genes, complete cds; and acyl-CoA oxidase (aco) gene, partial cds.	54,683	28-Jan-98

Table 4 (continued)

rx00567	714	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	42,090	17-Jun-98
		GB_BA1:CGBP116	962	Y12472	C.glutamicum DNA, attachment site bacteriophage Phi-16.	Corynebacterium glutamicum	40,000	05-MAR-1999
rx00621	906	GB_BA1:ECOCPLPA	1236	J05534	Escherichia coli ATP-dependent clip protease proteolytic component (clipP) gene, complete cds.	Escherichia coli	52,119	26-Apr-93
		GB_EST1:D36491	360	D36491	CELK033GYF Yujii Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk33g11 5', mRNA sequence.	Caenorhabditis elegans	40,390	8-Aug-94
		GB_IN2:CELC16A3	34968	U41534	Caenorhabditis elegans cosmid C16A3.	Caenorhabditis elegans	35,477	18-MAY-1999
		GB_HTG3:AC009311	160198	AC009311	Homo sapiens clone NH0311L03, *** SEQUENCING IN PROGRESS	Homo sapiens	38,636	13-Aug-99
				***, 3 unordered pieces.				
rx00622	1539	GB_BA1:AB004795	3039	AB004795	Pseudomonas sp. gene for dipeptidyl aminopeptidase, complete cds.	Pseudomonas sp.	54,721	5-Feb-99
		GB_BA1:MBOP11	2392	D38405	Moraxella lacunata gene for protease II, complete cds.	Moraxella lacunata	50,167	8-Feb-99
		GB_IN2:AF078916	2960	AF078916	Trypanosoma brucei oligopeptidase B (opb) gene, complete cds.	Trypanosoma brucei	48,076	08-OCT-1999
rx00650	759	GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	51,319	9-Sep-99
		GB_PL2:ATAC006533	99188	AC006533	Arabidopsis thaliana chromosome II BAC F20M17 genomic sequence, complete sequence.	Arabidopsis thaliana	38,051	26-MAY-1999
		GB_PL2:ATAC006533	99188	AC006533	Arabidopsis thaliana chromosome II BAC F20M17 genomic sequence, complete sequence.	Arabidopsis thaliana	35,403	26-MAY-1999
rx00675	915	GB_BA1:SC3C8	33095	AL023861	Streptomyces coelicolor cosmid 3C8.	Streptomyces coelicolor	36,836	15-Jan-99
		GB_PR3:AC005736	215441	AC005736	Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.	Homo sapiens	42,027	01-OCT-1998
		GB_IN2:AC005719	188357	AC005719	Drosophila melanogaster, chromosome 2L, region 38A5-38B4, BAC clone BACR48M05, complete sequence.	Drosophila melanogaster	35,531	27-OCT-1999
rx00689	1614	GB_PAT:E07294	2975	E07294	genomic DNA encoding dehydrogenase of Bacillus stearothermophilus.	Bacillus stearothermophilus	45,677	29-Sep-97
		GB_BA1:BACALDHT	1975	D13846	B. stearothermophilus aldH gene for aldehyde dehydrogenase, complete cds.	Bacillus stearothermophilus	45,677	20-Feb-99
		GB_BA2:PPU96338	5276	U96338	Pseudomonas putida NCIMB 9866 plasmid pRA4000 p-cresol degradative pathway genes, p-hydroxybenzaldehyde dehydrogenase (pchA), p-cresol methylhydroxylase, cytochrome subunit precursor (pchC), unknown (pchX) and p-cresol methylhydroxylase, flavoprotein subunit (pchF) genes, complete cds.	Pseudomonas putida	44,317	13-MAY-1999
rx00715	918	GB_EST30:AI647104	218	AI647104	vn15c01.y1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1021248 5', mRNA sequence.	Mus musculus	58,511	29-Apr-99
		GB_EST17:AA636159	447	AA636159	vn15c01.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1021248 5', mRNA sequence.	Mus musculus	41,195	22-OCT-1997

Table 4 (continued)

rx00744	1065	GB_EST10:AA184468	583	AA184468	mi52h05.r1 Siratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:63561 5' similar to gb:D10918 Mouse mRNA for ubiquitin like protein, partial sequence (MOUSE); mRNA sequence.	40,426	12-Feb-97
		GB_HTG3:AC009855	167592	AC009855	Homo sapiens clone 1_C_5, *** SEQUENCING IN PROGRESS *** 13 unordered pieces.	36,673	3-Sep-99
		GB_HTG3:AC009855	167592	AC009855	Homo sapiens clone 1_C_5, *** SEQUENCING IN PROGRESS *** 13 unordered pieces.	36,673	3-Sep-99
		GB_PR4:AC005082	169739	AC005082	Homo sapiens clone RG271G13, complete sequence.	39,557	8-Sep-99
rx00756	1119	GB_BA1:MLCB596	38426	AL035472	Mycobacterium leprae cosmid B596.	54,562	27-Aug-99
		GB_GSS12:AQ368028	652	AQ368028	tox0001N11r CUGI Tomato BAC Library Lycopersicon esculentum genomic clone tox0001N11r, genomic survey sequence.	42,657	5-Feb-99
		GB_HTG3:AC008067	151242	AC008067	Homo sapiens clone NH0303104, *** SEQUENCING IN PROGRESS *** 2 unordered pieces.	37,239	8-Sep-99
rx00773	1266	GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	36,616	09-MAR-1995
		GB_BA1:MSGL611CS	37769	L78822	Mycobacterium leprae cosmid L611 DNA sequence.	35,714	15-Jun-96
		GB_GSS14:AQ578181	728	AQ578181	nbxb0083P08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0083P08r, genomic survey sequence.	39,246	2-Jun-99
rx00793	1299	GB_GSS5:AQ769737	519	AQ769737	HS_3160_A2_G04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3160 Col=8 Row=M, genomic survey sequence.	37,765	28-Jul-99
		GB_BA1:RTU08434	2400	U08434	Rhizobium trifolii orotate phosphoribosyltransferase (pyrE) and fructokinase (frk) genes, complete cds.	40,700	16-Apr-97
		GB_EST31:F33810	243	F33810	HSPD27491 HM3 Homo sapiens cDNA clone s3000041E12, mRNA sequence.	41,564	13-MAY-1999
rx00820	486	GB_PR4:AC005868	96180	AC005868	Homo sapiens 12q24.2 PAC RPC15-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	32,298	27-Feb-99
		GB_EST8:AA000903	396	AA000903	mg38b04.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:426031 5', mRNA sequence.	42,045	18-Jul-96
		GB_EST25:AI317789	696	AI317789	uj20g09.y1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:1920544 5' similar to WP:C13C4.5 CE08130 SUGAR TRANSPORTER ; mRNA sequence.	38,557	17-DEC-1998
rx00833	618	GB_PHI:BPH6589	41489	AJ006589	Bacteriophage phi-C31 complete genome.	41,806	29-Apr-99
		GB_HTG2:AC006887	215801	AC006887	Caenorhabditis elegans clone Y59H11, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	35,798	24-Feb-99
		GB_HTG2:AC006887	215801	AC006887	Caenorhabditis elegans clone Y59H11, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	35,798	24-Feb-99
rx00844	957	GB_GSS15:AQ605195	459	AQ605195	HS_2136_B1_C12_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2136 Col=23 Row=F, genomic survey sequence.	38,074	10-Jun-99

Table 4 (continued)

GB_HTG1:CNS00M8S	214599	AL079302	Homo sapiens chromosome 14 clone R-1089B7, *** SEQUENCING IN PROGRESS ***; in ordered pieces.	Homo sapiens	38,120	15-OCT-1999
GB_HTG1:CNS00M8S	214599	AL079302	Homo sapiens chromosome 14 clone R-1089B7, *** SEQUENCING IN PROGRESS ***; in ordered pieces.	Homo sapiens	38,120	15-OCT-1999
GB_BA1:CGORF4GEN	2398	X95649	C.glutamicum ORF4 gene.	Corynebacterium glutamicum	99,273	10-MAR-1998
GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,301	16-Aug-93
GB_PAT:E14517	1411	E14517	DNA encoding Brevibacterium dihydrodipicolinic acid reductase.	Corynebacterium glutamicum	99,659	28-Jul-99
GB_PAT:192050	567	I92050	Sequence 17 from patent US 5726299.	Unknown.	62,787	01-DEC-1998
GB_PAT:178760	567	I78760	Sequence 16 from patent US 5693781.	Unknown.	62,787	3-Apr-98
GB_BA2:AE000426	10240	AE000426	Escherichia coli K-12 MG1655 section 316 of 400 of the complete genome.	Escherichia coli	36,456	12-Nov-98
GB_BA2:AE001598	11136	AE001598	Chlamydia pneumoniae section 14 of 103 of the complete genome.	Chlamydia pneumoniae	32,782	08-MAR-1999
GB_PL2:AF079370	2897	AF079370	Kluyveromyces lactis invertase (INV1) gene, complete cds.	Kluyveromyces lactis	35,849	4-Aug-99
GB_BA2:AE001598	11136	AE001598	Chlamydia pneumoniae section 14 of 103 of the complete genome.	Chlamydia pneumoniae	40,138	08-MAR-1999
GB_PR2:HSQ15C24	73192	AJ239325	Homo sapiens chromosome 21 from cosmid LLNLC116 1C16 and LLNLC116 15C24 map 21q22.3 region D21S171-LA161, complete sequence.	Homo sapiens	35,076	28-Sep-99
GB_GSS4:AQ691923	446	AQ691923	HS_5400_B2_G04_SP6E RPCL-11 Human Male BAC Library Homo sapiens genomic clone Plate=976 Col=8 Row=N, genomic survey sequence.	Homo sapiens	33,500	6-Jul-99
GB_EST37:A1967802	479	A1967802	Ljirmp12-930-d6 Ljirmp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP930-12-d6 5' similar to 60S ribosomal protein L7A, mRNA sequence.	Lotus japonicus	41,127	24-Aug-99
GB_PAT:178750	588	I78750	Sequence 6 from patent US 5693781.	Unknown.	97,071	3-Apr-98
GB_PAT:192039	588	I92039	Sequence 6 from patent US 5726299.	Unknown.	97,071	01-DEC-1998
GB_PR3:HS929C8	139190	AL020994	Human DNA sequence from clone 929C8 on chromosome 22q12.1-12.3 Contains CA repeat, GSS, STS, complete sequence.	Homo sapiens	39,016	23-Nov-99
GB_PAT:178750	588	I78750	Sequence 6 from patent US 5693781.	Unknown.	97,561	3-Apr-98
GB_PAT:192039	588	I92039	Sequence 6 from patent US 5726299.	Unknown.	97,561	01-DEC-1998
GB_PAT:178750	588	I78750	Sequence 6 from patent US 5693781.	Unknown.	37,222	3-Apr-98
GB_BA1:AB032799	9077	AB032799	Chromobacterium violaceum violacein biosynthetic gene cluster (vio A, vio B, vio C, vio D), complete cds.	Chromobacterium violaceum	39,868	02-OCT-1999
GB_BA2:AF172851	10094	AF172851	Chromobacterium violaceum violacein biosynthetic gene cluster, complete sequence.	Chromobacterium violaceum	42,760	30-Aug-99
GB_BA1:AB032799	9077	AB032799	Chromobacterium violaceum violacein biosynthetic gene cluster (vio A, vio B, vio C, vio D), complete cds.	Chromobacterium violaceum	39,551	02-OCT-1999

Table 4 (continued)

rx000982	1629	GB_BA1:BLARGS	2501	Z21501	B.lactofermentum argS and lysA genes for arginyl-tRNA synthetase and diaminopimelate decarboxylase (partial).	Corynebacterium glutamicum	39,003	28-DEC-1993
		GB_BA1:CGXLYSA	2344	X54740	Corynebacterium glutamicum argS-lysA operon gene for the upstream region of the arginyl-tRNA synthetase and diaminopimelate decarboxylase (EC 4.1.1.20).	Corynebacterium glutamicum	41,435	30-Jun-93
		GB_PAT:E14508	3579	E14508	DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase.	Corynebacterium glutamicum	40,566	28-Jul-99
rx000983	1599	GB_HTG2:AC008152	24000	AC008152	Leishmania major chromosome 35 clone L7936 strain Friedlin, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Leishmania major	38,658	28-Jul-99
		GB_HTG2:AC008152	24000	AC008152	Leishmania major chromosome 35 clone L7936 strain Friedlin, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Leishmania major	38,658	28-Jul-99
		GB_HTG3:AC008648	87249	AC008648	Homo sapiens chromosome 5 clone CIT978SKB_186E14, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Homo sapiens	36,102	3-Aug-99
rx000984	440	GB_BA1:MVINED	3098	D01045	Micromonospora viridifaciens DNA for nedR protein and neuraminidase, complete cds.	Micromonospora viridifaciens	59,226	2-Feb-99
		GB_PAT:E02375	1881	E02375	Neuraminidase gene.	Micromonospora viridifaciens	59,226	29-Sep-97
		GB_PR4:HUAC004513	101311	AC004513	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-928E7, complete sequence.	Homo sapiens	41,204	23-Nov-99
rx01014	2724	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	56,167	17-Jun-98
		GB_BA1:STMAMPEPN	2849	L23172	Streptomyces lividans aminopeptidase N gene, complete cds.	Streptomyces lividans	57,067	18-MAY-1994
		GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	37,551	2-Aug-99
rx01059	732	GB_HTG3:AC008154	172241	AC008154	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 26 unordered pieces.	Homo sapiens	39,499	8-Sep-99
		GB_HTG3:AC008154	172241	AC008154	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 26 unordered pieces.	Homo sapiens	39,499	8-Sep-99
		GB_EST32:AI756574	299	AI756574	ea02f10.y1 Eimeria M5-6 Merozoite stage Eimeria tenella cDNA 5' mRNA sequence.	Eimeria tenella	37,793	23-Jun-99
rx01073	954	GB_BA1:BACOUTB	1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	Bacillus subtilis	53,723	26-Apr-93
		GB_PR4:AC007938	167237	AC007938	Homo sapiens clone UWGC:djs201 from 7q31, complete sequence.	Homo sapiens	34,322	1-Jul-99
		GB_PL2:ATAC006282	92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	Arabidopsis thaliana	36,181	13-MAR-1999
rx01120	1401	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	36,715	17-Jun-98
		GB_BA1:CAJ10321	6710	AJ010321	Caulobacter crescentus partial tig gene and clpP, clpA, clpX, lon genes.	Caulobacter crescentus	63,311	01-OCT-1998

Table 4 (continued)

GB_BA2:AF150957	4440	AF150957	Azospirillum brasilense trigger factor (tig), heat-shock protein ClpP (clpP), and heat-shock protein ClpX (clpX) genes, complete cds; and Lon protease (lon) gene, partial cds.	Azospirillum brasilense	60,613	7-Jun-99
GB_PR3:HS408N23	97916	Z98048	Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.	Homo sapiens	34,567	23-Nov-99
GB_BA2:AE001227	26849	AE001227	Treponema pallidum section 43 of 87 of the complete genome.	Treponema pallidum	37,564	16-Jul-98
GB_PR3:HS408N23	97916	Z98048	Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.	Homo sapiens	34,911	23-Nov-99
GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	38,789	17-Jun-98
GB_HTG4:AC009849	114993	AC009849	Drosophila melanogaster chromosome 2 clone BACR07H08 (D864) RPCI-98 07.H.8 map 31B-31C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 55 unordered pieces.	Drosophila melanogaster	39,213	25-OCT-1999
GB_HTG4:AC009849	114993	AC009849	Drosophila melanogaster chromosome 2 clone BACR07H08 (D864) RPCI-98 07.H.8 map 31B-31C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 55 unordered pieces.	Drosophila melanogaster	39,213	25-OCT-1999
GB_BA2:AF176799	2943	AF176799	Lactobacillus pentosus PepQ (pepQ) and catabolite control protein A (ccpA) genes, complete cds.	Lactobacillus pentosus	37,043	5-Sep-99
GB_BA2:AF012084	3082	AF012084	Lactobacillus helveticus prolidase (pepQ) gene, complete cds.	Lactobacillus helveticus	46,796	1-Jul-98
GB_EST32:A1728955	611	A1728955	BNLGH12114 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004481) putative permease [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	37,647	11-Jun-99
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,570	22-Aug-97
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	60,434	17-Jun-98
GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	Streptomyces coelicolor A3(2)	57,011	22-Jul-99
GB_HTG1:CEY116A8_2110000	2110000	Z98858	Caenorhabditis elegans chromosome IV clone Y116A8, *** SEQUENCING IN PROGRESS ***. in unordered pieces.	Caenorhabditis elegans	34,843	26-Oct-99
GB_HTG1:CEY116A8_2110000	2110000	Z98858	Caenorhabditis elegans chromosome IV clone Y116A8, *** SEQUENCING IN PROGRESS ***. in unordered pieces.	Caenorhabditis elegans	34,843	26-Oct-99
GB_IN1:CEY116A8C	260341	AL117204	Caenorhabditis elegans cosmid Y116A8C, complete sequence.	Caenorhabditis elegans	34,843	19-Nov-99
GB_BA1:D90915	130001	D90915	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259.	Synechocystis sp.	36,538	7-Feb-99
GB_BA1:D90915	130001	D90915	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259.	Synechocystis sp.	34,512	7-Feb-99

Table 4 (continued)

rx01192	681	GB_HTG3:AC010515	41038	AC010515	Homo sapiens chromosome 19 clone LLNL-R_249H9, *** SEQUENCING IN PROGRESS *** , 31 unordered pieces.	Homo sapiens	33,564	15-Sep-99
		GB_OM:CFP180RRC	5425	X87224	Canis familiaris mRNA for ribosome receptor, p180.	Canis familiaris	41,229	22-Jan-99
		GB_OM:CFP180RRC	5425	X87224	Canis familiaris mRNA for ribosome receptor, p180.	Canis familiaris	38,187	22-Jan-99
rx01214	1614	GB_IN1:CEY47D3A	199814	AL117202	Caenorhabditis elegans cosmid Y47D3A, complete sequence.	Caenorhabditis elegans	36,604	19-Nov-99
		GB_PR4:AC006039	176257	AC006039	Homo sapiens clone NH0319F03, complete sequence.	Homo sapiens	34,984	05-MAY-1999
		GB_PR4:AC006039	176257	AC006039	Homo sapiens clone NH0319F03, complete sequence.	Homo sapiens	35,951	05-MAY-1999
rx01224	1146	GB_EST22:AI070047	479	AI070047	UI-R-C1-In-f-08-0-UI.s1 UI-R-C1 Rattus norvegicus cDNA clone UI-R:Rattus norvegicus C1-In-f-08-0-UI 3', mRNA sequence.	UI-R:Rattus norvegicus	36,975	5-Jul-99
		GB_RO:S75965	625	S75965	THP=Tamm-Horsfall protein (promoter) [rats, Genomic, 625 nt].	Rattus sp.	34,400	27-Jul-95
		GB_EST5:H96951	459	H96951	yu01g03.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232564 5', mRNA sequence.	Homo sapiens	32,969	11-DEC-1995
rx01250	588	GB_PL1:NEULCCB	2656	M18334	N.crassa (strain TS) laccase gene, complete cds.	Neurospora crassa	44,330	03-MAY-1994
		GB_OV:MTRACOMPL	16714	Y16884	Rhea americana complete mitochondrial genome.	Mitochondrion Rhea americana	35,094	19-Jul-99
		GB_OV:AF090339	16704	AF090339	Rhea americana mitochondrion, complete genome.	Mitochondrion Rhea americana	35,094	27-MAY-1999
rx01277	2127	GB_PL2:AF111709	52684	AF111709	Onyza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences; and unknown genes.	Onyza sativa subsp. indica	37,410	26-Apr-99
		GB_IN1:CELZC250	34372	AF003383	Caenorhabditis elegans cosmid ZC250.	Caenorhabditis elegans	35,506	14-MAY-1997
		GB_EST1:Z14808	331	Z14808	CEL5E4 Chris Martin sorted cDNA library Caenorhabditis elegans cDNA clone cm5e4 5', mRNA sequence.	Caenorhabditis elegans	36,890	19-Jun-97
rx01302	576	GB_BA1:MTC165	34331	Z95584	Mycobacterium tuberculosis H37Rv complete genome; segment 50/162.	Mycobacterium tuberculosis	59,298	17-Jun-98
		GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,227	10-DEC-1996
rx01303	1458	GB_BA1:SC5C7	41906	AL031515	Streptomyces coelicolor cosmid 5C7.	Streptomyces coelicolor	39,261	7-Sep-98
		GB_BA1:TTAJ5043	837	AJ225043	Thermus thermophilus partial narK gene.	Thermus thermophilus	55,245	18-Jun-98
		GB_PL2:AC010675	84723	AC010675	Arabidopsis thaliana chromosome 1 BAC T17F3 genomic sequence, complete sequence.	Arabidopsis thaliana	37,058	11-Nov-99
		GB_GSS9:AA170862	518	AQ170862	HS_3165_B2_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=6 Row=L, genomic survey sequence.	Homo sapiens	38,610	17-OCT-1998
rx01308	2503	GB_BA1:D90757	17621	D90757	Escherichia coli genomic DNA. (27.3 - 27.7 min).	Escherichia coli	55,445	7-Feb-99
		GB_BA1:D90787	15942	D90787	E.coli genomic DNA, Kohara clone #276(33.0-33.3 min.).	Escherichia coli	36,815	29-MAY-1997
		GB_BA1:D90758	13860	D90758	Escherichia coli genomic DNA. (27.6 - 27.9 min).	Escherichia coli	54,942	7-Feb-99
rx01309	824	GB_BA1:SCJ12	35302	AL109989	Streptomyces coelicolor cosmid J12.	Streptomyces coelicolor	62,423	24-Aug-99
		GB_BA1:BSNARYWI	12450	Z49884	B.subtilis narf[G.H.I.J.K], ywi[C.D.E] and argS genes.	A3(2) Bacillus subtilis	57,447	24-Jun-98

Table 4 (continued)

rx01358	1644	GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21); from 3798401 to Bacillus subtilis 4010550.	37,129	26-Nov-97
		GB_GSS11:AQ260413	453	AQ260413	CITBI-E1-2510B12.TF CITBI-E1 Homo sapiens genomic clone 2510B12, genomic survey sequence.	41,531	24-OCT-1998
		GB_EST20:AA840582	326	AA840582	vw77h07.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1261021 5' similar to gb.J04181 Mouse A-X actin mRNA, complete cds (MOUSE); mRNA sequence.	42,901	27-Feb-98
rx01385	2004	GB_PAT:A39944	3836	A39944	Sequence 1 from Patent WO9421807.	38,764	05-MAR-1997
		GB_BA1:FVBPEA	2519	M98557	Flavobacterium sp. pentachlorophenol 4-monoxygenase gene, complete mRNA.	40,855	26-Apr-93
		GB_PAT:I19994	2516	I19994	Sequence 2 from patent US 5512478.	40,855	07-OCT-1996
		GB_BA2:AF059680	2410	AF059680	Sphingomonas sp. UG30 pentachlorophenol 4-monoxygenase (pcpB) gene, complete cds; and pentachlorophenol 4-monoxygenase reductase (pcpD) gene, partial cds.	42,993	27-Apr-99
rx01412	327	GB_GSS12:AQ332469	459	AQ332469	HS_5003_A1_H08_SPEE RPC111 Human Male BAC Library Homo sapiens genomic clone Plate=579 Col=15 Row=O, genomic survey sequence.	38,208	06-MAR-1999
		GB_EST27:AA998532	453	AA998532	UI-R-CO-ic-d-11-0-UI.s1 UI-R-CO Rattus norvegicus cDNA clone UI-R-CO-ic-d-11-0-UI.3', mRNA sequence.	39,336	09-MAR-1999
		GB_HTG1:HASA342D11	178183	AL121748	Homo sapiens chromosome 10 clone RP11-342D11, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	40,550	23-Nov-99
rx01458	1173	GB_BA2:AE000745	15085	AE000745	Aquifex aeolicus section 77 of 109 of the complete genome.	37,694	25-MAR-1998
		GB_BA2:AE000745	15085	AE000745	Aquifex aeolicus section 77 of 109 of the complete genome.	35,567	25-MAR-1998
rx01571	723	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	57,500	7-Aug-98
		GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	35,655	7-Aug-98
rx01607	753	GB_PR4:AC005005	133893	AC005005	Homo sapiens PAC clone DJ412A9 from 22, complete sequence.	38,399	02-MAR-1999
		GB_HTG3:AC008257	109187	AC008257	Drosophila melanogaster chromosome 2 clone BACR08A11 (D916) RPCI-98.08.A.11 map 42A-42A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	33,741	08-OCT-1999
		GB_HTG3:AC008257	109187	AC008257	Drosophila melanogaster chromosome 2 clone BACR08A11 (D916) RPCI-98.08.A.11 map 42A-42A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	33,741	08-OCT-1999
rx01609	996	GB_BA1:MTV003	13246	AL008883	Mycobacterium tuberculosis H37Rv complete genome; segment 125/162.	39,369	17-Jun-98
		GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	60,624	15-Jun-96
		GB_BA1:AB024601	14807	AB024601	Pseudomonas aeruginosa dapD gene for tetrahydrodipicolinate N-succinyltransferase, complete cds, strain PAO1.	41,603	12-MAR-1999

Table 4 (continued)

rx01654	1119	GB_GSS4: AQ704352	532	AQ704352	HS_2147_A2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2147 Col=8 Row=O, genomic survey sequence.	Homo sapiens	37,838	7-Jul-99
		GB_RO:MMAE000663	250611	AE000663	Mus musculus TCR beta locus from bases 1 to 250611 (section 1 of 3) of the complete sequence.	Mus musculus	35,799	4-Sep-97
		GB_EST23:AI158428	511	AI158428	ud24f12.r1 Soares 2N6MT Mus musculus cDNA clone IMAGE:1446863 5', mRNA sequence.	Mus musculus	41,337	30-Sep-98
rx01664	945	GB_OV:AF026198	63155	AF026198	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete sequence.	Fugu rubripes	35,187	02-MAY-1998
		GB_PR3:AC004466	122186	AC004466	Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	37,382	17-Sep-98
		GB_PR3:AC004466	122186	AC004466	Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	37,325	17-Sep-98
rx01795	720	GB_BA2:CGU13922	4412	U13922	Corynebacterium glutamicum putative type II 5-cytosine methyltransferase (cgIIIM) and putative type II restriction endonuclease (cgIIR) and putative type I or type III restriction endonuclease (cgIIR) genes, complete cds.	Corynebacterium glutamicum	99,444	3-Feb-98
		GB_BA1:S86113	1044	S86113	ORF 1 [Neisseria gonorrhoeae, Genomic, 1044 nt].	Neisseria gonorrhoeae	58,320	07-MAY-1993
		GB_PAT:I22080	850	I22080	Sequence 1 from patent US 5525717.	Unknown.	57,722	07-OCT-1996
rx01802	954	GB_BA2:AE001519	14062	AE001519	Helicobacter pylori, strain J99 section 80 of 132 of the complete genome.	Helicobacter pylori J99	33,510	20-Jan-99
		GB_GSS5: AQ774071	552	AQ774071	HS_2269_B1_C10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2269 Col=19 Row=F, genomic survey sequence.	Homo sapiens	37,967	29-Jul-99
		GB_PR4:AC007459	40907	AC007459	Homo sapiens chromosome 16 clone 306C6, complete sequence.	Homo sapiens	39,140	04-MAY-1999
rx01838	842	GB_BA1:SCE15	26440	AL049707	Streptomyces coelicolor cosmid E15.	Streptomyces coelicolor	36,297	22-Apr-99
		GB_HTG3:AC009545	165042	AC009545	Homo sapiens chromosome 11 clone 131_J_04 map 11, *** SEQUENCING IN PROGRESS *** 8 unordered pieces.	Homo sapiens	37,651	01-OCT-1999
		GB_HTG3:AC009545	165042	AC009545	Homo sapiens chromosome 11 clone 131_J_04 map 11, *** SEQUENCING IN PROGRESS *** 8 unordered pieces.	Homo sapiens	37,651	01-OCT-1999
rx01848	867	GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome, segment 124/162.	Mycobacterium tuberculosis	38,270	17-Jun-98
		GB_EST21:C89252	587	C89252	C89252 Mouse early blastocyst cDNA Mus musculus cDNA clone 01B00061JC08, mRNA sequence.	Mus musculus	37,219	28-MAY-1998
		GB_EST14:AA423340	457	AA423340	ve39d04.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:820519 5', mRNA sequence.	Mus musculus	38,377	16-OCT-1997

Table 4 (continued)

rx01849	1224	GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	39,950	17-Jun-98
		GB_BA2:RCPHSYNG	45959	Z11165	R. capsulatus complete photosynthesis gene cluster.	Rhodobacter capsulatus	37,344	2-Sep-99
		GB_BA1:RSPD10302	40707	AJ010302	Rhodobacter sphaeroides photosynthetic gene cluster.	Rhodobacter sphaeroides	40,998	27-Aug-99
rx01868	2049	GB_BA1:MTV033	21620	AL021928	Mycobacterium tuberculosis H37Rv complete genome; segment 11/162.	Mycobacterium tuberculosis	38,679	17-Jun-98
		GB_BA1:MLCL622	42498	Z95398	Mycobacterium leprae cosmid L622.	Mycobacterium leprae	38,911	24-Jun-97
		GB_BA1:MSG8983CS	36788	L78828	Mycobacterium leprae cosmid B983 DNA sequence.	Mycobacterium leprae	38,933	15-Jun-96
rx01885	924	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	51,094	17-Jun-98
		GB_PR3:HSU220B11	41247	Z69908	Human DNA sequence from cosmid cu220B11, between markers DXS6791 and DXS8038 on chromosome X.	Homo sapiens	39,038	23-Nov-99
		GB_BA1:PDU17435	993	U17435	Paracoccus denitrificans Fnr-like transcriptional activator (nfr) gene, complete cds.	Paracoccus denitrificans	39,390	19-Jul-95
rx01914	526	GB_PR3:AC005796	43843	AC005796	Homo sapiens chromosome 19, cosmid R31408, complete sequence.	Homo sapiens	34,961	06-OCT-1998
		GB_PR3:HS390C10	114231	AL008721	Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga and tat repeat polymorphisms, complete sequence.	Homo sapiens	39,600	23-Nov-99
		GB_PR3:AC005796	43843	AC005796	Homo sapiens chromosome 19, cosmid R31408, complete sequence.	Homo sapiens	37,725	06-OCT-1998
rx01932	1020	GB_PR3:AC003025	112309	AC003025	Human Chromosome 11p12.2 PAC clone pDJ466a11, complete sequence.	Homo sapiens	35,585	23-Jul-98
		GB_GSS3:B78728	312	B78728	CIT-HSP-431E3 TV CIT-HSP Homo sapiens genomic clone 431E3, genomic survey sequence.	Homo sapiens	38,907	25-Jun-98
		GB_PR3:AC003025	112309	AC003025	Human Chromosome 11p12.2 PAC clone pDJ466a11, complete sequence.	Homo sapiens	35,859	23-Jul-98
rx01933	726	GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	35,302	27-Aug-99
		GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	35,302	27-Aug-99
		GB_PR4:AC006032	170282	AC006032	Homo sapiens BAC clone NH0115E20 from Y, complete sequence.	Homo sapiens	37,640	27-Feb-99
rx01971	954	GB_HTG3:AC008230	108469	AC008230	Drosophila melanogaster chromosome 2 clone BACR17117 (D934) RPCI-98 17.1.17 map 53A-53C strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** 108 unordered pieces.	Drosophila melanogaster	35,466	10-Aug-99
		GB_HTG3:AC008230	108469	AC008230	Drosophila melanogaster chromosome 2 clone BACR17117 (D934) RPCI-98 17.1.17 map 53A-53C strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** 108 unordered pieces.	Drosophila melanogaster	35,466	10-Aug-99

Table 4 (continued)

rx02016	900	GB_PR3:AF064860	165382	AF064860	Homo sapiens chromosome 21q22.3 PAC 70124, complete sequence.	Homo sapiens	39,716	2-Jun-98
		GB_EST2:D48846	459	D48846	RICS15292A Rice green shoot Oryza sativa cDNA, mRNA sequence.	Oryza sativa	37,118	2-Aug-95
		GB_GSS10:AQ195886	595	AQ195886	RPC111-66O13.TJ RPC11-11 Homo sapiens genomic clone RPC11-11-66O13, genomic survey sequence.	Homo sapiens	41,000	20-Apr-99
		GB_GSS10:AQ195886	595	AQ195886	RPC111-66O13.TJ RPC11-11 Homo sapiens genomic clone RPC11-11-66O13, genomic survey sequence.	Homo sapiens	34,790	20-Apr-99
rx02017	807	GB_EST20:AA855266	406	AA855266	vw70b08.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1260279 5', mRNA sequence.	Mus musculus	42,638	06-MAR-1998
		GB_EST20:AA855266	406	AA855266	vw70b08.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1260279 5', mRNA sequence.	Mus musculus	37,183	06-MAR-1998
rx02018	1073	GB_BA1:SC5C7	41906	AL031515	Streptomyces coelicolor cosmid 5C7.	Streptomyces coelicolor	41,732	7-Sep-98
		GB_BA1:MTC165	34331	Z95584	Mycobacterium tuberculosis H37Rv complete genome, segment 50/162.	Mycobacterium tuberculosis	62,395	17-Jun-98
		GB_BA1:SCJ12	35302	AL109989	Streptomyces coelicolor cosmid J12.	Streptomyces coelicolor	61,603	24-Aug-99
rx02048	1497	GB_PAT:E15823	2323	E15823	DNA encoding cell surface protein from Corynebacterium ammoniagenes.	Corynebacterium ammoniagenes	53,942	28-Jul-99
		GB_OM:SSAMPTDN	3387	Z29522	S.scrofa mRNA for aminopeptidase N.	Sus scrofa	42,672	26-Sep-94
		GB_OV:D87992	3181	D87992	Gallus gallus mRNA for aminopeptidase Ey, complete cds.	Gallus gallus	41,554	5-Jun-99
rx02101	1386	GB_BA1:AP000064	247695	AP000064	Aeropyrum pernix genomic DNA, section 717.	Aeropyrum pernix	39,882	22-Jun-99
		GB_PL2:ATAC006587	79262	AC006587	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence.	Arabidopsis thaliana	38,490	23-MAR-1999
		GB_PL2:ATAC006587	79262	AC006587	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence.	Arabidopsis thaliana	34,863	23-MAR-1999
rx02265	423	GB_BA2:AF120718	4137	AF120718	Lactobacillus fermentum urease operon, partial sequence.	Lactobacillus fermentum	56,265	31-MAR-1999
		GB_PAT:E03531	2896	E03531	DNA sequence coding for acid urease.	Lactobacillus fermentum	56,265	29-Sep-97
		GB_BA1:LBAUURE	2896	D10605	L.fermentum gene for acid urease.	Lactobacillus fermentum	56,265	2-Feb-99
rx02276	801	GB_GSS10:AQ242920	451	AQ242920	HS_2061_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=15 Row=1, genomic survey sequence.	Homo sapiens	37,916	03-OCT-1998
		GB_IN1:SLMMTPMF	14503	D29637	Physarum polycephalum mitochondrial DNA.	Mitochondrion Physarum polycephalum	40,335	12-MAY-1999
		GB_IN2:AF012249	5542	AF012249	Physarum polycephalum strain aux2-S region of mitochondria derived from mF plasmid, including URFA', URFC, URFD, URFE, URFF, and URFG genes, complete cds, and URFH gene, partial cds.	Mitochondrion Physarum polycephalum	40,335	08-MAY-1998
rx02277	738	GB_BA2:AF048784	681	AF048784	Actinomyces naeslundii urease accessory protein (ureG) gene, complete cds.	Actinomyces naeslundii	66,814	9-Feb-99

Table 4 (continued)

GB_BA2:AF056321	5482	AF056321	Actinomyces naeslundii urease gamma subunit UreA (ureA), urease beta subunit UreB (ureB), urease alpha subunit UreC (ureC), urease accessory protein UreE (ureE), urease accessory protein UreF (ureF), urease accessory protein UreG (ureG), and urease accessory protein UreD (ureD) genes, complete cds.	Actinomyces naeslundii	63,686	9-Feb-99
GB_BA2:SSU35248	5773	U35248	Streptococcus salivarius ure cluster nickel transporter homolog (ureI) gene, partial cds, and urease beta subunit (ureA), gamma subunit (ureB), alpha subunit (ureC), and accessory proteins (ureE), (ureF), (ureG), and (ureD) genes, complete cds.	Streptococcus salivarius	61,931	26-Jan-96
GB_GSS3:B49054	543	B49054	RPC11-4113. TV RPC11-11 Homo sapiens genomic clone RPC11-4113, genomic survey sequence.	Homo sapiens	39,161	8-Apr-99
GB_PL1:PMCMSGI	3363	L27092	Pneumocystis carinii B-cell receptor (msg1) gene, 3' end.	Pneumocystis carinii	39,819	26-Sep-94
GB_PL2:AF038556	12792	AF038556	Pneumocystis carinii f. sp. hominis variant regions of major surface glycoproteins (msg1, msg3, msg4) genes, partial cds.	Pneumocystis carinii f. sp. hominis	33,832	10-Sep-98
GB_GSS8:AQ051031	914	AQ051031	nbxb0004dG10r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0004N20r, genomic survey sequence.	Oryza sativa	32,299	24-MAR-1999
GB_GSS8:AQ051031	914	AQ051031	nbxb0004dG10r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0004N20r, genomic survey sequence.	Oryza sativa	34,573	24-MAR-1999
GB_BA1:CGU35023	3195	U35023	Corynebacterium glutamicum thiosulfate sulfurtransferase (thtR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds.	Corynebacterium glutamicum	100,000	16-Jan-97
GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	60,380	10-Feb-99
GB_BA1:UD0012	33312	U00012	Mycobacterium leprae cosmid B1308.	Mycobacterium leprae	37,660	30-Jan-96
GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	35,973	03-DEC-1999
GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	35,973	03-DEC-1999
GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,992	03-DEC-1999
GB_BA1:AB020624	1605	AB020624	Corynebacterium glutamicum murl gene for D-glutamate racemase, complete cds.	Corynebacterium glutamicum	99,227	24-Jul-99
GB_EST4:H51527	294	H51527	yo33b09.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179705 3' mRNA sequence.	Homo sapiens	40,411	18-Sep-95
GB_GSS1:CNS003CM	1101	AL064136	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR08C19 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	37,674	3-Jun-99

Table 4 (continued)

rx02477	744	GB_HTG4:AC010054	130191	AC010054	Drosophila melanogaster chromosome 3L74E2 clone RPC198-15E10, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,466	16-OCT-1999
		GB_HTG4:AC010054	130191	AC010054	Drosophila melanogaster chromosome 3L74E2 clone RPC198-15E10, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,466	16-OCT-1999
		GB_HTG4:AC009375	137069	AC009375	Drosophila melanogaster chromosome 3L75A1 clone RPC198-44L18, *** SEQUENCING IN PROGRESS ***; 59 unordered pieces.	Drosophila melanogaster	39,118	16-OCT-1999
rx02513	832	GB_BA1:MTER260	373	X92572	M.terrae gene for 32 kDa protein (partial).	Mycobacterium terrae	42,895	15-Jan-98
		GB_PL1:AB019229	84294	AB019229	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence.	Arabidopsis thaliana	36,084	20-Nov-99
		GB_PL1:AB019229	84294	AB019229	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence.	Arabidopsis thaliana	35,244	20-Nov-99
rx02531	834	GB_BA1:CGLATTB	271	X99850	C.glutamicum DNA for attB region.	Corynebacterium glutamicum	40,590	8-Aug-96
		GB_EST11:AA239557	423	AA239557	mv25f04.r1 GuayWoodford Beiler mouse kidney day 0 Mus musculus cDNA clone IMAGE:656095 5' similar to gb:X52634 Murine tm oncogene for tm protein (MOUSE); mRNA sequence.	Mus musculus	38,760	12-MAR-1997
		GB_BA1:RSPYPPCL	6500	AJ002398	Rhodobacter sphaeroides pyp and pcl genes, and orfA, orfB, orfC, orfD, orfE, orfF.	Rhodobacter sphaeroides	37,091	17-DEC-1998
rx02548	314	GB_BA2:AF127374	63734	AF127374	Streptomyces lavendulae LinA homolog, cytochrome P450 hydroxylase ORF4, cytochrome P450 hydroxylase ORF3, MitT (mitT), MitS (mitS), MitR (mitR), MitQ (mitQ), MiIP (miIP), MitO (mitO), MitN (mitN), MitM (mitM), MitL (mitL), MitK (mitK), MitJ (mitJ), MitI (mitI), MitH (mitH), MitG (mitG), MitF (mitF), MitE (mitE), MitD (mitD), MitC (mitC), MitB (mitB), MitA (mitA), MmcA (mmcA), MmcB (mmcB), MmcC (mmcC), MmcD (mmcD), MmcE (mmcE), MmcF (mmcF), MmcG (mmcG), MmcH (mmcH), MmcI (mmcI), MmcJ (mmcJ), MmcK (mmcK), MmcL (mmcL), MmcM (mmcM), MmcN (mmcN), MmcO (mmcO), MmcP (mmcP), MmcQ (mmcQ), MmcR (mmcR), MmcS (mmcS), MmcT (mmcT), MmcU (mmcU), MmcV (mmcV), Mct (mct), MmcW (mmcW), MmcX (mmcX), and MmcY (mmcY) genes, complete cds; and unknown genes.	Streptomyces lavendulae	66,242	27-MAY-1999

Table 4 (continued)

GB_BA2:AF127374	63734	AF127374	Streptomyces lavendulae LinA homolog, cytochrome P450 hydroxylase ORF4, cytochrome P450 hydroxylase ORF3, MitT (mitT), MitS (mitS), MitR (mitR), MitQ (mitQ), MitP (mitP), MitO (mitO), MitN (mitN), MitM (mitM), MitL (mitL), MitK (mitK), MitJ (mitJ), MitI (mitI), MitH (mitH), MitG (mitG), MitF (mitF), MitE (mitE), MitD (mitD), MitC (mitC), MitB (mitB), MitA (mitA), MmcA (mmcA), MmcB (mmcB), MmcC (mmcC), MmcD (mmcD), MmcE (mmcE), MmcF (mmcF), MmcG (mmcG), MmcH (mmch), MmcI (mmcl), MmcJ (mmcj), MmcK (mmck), MmcL (mmcl), MmcM (mmcm), MmcN (mmcn), MmcO (mmco), MmcP (mmcp), MmcQ (mmcq), MmcR (mmcr), MmcS (mmcs), MmcT (mmct), MmcU (mmcu), MmcV (mmcv), Mct (mct), MmcW (mmcw), MmcX (mmcX), and MmcY (mmcy) genes, complete cds; and unknown genes.	Streptomyces lavendulae	38,411	27-MAY-1999
GB_GSS4:AQ741886	742	AQ741886	HS_5569_B2_B02_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1145 Col=4 Row=D, genomic survey sequence.	Homo sapiens	38,907	16-Jul-99
GB_EST18:AA567307	741	AA567307	HLO1004.5prime HL Drosophila melanogaster head BlueScript Drosophila melanogaster cDNA clone HLO1004 5prime, mRNA sequence.	Drosophila melanogaster	38,736	28-Nov-98
GB_EST27:AI402394	630	AI402394	GH21610.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH21610 5prime, mRNA sequence.	Drosophila melanogaster	41,308	8-Feb-99
GB_GSS10:AQ237646	715	AQ237646	RPCI11-6119.TJB RPCI-11 Homo sapiens genomic clone RPCI-11-6119, genomic survey sequence.	Homo sapiens	44,340	21-Apr-99
GB_EST32:AI726448	562	AI726448	BNLGH15854 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U53418) UDP-glucose dehydrogenase [Glycine max], mRNA sequence.	Gossypium hirsutum	37,003	11-Jun-99
GB_EST32:AI726198	608	AI726198	BNLGH15243 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U53418) UDP-glucose dehydrogenase [Glycine max], mRNA sequence.	Gossypium hirsutum	40,925	11-Jun-99
GB_PR4:AC002992	154848	AC002992	Homo sapiens chromosome Y, clone 203M13, complete sequence.	Homo sapiens	38,039	13-OCT-1999
GB_EST4:H29653	415	H29653	ym58f01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52678 5' similar to SP:OXDD_BOVIN P31228 D-ASPARTATE OXIDASE, mRNA sequence.	Homo sapiens	39,036	17-Jul-95
GB_PR3:HSDJ261K5	131974	AL050350	Human DNA sequence from clone 261K5 on chromosome 6q21-22.1. Contains the 3' part of the gene for a novel organic cation transporter (BAC ORF RG331P03), the DDO gene for D-aspartate oxidase (EC 1.4.3.1), ESTs, STSs, GSSs and two putative CpG islands, complete sequence.	Homo sapiens	35,957	23-Nov-99

Table 4 (continued)

rx02589	888	GB_EST2:R20147	494	R20147	y918h02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32866 5' similar to SP:OXDD_BOVIN P31228 D-ASPARTATE OXIDASE; mRNA sequence.	Homo sapiens	36,437	17-Apr-95
		GB_HTG1:CEY6E2	186306	Z96799	Caenorhabditis elegans chromosome V clone Y6E2, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	37,979	02-OCT-1997
		GB_HTG1:CEY6E2	186306	Z96799	Caenorhabditis elegans chromosome V clone Y6E2, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	37,979	02-OCT-1997
		GB_HTG3:AC011690	72277	AC011690	Homo sapiens clone 17_E_13, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,814	10-OCT-1999
rx02592	894	GB_BA1:MSG8983CS	36788	L78828	Mycobacterium leprae cosmid B983 DNA sequence.	Mycobacterium leprae	53,235	15-Jun-96
		GB_GSS9:AQ170723	487	AQ170723	HS_2270_B2_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=10 Row=L, genomic survey sequence.	Homo sapiens	39,666	16-OCT-1998
		GB_GSS12:AQ349397	791	AQ349397	RPC11-118H16.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-118H16, genomic survey sequence.	Homo sapiens	34,204	07-MAY-1999
rx02603	1119	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	37,975	24-Jun-99
		GB_IN2:AC005714	177740	AC005714	Drosophila melanogaster, chromosome 2R, region 58D4-58E2, BAC clone BACR48M13, complete sequence.	Drosophila melanogaster	41,226	01-MAY-1999
		GB_EST19:AA775050	218	AA775050	ac76e10.s1 Striatagene lung (#937210) Homo sapiens cDNA clone IMAGE:888554 3' similar to gb:Y00371_ma1 HEAT SHOCK COGNATE 71 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	40,826	5-Feb-98
rx02630	1446	GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	49,015	27-Aug-99
		GB_BA1:MTV044	16150	AL021999	Mycobacterium tuberculosis H37Rv complete genome; segment 45/162.	Mycobacterium tuberculosis	49,192	17-Jun-98
rx02643	1167	GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	45,621	09-MAR-1995
		GB_EST37:AI950576	308	AI950576	wx52e08.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547302 3', mRNA sequence.	Homo sapiens	40,909	6-Sep-99
		GB_EST37:AI950576	308	AI950576	wx52e08.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547302 3', mRNA sequence.	Homo sapiens	40,288	6-Sep-99
rx02644	774	GB_EST34:AV149547	302	AV149547	AV149547 Mus musculus C57BL/6J 10-11 day embryo Mus musculus cDNA clone 2810489D03, mRNA sequence.	Mus musculus	38,627	5-Jul-99
		GB_EST35:AV156221	271	AV156221	AV156221 Mus musculus head C57BL/6J 12-day embryo Mus musculus cDNA clone 3000001C24, mRNA sequence.	Mus musculus	33,990	7-Jul-99
		GB_EST32:AV054919	274	AV054919	AV054919 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA clone 1810033C08, mRNA sequence.	Mus musculus	36,585	23-Jun-99
rx02745	902	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	39,298	17-Jun-98

Table 4 (continued)

GB_BA2:AF027770	30683	AF027770	Mycobacterium smegmatis FxbA (fxbA) gene, partial cds; FxbB (fxbB), FxbC (fxbC), and FxuD (fxuD) genes, complete cds; and unknown genes.	Mycobacterium smegmatis	55,125	03-DEC-1998
GB_BA2:SAU43537	3938	U43537	Streptomyces argillaceus mithramycin resistance determinant, ATP-binding protein (mtrA) and membrane protein (mtrB) genes, complete cds.	Streptomyces argillaceus	46,868	5-Sep-96
GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	100,000	14-MAY-1999
GB_BA1:MTCY338	29372	Z74697	Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.	Mycobacterium tuberculosis	39,785	17-Jun-98
GB_HTG3:AC008733	216140	AC008733	Homo sapiens chromosome 19 clone CITB-E1_2525J15, *** SEQUENCING IN PROGRESS ***; 72 unordered pieces.	Homo sapiens	35,688	3-Aug-99
GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	36,859	1-Feb-97
GB_IN1:CET04C10	20958	Z69885	Caenorhabditis elegans cosmid T04C10, complete sequence.	Caenorhabditis elegans	35,934	2-Sep-99
GB_EST35:AI823090	720	AI823090	L30-944T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-944 5' similar to 60S ribosomal protein L36 (AC004684)(Arabidopsis thaliana), mRNA sequence.	Mesembryanthemum crystallinum	35,770	21-Jul-99
GB_BA1:CJY13333	3315	Y13333	Campylobacter jejuni clpB gene.	Campylobacter jejuni	53,400	12-Apr-99
GB_BA2:AF065404	181654	AF065404	Bacillus anthracis virulence plasmid PX01, complete sequence.	Bacillus anthracis	45,168	20-OCT-1999
GB_PL2:AC006601	110684	AC006601	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence.	Arabidopsis thaliana	36,680	22-Feb-99

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \cdot \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \cdot 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 500 mg/l complexing agent
- 15 (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

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min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., Science, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

25

Example 4: *In vivo* Mutagenesis

30

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

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the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g., Martin, J.F. et al. (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see e.g., Yoshihama, M. et al. (1985) *J. Bacteriol.* 162:591-597, Martin J.F. et al. (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. et al. (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. et al. (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. et al. (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described e.g. in Schäfer, A et al.

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:
25 Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to
30 that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

- (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.
- 10 To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which
- 15 specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

20 **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

- Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der
- 25 Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose,
- 30 ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

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is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

10 For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance

15 of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates

20 (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

25

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered

30 enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods,

applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's
10 *Encyclopedia of Industrial Chemistry* (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using
15 reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed
20 according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired 25 Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired
30 product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical

- chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.*
- 5 (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of
- 10 Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the
- 15 production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and
- 20 measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

25 **Example 10: Purification of the Desired Product from *C. glutamicum* Culture**

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such
- 30 as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

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90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to HA nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to HA protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM, described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*. John Wiley and Sons: New York). The gene sequences of the invention

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were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a
5 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
10 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
15 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For
20 example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are
25 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose,
30 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (e.g., ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, e.g., Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (e.g., different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (e.g., metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

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Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an
5 HA protein, or a portion thereof, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule
encodes an HA protein involved in the production of a fine chemical.
- 10 3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the
group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the
Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does
not consist of any of the F-designated genes set forth in Table 1.
- 15 4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected
from the group consisting of those sequences set forth as even-numbered SEQ ID
NOs of the Sequence Listing, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
- 20 5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant
of a polypeptide selected from the group of amino acid sequences consisting of those
sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,
provided that the nucleic acid molecule does not consist of any of the F-designated
25 genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least
50% homologous to a nucleotide sequence selected from the group consisting of
those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or
30 a portion thereof, provided that the nucleic acid molecule does not consist of any of
the F-designated genes set forth in Table 1.

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7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

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17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
- 5 18. An isolated HA polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical production.
- 10 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 15 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
- 20 by any of the F-designated genes set forth in Table 1.
22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 25 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 30 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those

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sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

- 5 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 10 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 15 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of:
20 *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*,
Corynebacterium acetoacidophilum, *Corynebacterium acetoglutamicum*,
Corynebacterium acetophilum, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
Brevibacterium butanicum, *Brevibacterium divaricatum*, *Brevibacterium flavum*,
25 *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,
Brevibacterium paraffinolyticum, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
- 30 31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

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and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

- 5 32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
10 tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
15
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 440 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing
20 the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
25
37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the
30 Sequence Listing s.

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38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

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                               195                               200                               205

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gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile 90 95 100			403
gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala 105 110 115			451
acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac Thr Glu Ala Thr Val Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp 120 125 130			499
ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr 135 140 145			547
gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala 150 155 160 165			595
gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala 170 175 180			643
gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile 185 190 195			691
ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr 200 205 210			739
gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu 215 220 225			787
ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp 230 235 240 245			835
gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly 250 255 260			883
cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg 265 270 275			931
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<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

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Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser
  35           40           45

Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val
  50           55           60

Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala
  65           70           75           80

Val Arg Leu Pro Tyr Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val
  85           90           95

Ala Leu Glu Phe Ile Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys
 100           105           110

Asp Ala Thr Asp Ala Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu
 115           120           125

Pro Glu Leu Thr Asp Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg
 130           135           140

Met Val Ala Gln Tyr Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile
 145           150           155           160

Gly Thr Asp His Ala Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe
 165           170           175

Gly Asp Gly Ala Ala Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg
 180           185           190

Gln Gly Ala Ala Ile Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp
 195           200           205

Thr Lys Val Pro Thr Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro
 210           215           220

Asp Glu Glu Ala Leu Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu
 225           230           235           240

Glu Asn Lys Pro Asp Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His
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Glu Asn Trp Trp Arg
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 35 40 45

Ile Ser Phe Asp Arg Ser Glu Gly Tyr Gly Phe Arg Leu Asp Ile Pro
 50 55 60

Ser Gly Thr Ala Val Arg Leu Glu Pro Gly Asp Ala Arg Thr Val Asn
 65 70 75 80

Leu Val Ala Ile Gly Gly Asp Arg Ile Val Ala Gly Phe Arg Asp Leu
 85 90 95

Val Asp Gly Pro Leu Glu Asp Leu Lys Val Asn Val Trp Glu Gly Arg
 100 105 110

Glu Asp Gly Trp Arg Arg Ser Ser Ala Ala Gly Asp Ala Pro Gln Glu
 115 120 125

Leu Pro Gln Val Glu Ala Ala Glu Arg Gly Arg Lys Leu Asp Asp Ala
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Thr Asp Val Asp Thr Asn Val Gly Thr Glu Glu Gly Phe Glu Glu Gly
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(220)

<223> FRXA02264

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 Met Ile Pro Gly Glu
 1 5

tac atc ctg tcc agc gaa tca ctc acc gga aat gtt ggg cgc gag gcc 163
 Tyr Ile Leu Ser Ser Glu Ser Leu Thr Gly Asn Val Gly Arg Glu Ala
 10 15 20

aaa acc atc gaa atc atc aac acc ggt gat agg cct gtg cag att ggt 211

aaa gct gac gtt gcg ctt cga gat ggc aaa atc ttc cga atc gga aag	403
Lys Ala Asp Val Ala Leu Arg Asp Gly Lys Ile Phe Arg Ile Gly Lys	
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gcc gga aac ccg aat gtc atg gaa aac gtc gac atc gtc atc ggc gtt	451
Ala Gly Asn Pro Asn Val Met Glu Asn Val Asp Ile Val Ile Gly Val	
105 110 115	
gcc acc gac atc att gct ggt gaa ggc aaa atc ctt acc gca ggt ggc	499
Ala Thr Asp Ile Ile Ala Gly Glu Gly Lys Ile Leu Thr Ala Gly Gly	
120 125 130	
atc gac acg cac gtg cac ttc ttg ggc aca gac cag gtc aac act gca	547
Ile Asp Thr His Val His Phe Leu Gly Thr Asp Gln Val Asn Thr Ala	
135 140 145	
tta gca tca ggt atc acc acg atg atc ggt gga ggc acc ggc cca agc	595
Leu Ala Ser Gly Ile Thr Thr Met Ile Gly Gly Thr Gly Pro Ser	
150 155 160 165	
cag gcg tcg atg gct aca act gtc acg cca ggt cag tgg aat acc tac	643
Gln Ala Ser Met Ala Thr Thr Val Thr Pro Gly Gln Trp Asn Thr Tyr	
170 175 180	
aac atg ctt agt gct ttt gaa ggc atg ccc atg aac ttt ggc att ttg	691
Asn Met Leu Ser Ala Phe Glu Gly Met Pro Met Asn Phe Gly Ile Leu	
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ggt aaa ggc cat ggt tct tcc aaa tct ccg ctg gct gag cag gtt cgt	739
Gly Lys Gly His Gly Ser Ser Lys Ser Pro Leu Ala Glu Gln Val Arg	
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gcg ggt gca atc ggt ctg aaa att cac gag gac tgg ggt gcc aca cca	787
Ala Gly Ala Ile Gly Leu Lys Ile His Glu Asp Trp Gly Ala Thr Pro	
215 220 225	
tcg tcg atc aac act gcc cta gaa gta gcc gat gac atg gac atc cag	835
Ser Ser Ile Asn Thr Ala Leu Glu Val Ala Asp Asp Met Asp Ile Gln	
230 235 240 245	
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Val Ala Leu His Ser Asp Thr Leu Asn Glu Ala Gly Phe Val Glu Asp	
250 255 260	
acc att gaa gcc att gcg ggc cga gtc atc cat acc ttc cac acc gaa	931
Thr Ile Glu Ala Ile Ala Gly Arg Val Ile His Thr Phe His Thr Glu	
265 270 275	
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Gly Ala Gly Gly Gly His Ala Pro Asp Leu Ile Arg Val Ala Ala Leu	
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cca aac gtg ttg cct gca tcc acc aac cca acg ctc cca tac acc cga	1027
Pro Asn Val Leu Pro Ala Ser Thr Asn Pro Thr Leu Pro Tyr Thr Arg	
295 300 305	
aac act gtt gaa gag cac ctg gac atg gtg atg gtt gcc cac cac ctc	1075
Asn Thr Val Glu Glu His Leu Asp Met Val Met Val Ala His His Leu	
310 315 320 325	
aac cca gat att cca gaa gac gtg gct ttt gcg gat tcc cga att cgt	1123

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gcc	gaa	acg	att	gca	gcc	gaa	gat	gtg	ctt	cac	gat	atg	ggt	atc	ttc	1171	
Ala	Glu	Thr	Ile	Ala	Ala	Glu	Asp	Val	Leu	His	Asp	Met	Gly	Ile	Phe		
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tct	atc	acc	tct	tcg	gat	tcc	cag	gcg	atg	ggc	cga	gta	gga	gag	acc	1219	
Ser	Ile	Thr	Ser	Ser	Asp	Ser	Gln	Ala	Met	Gly	Arg	Val	Gly	Glu	Thr		
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atc	acg	cgc	acg	tgg	cag	gtc	gcc	gac	cat	atg	aaa	cgc	acc	cgt	gga	1267	
Ile	Thr	Arg	Thr	Trp	Gln	Val	Ala	Asp	His	Met	Lys	Arg	Thr	Arg	Gly		
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tca	cta	acg	gga	gat	gct	cca	tac	aac	gac	aac	aac	cgc	ttg	cgt	cga	1315	
Ser	Leu	Thr	Gly	Asp	Pro	Tyr	Asn	Asp	Asn	Asn	Arg	Leu	Arg	Arg	Arg		
390					395				400						405		
ttc	atc	gca	aaa	tac	acc	atc	aac	cct	gcg	att	gcg	cac	ggt	gtg	gat	1363	
Phe	Ile	Ala	Lys	Tyr	Thr	Ile	Asn	Pro	Ala	Ile	Ala	His	Gly	Val	Asp		
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Tyr	Val	Val	Arg	Ser	Val	Glu	Glu	Gly	Lys	Phe	Ala	Asp	Leu	Val	Leu		
			425					430					435				
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Trp	Asp	Pro	Lys	Phe	Phe	Gly	Val	Lys	Pro	Asp	Leu	Val	Ile	Lys	Gly		
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ggg	ttg	atg	gtc	aat	tcc	ctc	atg	ggt	gat	tcc	aac	ggt	tcc	att	cca	1507	
Gly	Leu	Met	Val	Asn	Ser	Leu	Met	Gly	Asp	Ser	Asn	Gly	Ser	Ile	Pro		
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Thr	Pro	Gln	Pro	Arg	Thr	Leu	Arg	Asn	Thr	Trp	Gly	Ala	Phe	Gly	Gln		
470					475					480					485		
gca	gtt	tcc	aga	agc	tcc	att	aca	ttc	cta	tcc	cag	gac	gct	atc	gat	1603	
Ala	Val	Ser	Arg	Ser	Ser	Ile	Thr	Phe	Leu	Ser	Gln	Asp	Ala	Ile	Asp		
			490					495					500				
gca	aat	gtt	cct	gat	ctg	ctg	aat	ctg	agg	aag	cag	atc	cgg	ggc	gtt	1651	
Ala	Asn	Val	Pro	Asp	Leu	Leu	Asn	Leu	Arg	Lys	Gln	Ile	Arg	Gly	Val		
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cga	ggt	gta	agg	aat	ctg	acc	aaa	cga	gac	atg	aaa	ctc	aat	gca	gaa	1699	
Arg	Gly	Val	Arg	Asn	Leu	Thr	Lys	Arg	Asp	Met	Lys	Leu	Asn	Ala	Glu		
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atg	cct	gat	att	cgt	gtc	gat	cca	gag	acc	tac	cag	gtg	ttt	gtc	aac	1747	
Met	Pro	Asp	Ile	Arg	Val	Asp	Pro	Glu	Thr	Tyr	Gln	Val	Phe	Val	Asn		
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ggt	gag	ttg	atc	acc	agc	aag	cca	gca	gag	aca	gtg	cca	atg	gca	cgt	1795	
Gly	Glu	Leu	Ile	Thr	Ser	Lys	Pro	Ala	Glu	Thr	Val	Pro	Met	Ala	Arg		
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Arg	Tyr	Phe	Leu	Phe													

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 Gly Lys Val Ile Arg Asp Gly Met Gly Gln Asn Gly Thr Leu Val Arg
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 Asp Val Asp Ile Pro Asp Thr Val Ile Thr Asn Val Ile Val Leu Asp
 65 70 75 80
 Tyr Thr Gly Val Tyr Lys Ala Asp Val Ala Leu Arg Asp Gly Lys Ile
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 Phe Arg Ile Gly Lys Ala Gly Asn Pro Asn Val Met Glu Asn Val Asp
 100 105 110
 Ile Val Ile Gly Val Ala Thr Asp Ile Ile Ala Gly Glu Gly Lys Ile
 115 120 125
 Leu Thr Ala Gly Gly Ile Asp Thr His Val His Phe Leu Gly Thr Asp
 130 135 140
 Gln Val Asn Thr Ala Leu Ala Ser Gly Ile Thr Thr Met Ile Gly Gly
 145 150 155 160
 Gly Thr Gly Pro Ser Gln Ala Ser Met Ala Thr Thr Val Thr Pro Gly
 165 170 175
 Gln Trp Asn Thr Tyr Asn Met Leu Ser Ala Phe Glu Gly Met Pro Met
 180 185 190
 Asn Phe Gly Ile Leu Gly Lys Gly His Gly Ser Ser Lys Ser Pro Leu
 195 200 205
 Ala Glu Gln Val Arg Ala Gly Ala Ile Gly Leu Lys Ile His Glu Asp
 210 215 220
 Trp Gly Ala Thr Pro Ser Ser Ile Asn Thr Ala Leu Glu Val Ala Asp
 225 230 235 240
 Asp Met Asp Ile Gln Val Ala Leu His Ser Asp Thr Leu Asn Glu Ala
 245 250 255
 Gly Phe Val Glu Asp Thr Ile Glu Ala Ile Ala Gly Arg Val Ile His
 260 265 270
 Thr Phe His Thr Glu Gly Ala Gly Gly Gly His Ala Pro Asp Leu Ile

275	280	285
Arg Val Ala Ala Leu Pro Asn Val Leu Pro Ala Ser Thr Asn Pro Thr 290 295 300		
Leu Pro Tyr Thr Arg Asn Thr Val Glu Glu His Leu Asp Met Val Met 305 310 315 320		
Val Ala His His Leu Asn Pro Asp Ile Pro Glu Asp Val Ala Phe Ala 325 330 335		
Asp Ser Arg Ile Arg Ala Glu Thr Ile Ala Ala Glu Asp Val Leu His 340 345 350		
Asp Met Gly Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly 355 360 365		
Arg Val Gly Glu Thr Ile Thr Arg Thr Trp Gln Val Ala Asp His Met 370 375 380		
Lys Arg Thr Arg Gly Ser Leu Thr Gly Asp Ala Pro Tyr Asn Asp Asn 385 390 395 400		
Asn Arg Leu Arg Arg Phe Ile Ala Lys Tyr Thr Ile Asn Pro Ala Ile 405 410 415		
Ala His Gly Val Asp Tyr Val Val Arg Ser Val Glu Glu Gly Lys Phe 420 425 430		
Ala Asp Leu Val Leu Trp Asp Pro Lys Phe Phe Gly Val Lys Pro Asp 435 440 445		
Leu Val Ile Lys Gly Gly Leu Met Val Asn Ser Leu Met Gly Asp Ser 450 455 460		
Asn Gly Ser Ile Pro Thr Pro Gln Pro Arg Thr Leu Arg Asn Thr Trp 465 470 475 480		
Gly Ala Phe Gly Gln Ala Val Ser Arg Ser Ser Ile Thr Phe Leu Ser 485 490 495		
Gln Asp Ala Ile Asp Ala Asn Val Pro Asp Leu Leu Asn Leu Arg Lys 500 505 510		
Gln Ile Arg Gly Val Arg Gly Val Arg Asn Leu Thr Lys Arg Asp Met 515 520 525		
Lys Leu Asn Ala Glu Met Pro Asp Ile Arg Val Asp Pro Glu Thr Tyr 530 535 540		
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<212> DNA

<213> Corynebacterium glutamicum

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 <222> (1)..(1602)
 <223> FRXA02274

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 Arg Asp Gly Met Gly Gln Asn Gly Thr Leu Val Arg Asp Val Asp Ile
 20 25 30
 ccc gat acc gtc atc acc aac gtc atc gtc ctt gac tat acg ggt gtg 144
 Pro Asp Thr Val Ile Thr Asn Val Ile Val Leu Asp Tyr Thr Gly Val
 35 40 45
 tac aaa gct gac gtt gcg ctt cga gat ggc aaa atc ttc cga atc gga 192
 Tyr Lys Ala Asp Val Ala Leu Arg Asp Gly Lys Ile Phe Arg Ile Gly
 50 55 60
 aag gcc gga aac ccg aat gtc atg gaa aac gtc gac atc gtc atc ggc 240
 Lys Ala Gly Asn Pro Asn Val Met Glu Asn Val Asp Ile Val Ile Gly
 65 70 75 80
 gtt gcc acc gac atc att gct ggt gaa ggc aaa atc ctt acc gca ggt 288
 Val Ala Thr Asp Ile Ile Ala Gly Glu Gly Lys Ile Leu Thr Ala Gly
 85 90 95
 ggc atc gac acg cac gtg cac ttc ttg ggc aca gac cag gtc aac act 336
 Gly Ile Asp Thr His Val His Phe Leu Gly Thr Asp Gln Val Asn Thr
 100 105 110
 gca tta gca tca ggt atc acc acg atg atc ggt gga ggc acc ggc cca 384
 Ala Leu Ala Ser Gly Ile Thr Thr Met Ile Gly Gly Gly Thr Gly Pro
 115 120 125
 agc cag gcg tcg atg gct aca act gtc acg cca ggt cag tgg aat acc 432
 Ser Gln Ala Ser Met Ala Thr Thr Val Thr Pro Gly Gln Trp Asn Thr
 130 135 140
 tac aac atg ctt agt gct ttt gaa ggc atg ccc atg aac ttt ggc att 480
 Tyr Asn Met Leu Ser Ala Phe Glu Gly Met Pro Met Asn Phe Gly Ile
 145 150 155 160
 ttg ggt aaa ggc cat ggt tct tcc aaa tct ccg ctg gct gag cag gtt 528
 Leu Gly Lys Gly His Gly Ser Ser Lys Ser Pro Leu Ala Glu Gln Val
 165 170 175
 cgt gcg ggt gca atc ggt ctg aaa att cac gag gac tgg ggt gcc aca 576
 Arg Ala Gly Ala Ile Gly Leu Lys Ile His Glu Asp Trp Gly Ala Thr
 180 185 190
 cca tcg tcg atc aac act gcc cta gaa gta gcc gat gac atg gac atc 624
 Pro Ser Ser Ile Asn Thr Ala Leu Glu Val Ala Asp Asp Met Asp Ile
 195 200 205
 cag gtg gca ctc cac tcc gat acc ttg aat gag gcc ggt ttt gtg gaa 672
 Gln Val Ala Leu His Ser Asp Thr Leu Asn Glu Ala Gly Phe Val Glu

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Glu Gly Ala Gly Gly Gly His Ala Pro Asp Leu Ile Arg Val Ala Ala			
	245	250	255
ctg cca aac gtg ttg cct gca tcc acc aac cca acg ctc cca tac acc			816
Leu Pro Asn Val Leu Pro Ala Ser Thr Asn Pro Thr Leu Pro Tyr Thr			
	260	265	270
cga aac act gtt gaa gag cac ctg gac atg gtg atg gtt gcc cac cac			864
Arg Asn Thr Val Glu Glu His Leu Asp Met Val Met Val Ala His His			
	275	280	285
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Leu Asn Pro Asp Ile Pro Glu Asp Val Ala Phe Ala Asp Ser Arg Ile			
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cgt gcc gaa acg att gca gcc gaa gat gtg ctt cac gat atg ggt atc			960
Arg Ala Glu Thr Ile Ala Ala Glu Asp Val Leu His Asp Met Gly Ile			
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ttc tct atc acc tct tcg gat tcc cag gcg atg ggc cga gta gga gag			1008
Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Val Gly Glu			
	325	330	335
acc atc acg cgc acg tgg cag gtc gcc gac cat atg aaa cgc acc cgt			1056
Thr Ile Thr Arg Thr Trp Gln Val Ala Asp His Met Lys Arg Thr Arg			
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Gly Ser Leu Thr Gly Asp Ala Pro Tyr Asn Asp Asn Asn Arg Leu Arg			
	355	360	365
cga ttc atc gca aaa tac acc atc aac cct gcg att gcg cac ggt gtg			1152
Arg Phe Ile Ala Lys Tyr Thr Ile Asn Pro Ala Ile Ala His Gly Val			
	370	375	380
gat tat gtt gtt cgt tca gtg gag gaa ggc aag ttc gct gac ctc gtg			1200
Asp Tyr Val Val Arg Ser Val Glu Glu Gly Lys Phe Ala Asp Leu Val			
	385	390	395
ctg tgg gat cca aag ttc ttt ggt gtg aaa cct gat ctg gtg atc aag			1248
Leu Trp Asp Pro Lys Phe Phe Gly Val Lys Pro Asp Leu Val Ile Lys			
	405	410	415
ggt ggg ttg atg gtc aat tcc ctc atg ggt gat tcc aac ggt tcc att			1296
Gly Gly Leu Met Val Asn Ser Leu Met Gly Asp Ser Asn Gly Ser Ile			
	420	425	430
cca act ccg cag ccc cgc acc ctg cgc aat act tgg ggt gcg ttt gcc			1344
Pro Thr Pro Gln Pro Arg Thr Leu Arg Asn Thr Trp Gly Ala Phe Gly			
	435	440	445
cag gca gtt tcc aga agc tcc att aca ttc cta tcc cag gac gct atc			1392
Gln Ala Val Ser Arg Ser Ser Ile Thr Phe Leu Ser Gln Asp Ala Ile			
	450	455	460

gat gca aat gtt cct gat ctg ctg aat ctg agg aag cag atc cgg ggc 1440
 Asp Ala Asn Val Pro Asp Leu Leu Asn Leu Arg Lys Gln Ile Arg Gly
 465 470 475 480

gtt cga ggt gta agg aat ctg acc aaa cga gac atg aaa ctc aat gca 1488
 Val Arg Gly Val Arg Asn Leu Thr Lys Arg Asp Met Lys Leu Asn Ala
 485 490 495

gaa atg cct gat att cgt gtc gat cca gag acc tac cag gtg ttt gtc 1536
 Glu Met Pro Asp Ile Arg Val Asp Pro Glu Thr Tyr Gln Val Phe Val
 500 505 510

aac ggt gag ttg atc acc agc aag cca gca gag aca gtg cca atg gca 1584
 Asn Gly Glu Leu Ile Thr Ser Lys Pro Ala Glu Thr Val Pro Met Ala
 515 520 525

cgt cgc tac ttc ttg ttc taatccgccca acaaggaagg aag 1625
 Arg Arg Tyr Phe Leu Phe
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<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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Pro Asp Thr Val Ile Thr Asn Val Ile Val Leu Asp Tyr Thr Gly Val
 35 40 45

Tyr Lys Ala Asp Val Ala Leu Arg Asp Gly Lys Ile Phe Arg Ile Gly
 50 55 60

Lys Ala Gly Asn Pro Asn Val Met Glu Asn Val Asp Ile Val Ile Gly
 65 70 75 80

Val Ala Thr Asp Ile Ile Ala Gly Glu Gly Lys Ile Leu Thr Ala Gly
 85 90 95

Gly Ile Asp Thr His Val His Phe Leu Gly Thr Asp Gln Val Asn Thr
 100 105 110

Ala Leu Ala Ser Gly Ile Thr Thr Met Ile Gly Gly Gly Thr Gly Pro
 115 120 125

Ser Gln Ala Ser Met Ala Thr Thr Val Thr Pro Gly Gln Trp Asn Thr
 130 135 140

Tyr Asn Met Leu Ser Ala Phe Glu Gly Met Pro Met Asn Phe Gly Ile
 145 150 155 160

Leu Gly Lys Gly His Gly Ser Ser Lys Ser Pro Leu Ala Glu Gln Val
 165 170 175

Arg Ala Gly Ala Ile Gly Leu Lys Ile His Glu Asp Trp Gly Ala Thr
 180 185 190
 Pro Ser Ser Ile Asn Thr Ala Leu Glu Val Ala Asp Asp Met Asp Ile
 195 200 205
 Gln Val Ala Leu His Ser Asp Thr Leu Asn Glu Ala Gly Phe Val Glu
 210 215 220
 Asp Thr Ile Glu Ala Ile Ala Gly Arg Val Ile His Thr Phe His Thr
 225 230 235 240
 Glu Gly Ala Gly Gly Gly His Ala Pro Asp Leu Ile Arg Val Ala Ala
 245 250 255
 Leu Pro Asn Val Leu Pro Ala Ser Thr Asn Pro Thr Leu Pro Tyr Thr
 260 265 270
 Arg Asn Thr Val Glu Glu His Leu Asp Met Val Met Val Ala His His
 275 280 285
 Leu Asn Pro Asp Ile Pro Glu Asp Val Ala Phe Ala Asp Ser Arg Ile
 290 295 300
 Arg Ala Glu Thr Ile Ala Ala Glu Asp Val Leu His Asp Met Gly Ile
 305 310 315 320
 Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Val Gly Glu
 325 330 335
 Thr Ile Thr Arg Thr Trp Gln Val Ala Asp His Met Lys Arg Thr Arg
 340 345 350
 Gly Ser Leu Thr Gly Asp Ala Pro Tyr Asn Asp Asn Asn Arg Leu Arg
 355 360 365
 Arg Phe Ile Ala Lys Tyr Thr Ile Asn Pro Ala Ile Ala His Gly Val
 370 375 380
 Asp Tyr Val Val Arg Ser Val Glu Glu Gly Lys Phe Ala Asp Leu Val
 385 390 395 400
 Leu Trp Asp Pro Lys Phe Phe Gly Val Lys Pro Asp Leu Val Ile Lys
 405 410 415
 Gly Gly Leu Met Val Asn Ser Leu Met Gly Asp Ser Asn Gly Ser Ile
 420 425 430
 Pro Thr Pro Gln Pro Arg Thr Leu Arg Asn Thr Trp Gly Ala Phe Gly
 435 440 445
 Gln Ala Val Ser Arg Ser Ser Ile Thr Phe Leu Ser Gln Asp Ala Ile
 450 455 460
 Asp Ala Asn Val Pro Asp Leu Leu Asn Leu Arg Lys Gln Ile Arg Gly
 465 470 475 480
 Val Arg Gly Val Arg Asn Leu Thr Lys Arg Asp Met Lys Leu Asn Ala
 485 490 495
 Glu Met Pro Asp Ile Arg Val Asp Pro Glu Thr Tyr Gln Val Phe Val

500

505

510

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Arg Arg Tyr Phe Leu Phe
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<220>
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 <223> RXA02265

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 Leu His Ile Thr Pro
 1 5
 cgt gaa caa gaa aaa ctg atg atc gtg gtg gcg gct gac ctt gca cgt 163
 Arg Glu Gln Glu Lys Leu Met Ile Val Val Ala Ala Asp Leu Ala Arg
 10 15 20
 cgc cgt aaa gat cgc ggc cta aaa ctt aac cac cca gag gcc gtc gcc 211
 Arg Arg Lys Asp Arg Gly Leu Lys Leu Asn His Pro Glu Ala Val Ala
 25 30 35
 ctc atc acg tat gaa ctg att gaa ggc gcc cgt gac gga cgc aca gtc 259
 Leu Ile Thr Tyr Glu Leu Ile Glu Gly Ala Arg Asp Gly Arg Thr Val
 40 45 50
 gca gac ctt atg agc tgg gga agc acc att ttg act agg gat gat gtc 307
 Ala Asp Leu Met Ser Trp Gly Ser Thr Ile Leu Thr Arg Asp Asp Val
 55 60 65
 tta gaa ggc atc cca gag atg atc cct gac atc cag gtt gaa gca acg 355
 Leu Glu Gly Ile Pro Glu Met Ile Pro Asp Ile Gln Val Glu Ala Thr
 70 75 80 85
 ttt gat gac ggc acc aag ctc gtc acc gtg cac aat ccc atc cga 400
 Phe Asp Asp Gly Thr Lys Leu Val Thr Val His Asn Pro Ile Arg
 90 95 100
 taacccttga tggttttagg agt 423

<210> 18
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 <213> Corynebacterium glutamicum

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Met Thr Gln Thr Gln																		
1 5																		
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Pro Val Gly Thr Leu Arg Leu Thr Ile Asp Asp Gln Gly Pro Gln Gly																		
10 15 20																		
caa agc cgt gcg gtg gag caa ttt cac cag ggt gcg ctt cga gtc atc																		211
Gln Ser Arg Ala Val Glu Gln Phe His Gln Gly Ala Leu Arg Val Ile																		
25 30 35																		
cgg cca cac tac ttg gat gat tcc gga cag gtt tgc tac acc atc att																		259
Arg Pro His Tyr Leu Asp Asp Ser Gly Gln Val Cys Tyr Thr Ile Ile																		
40 45 50																		
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Ala Ile Gly Gly Gly Tyr Leu Gly Gly Asp Val Tyr Glu Gln Gln Phe																		
55 60 65																		
acg atc aaa gac aac gca aaa gct ttg atc acc acg caa tcg gcc acc																		355
Thr Ile Lys Asp Asn Ala Lys Ala Leu Ile Thr Thr Gln Ser Ala Thr																		
70 75 80 85																		
aag att tat cgc aca ccg caa gga cca gcc acg cag cac acc gaa atc																		403
Lys Ile Tyr Arg Thr Pro Gln Gly Pro Ala Thr Gln His Thr Glu Ile																		
90 95 100																		

aac gtc ggt gaa aat gct gtg ctg gaa tac ttg gcg gat caa acc atc 451
 Asn Val Gly Glu Asn Ala Val Leu Glu Tyr Leu Ala Asp Gln Thr Ile
 105 110 115
 gcg tac cgg gag gcc acc tat cat caa ttc acc aag gtg gcg ctg cac 499
 Ala Tyr Arg Glu Ala Thr Tyr His Gln Phe Thr Lys Val Ala Leu His
 120 125 130
 ccg agc gca acg ttt gtg atg agc gaa caa atc acc cca ggc tgg cac 547
 Pro Ser Ala Thr Phe Val Met Ser Glu Gln Ile Thr Pro Gly Trp His
 135 140 145
 ccc gac ggc aaa cac ttt gct tac gat gaa atg cgt cta cac acc gaa 595
 Pro Asp Gly Lys His Phe Ala Tyr Asp Glu Met Arg Leu His Thr Glu
 150 155 160 165
 atc acg gac tcc acc aca ggg cga ctc gtg ctc ttg gat aat tta ctg 643
 Ile Thr Asp Ser Thr Thr Gly Arg Leu Val Leu Leu Asp Asn Leu Leu
 170 175 180
 ctc cgg ccg gac tcc cga gag gga agt ttt ggg tgg acg gaa cag tac 691
 Leu Arg Pro Asp Ser Arg Glu Gly Ser Phe Gly Trp Thr Glu Gln Tyr
 185 190 195
 aca cat tca ggg cag atg att gtg atg ggg gaa ggc gtc gat aag cag 739
 Thr His Ser Gly Gln Met Ile Val Met Gly Glu Gly Val Asp Lys Gln
 200 205 210
 ctt gtt gct gag ctg aat gag caa ctt gcc gcg cac cct gat gtg tac 787
 Leu Val Ala Glu Leu Asn Glu Gln Leu Ala Ala His Pro Asp Val Tyr
 215 220 225
 ggc gcc gtc aat ttc tta agc gcg ccg ggc acg tta ctg cgc gga ttt 835
 Gly Ala Val Asn Phe Leu Ser Ala Pro Gly Thr Leu Leu Arg Gly Phe
 230 235 240 245
 att gcg cgc acg ctg agc aac cgc act gag gag ttg att aac ctg cac 883
 Ile Ala Arg Thr Leu Ser Asn Arg Thr Glu Glu Leu Ile Asn Leu His
 250 255 260
 gaa cac att gcg tcg ctg ttg cgc ggg cgg tgg cgc ggg cag gaa ccg 931
 Glu His Ile Ala Ser Leu Leu Arg Gly Arg Trp Arg Gly Gln Glu Pro
 265 270 275
 gtg aat ttg cgg aag tac tagacggcgt cgagaaatcg aag 972
 Val Asn Leu Arg Lys Tyr
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<210> 20

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

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Ala Leu Arg Val Ile Arg Pro His Tyr Leu Asp Asp Ser Gly Gln Val
 35 40 45
 Cys Tyr Thr Ile Ile Ala Ile Gly Gly Gly Tyr Leu Gly Gly Asp Val
 50 55 60
 Tyr Glu Gln Gln Phe Thr Ile Lys Asp Asn Ala Lys Ala Leu Ile Thr
 65 70 75 80
 Thr Gln Ser Ala Thr Lys Ile Tyr Arg Thr Pro Gln Gly Pro Ala Thr
 85 90 95
 Gln His Thr Glu Ile Asn Val Gly Glu Asn Ala Val Leu Glu Tyr Leu
 100 105 110
 Ala Asp Gln Thr Ile Ala Tyr Arg Glu Ala Thr Tyr His Gln Phe Thr
 115 120 125
 Lys Val Ala Leu His Pro Ser Ala Thr Phe Val Met Ser Glu Gln Ile
 130 135 140
 Thr Pro Gly Trp His Pro Asp Gly Lys His Phe Ala Tyr Asp Glu Met
 145 150 155 160
 Arg Leu His Thr Glu Ile Thr Asp Ser Thr Thr Gly Arg Leu Val Leu
 165 170 175
 Leu Asp Asn Leu Leu Leu Arg Pro Asp Ser Arg Glu Gly Ser Phe Gly
 180 185 190
 Trp Thr Glu Gln Tyr Thr His Ser Gly Gln Met Ile Val Met Gly Glu
 195 200 205
 Gly Val Asp Lys Gln Leu Val Ala Glu Leu Asn Glu Gln Leu Ala Ala
 210 215 220
 His Pro Asp Val Tyr Gly Ala Val Asn Phe Leu Ser Ala Pro Gly Thr
 225 230 235 240
 Leu Leu Arg Gly Phe Ile Ala Arg Thr Leu Ser Asn Arg Thr Glu Glu
 245 250 255
 Leu Ile Asn Leu His Glu His Ile Ala Ser Leu Leu Arg Gly Arg Trp
 260 265 270
 Arg Gly Gln Glu Pro Val Asn Leu Arg Lys Tyr
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<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(571)

<223> RXA02275

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Met Ile Ile Thr Ala
1 5

atc gac acc aac atc tac gat gaa ccg gag ttt gtt gaa gga cgc gat 163
Ile Asp Thr Asn Ile Tyr Asp Glu Pro Glu Phe Val Glu Gly Arg Asp
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gtc atc ggt gtg cgc ttt gaa gat tta gtt ttg gat aag cgc att caa 211
Val Ile Gly Val Arg Phe Glu Asp Leu Val Leu Asp Lys Arg Ile Gln
25 30 35

cgg gtt gca ctc ccc gga gga gaa gaa ctg ggg ttg cgg tta aac cac 259
Arg Val Ala Leu Pro Gly Gly Glu Glu Leu Gly Leu Arg Leu Asn His
40 45 50

ggg cat ccg att ctg cgt gaa ggt gat gtg ttg aaa gct gat gat aag 307
Gly His Pro Ile Leu Arg Glu Gly Asp Val Leu Lys Ala Asp Asp Lys
55 60 65

acg gta ttt gtg gtg gag att atc ccc acg gat gtt tta gtt atc acg 355
Thr Val Phe Val Val Glu Ile Ile Pro Thr Asp Val Leu Val Ile Thr
70 75 80 85

cca agc gat att cac cag atg gga ttt gtg gcg cac tcc ctg gga aac 403
Pro Ser Asp Ile His Gln Met Gly Phe Val Ala His Ser Leu Gly Asn
90 95 100

agg cac ctg cca gca cag ttt tcc aag cca ggt gaa ttg aca gag aag 451
Arg His Leu Pro Ala Gln Phe Ser Lys Pro Gly Glu Leu Thr Glu Lys
105 110 115

gca gcc atg atc gtg caa tac gat cac acg gtg gtc agc ttc ttg gat 499
Ala Ala Met Ile Val Gln Tyr Asp His Thr Val Val Ser Phe Leu Asp
120 125 130

gag cac ggc atc gag tat cag cgc acc gaa ctt gtt ccg cca att cct 547
Glu His Gly Ile Glu Tyr Gln Arg Thr Glu Leu Val Pro Pro Ile Pro
135 140 145

ttc agg cat agc ggg cac aca cat tgatggatct tgacgctgat ttt 594
Phe Arg His Ser Gly His Thr His
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<210> 22

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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20 25 30

Asp Lys Arg Ile Gln Arg Val Ala Leu Pro Gly Gly Glu Glu Leu Gly
35 40 45

Leu Arg Leu Asn His Gly His Pro Ile Leu Arg Glu Gly Asp Val Leu
 50 55 60
 Lys Ala Asp Asp Lys Thr Val Phe Val Val Glu Ile Ile Pro Thr Asp
 65 70 75 80
 Val Leu Val Ile Thr Pro Ser Asp Ile His Gln Met Gly Phe Val Ala
 85 90 95
 His Ser Leu Gly Asn Arg His Leu Pro Ala Gln Phe Ser Lys Pro Gly
 100 105 110
 Glu Leu Thr Glu Lys Ala Ala Met Ile Val Gln Tyr Asp His Thr Val
 115 120 125
 Val Ser Phe Leu Asp Glu His Gly Ile Glu Tyr Gln Arg Thr Glu Leu
 130 135 140
 Val Pro Pro Ile Pro Phe Arg His Ser Gly His Thr His
 145 150 155

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(778)
 <223> RXA02276

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 ttccgccaat tcctttcagg catagcgggc acacacattg atg gat ctt gac gct 115
 Met Asp Leu Asp Ala
 1 5
 gat ttt ctg ctg ttg cat tta tcg gat tca gca ctt cca acg gga gcg 163
 Asp Phe Leu Leu Leu His Leu Ser Asp Ser Ala Leu Pro Thr Gly Ala
 10 15 20
 ttt gcg cac tca ttt gga ttt gaa act tat atg gat gca gag cga atc 211
 Phe Ala His Ser Phe Gly Phe Glu Thr Tyr Met Asp Ala Glu Arg Ile
 25 30 35
 acc aat gca gag gag ttc caa gac tgg ctg aaa gtc ctg ctt aag gtg 259
 Thr Asn Ala Glu Glu Phe Gln Asp Trp Leu Lys Val Leu Leu Lys Val
 40 45 50
 caa ttg acc agc tct gat gct ttg gca atg agg atg ttt tac gcc acc 307
 Gln Leu Thr Ser Ser Asp Ala Leu Ala Met Arg Met Phe Tyr Ala Thr
 55 60 65
 ccg acg gtg tct gag ctg aaa cgg ctg gat gag cgc ctt ttt gct gga 355
 Pro Thr Val Ser Glu Leu Lys Arg Leu Asp Glu Arg Leu Phe Ala Gly
 70 75 80 85
 act ccg gcg aga gaa att cgg gaa gct aat gct cga atg ggt acg cgc 403
 Thr Pro Ala Arg Glu Ile Arg Glu Ala Asn Ala Arg Met Gly Thr Arg

	90	95	100	
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Met Ala Glu Ile Val Ala Glu Thr Tyr Ser Val Pro Leu Ile Val Glu				
	105	110	115	
tat ctc gaa ttg att caa cat cga gag cta tca ggg cac ccg gct ttg				499
Tyr Leu Glu Leu Ile Gln His Arg Glu Leu Ser Gly His Pro Ala Leu				
	120	125	130	
gct ttg gct ctt gcc acc cac agc gcg ggg att gat gtg gat cga gca				547
Ala Leu Ala Leu Ala Thr His Ser Ala Gly Ile Asp Val Asp Arg Ala				
	135	140	145	
atc cac gct cac ctc acg gca acg gtg agt tcg ctg atc caa aat gcg				595
Ile His Ala His Leu Thr Ala Thr Val Ser Ser Leu Ile Gln Asn Ala				
	150	155	160	165
gtt cgt ggc atc cca ctg ggg caa atg gca ggt cag cgg gtg atg ttc				643
Val Arg Gly Ile Pro Leu Gly Gln Met Ala Gly Gln Arg Val Met Phe				
	170	175	180	
gcc atg cgt gag cat atc ggt gcg gcc gtg aaa cgt agc gcg aac ttg				691
Ala Met Arg Glu His Ile Gly Ala Ala Val Lys Arg Ser Ala Asn Leu				
	185	190	195	
gat gag att gat ttc tgt tcg ggt gat cca ggc ttg gat att tca caa				739
Asp Glu Ile Asp Phe Cys Ser Gly Asp Pro Gly Leu Asp Ile Ser Gln				
	200	205	210	
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Met Val His Glu Thr Gln Arg Ala Arg Leu Phe Met Ser				
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<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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Leu	Pro	Thr	Gly	Ala	Phe	Ala	His	Ser	Phe	Gly	Phe	Glu	Thr	Tyr	Met
			20					25						30	

Asp	Ala	Glu	Arg	Ile	Thr	Asn	Ala	Glu	Glu	Phe	Gln	Asp	Trp	Leu	Lys
	35						40					45			

Val	Leu	Leu	Lys	Val	Gln	Leu	Thr	Ser	Ser	Asp	Ala	Leu	Ala	Met	Arg
	50					55					60				

Met	Phe	Tyr	Ala	Thr	Pro	Thr	Val	Ser	Glu	Leu	Lys	Arg	Leu	Asp	Glu
	65					70				75					80

Arg	Leu	Phe	Ala	Gly	Thr	Pro	Ala	Arg	Glu	Ile	Arg	Glu	Ala	Asn	Ala
				85					90					95	

Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala Ile Tyr Ser Val Ala
 200 205 210

tgg gat ttg gag caa gcg caa gat tat cgc tct gat att cat gct cgt 787
 Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser Asp Ile His Ala Arg
 215 220 225

gcc act gcc cag ggt cgc gag ccc atg ccg gtg ctt cct ggt ttg gtg 835
 Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val Leu Pro Gly Leu Val
 230 235 240 245

act ttt gtt ggc acg acc gtg gaa gaa gcg cgt gca aaa cag cag gct 883
 Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg Ala Lys Gln Gln Ala
 250 255 260

ctt aat gcg ttg ctg ccg gtc aaa gac tca cta aat cag ttg agt ttc 931
 Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu Asn Gln Leu Ser Phe
 265 270 275

ttt gtg ggt caa gat tgc tcg acg tgg gat ttg gat gca cct ccc cca 979
 Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu Asp Ala Pro Pro Pro
 280 285 290

cca ctg cca ccg cta gaa gag ttt tcc ggt cct aaa ggc agg tac gaa 1027
 Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro Lys Gly Arg Tyr Glu
 295 300 305

acg gtc ctg cgg 1039
 Thr Val Leu Arg
 310

<210> 440

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

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 20 25 30

Asp Gly Gln Ala Ile Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp
 35 40 45

Phe Leu Glu Pro Val Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn
 50 55 60

Asn Ile Gly Leu Ile Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe
 65 70 75 80

His Ala Ala Arg Met Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg
 85 90 95

Ala Gly Ile Asn Val Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn
 100 105 110

His Gly Met Asp Ala Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala
 115 120 125

Ala Glu Phe Ile Glu Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala
 130 135 140

Glu Ser Leu Val Met Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu
 145 150 155 160

Ile Lys Ser Ile Asp His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro
 165 170 175

Leu Asn Ile Pro Ser Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala
 180 185 190

Gly Ser Ser Pro Gln Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala
 195 200 205

Phe Tyr Ser Val Ala Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser
 210 215 220

Asp Ile His Ala Arg Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val
 225 230 235 240

Leu Pro Gly Leu Val Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg
 245 250 255

Ala Lys Gln Gln Ala Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu
 260 265 270

Asn Gln Leu Ser Phe Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu
 275 280 285

Asp Ala Pro Pro Pro Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro
 290 295 300

Lys Gly Arg Tyr Glu Thr Val Leu Arg
 305 310

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Ile Phe Val Glu Ser Gly Gly Asp Asn Leu Ser Ala Thr Phe Ser Pro
 100 105 110

Glu Leu Val Asp Phe Ser Ile Tyr Ile Ile Asp Val Ala Gln Gly Glu
 115 120 125

Lys Ile Pro Arg Lys Ala Gly Gln Gly Met Ile Lys Ser Asp Leu Phe
 130 135 140

Ile Ile Asn Lys Thr Asp Leu Ala Pro Tyr Val Gly Ala Asn Leu Asp
 145 150 155 160

Val Met Val Glu Asp Ala Lys Ala Phe Arg Lys Asn Lys Pro Phe Cys
 165 170 175

Leu Thr Asn Leu Arg Thr Asp Asp Gly Leu Asp Lys Val Leu Glu Trp
 180 185 190

Ile Arg His Glu Val Met Met Gln Asp Leu Gln Glu Ala
 195 200 205

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 <211> 1119
 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA02603

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 Val Ser Glu His Ala
 1 5

gct gaa cat cac cgc gat acc caa aat ttc tta acc tcc gaa ccg cac 163
 Ala Glu His His Arg Asp Thr Gln Asn Phe Leu Thr Ser Glu Pro His
 10 15 20

acc acg gca atc gaa gac aac aag aag cgc caa ccg ccg aaa aac ctt 211
 Thr Thr Ala Ile Glu Asp Asn Lys Lys Arg Gln Pro Pro Lys Asn Leu
 25 30 35

gct gac ggc atg atc aag gcg ctg cgc ccc aag cag tgg gtc aag aac 259
 Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys Gln Trp Val Lys Asn
 40 45 50

gtt ctt gtg cta gca gca cca ctt gct gct ggt gca gat gcg atc ttc 307
 Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly Ala Asp Ala Ile Phe
 55 60 65

aac cag cgc acg atc atc gac gtt gct atc gca ttc gta gtg ttc tgc 355
 Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala Phe Val Val Phe Cys
 70 75 80 85

ttc ggt gca tca gcc att tac ttg gtt aat gat gcc cgt gac gtg gaa 403
 Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp Ala Arg Asp Val Glu

90	95	100	
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cta tcc atc gga ctg tct ttc ctc gcc acc gac ggc gtg gca ctt gcc Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp Gly Val Ala Leu Ala 135 140 145			547
tgc gtg att ggc gtg tac att gcg ctg cag ctg gga tac tgc ttc ggt Cys Val Ile Gly Val Tyr Ile Ala Leu Gln Leu Gly Tyr Cys Phe Gly 150 155 160 165			595
tgg aag cac atg cca gtg atc gat att gcg ctt gtc tcc tcc gga ttc Trp Lys His Met Pro Val Ile Asp Ile Ala Leu Val Ser Ser Gly Phe 170 175 180			643
atg ctc cgc gca atg gca ggt ggt gtc gca gca ggc atc gag cta tcc Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala Gly Ile Glu Leu Ser 185 190 195			691
cag tgg ttc ctg cta gtc gct gcg ttt ggt tcc ctg ttc atg gca tct Gln Trp Phe Leu Leu Val Ala Ala Phe Gly Ser Leu Phe Met Ala Ser 200 205 210			739
gga aag cgc tac gca gaa atc ctt ctg cac gag cgc acc ggc gct aag Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu Arg Thr Gly Ala Lys 215 220 225			787
atc cgc aag tcc ctg gaa agc tac acc ccc acc tac ctg cgc ttc gtt Ile Arg Lys Ser Leu Glu Ser Tyr Thr Pro Thr Tyr Leu Arg Phe Val 230 235 240 245			835
tgg acc atg gca gca aca gca gtg gtc atg tcc tac gca ctg tgg ggc Trp Thr Met Ala Ala Thr Ala Val Val Met Ser Tyr Ala Leu Trp Gly 250 255 260			883
ttc gac ctt tcc caa cac tcc acc gac gca ggt ccg tgg tac caa atc Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly Pro Trp Tyr Gln Ile 265 270 275			931
tcc atg gtt cca ttc acc atc gcc atc ctg cgc tac gca gcc ggc gta Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg Tyr Ala Ala Gly Val 280 285 290			979
gac acc ggc gac ggc ggt gcc cct gac gaa gtg gca ctc agc gac aaa Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val Ala Leu Ser Asp Lys 295 300 305			1027
gtt ctg cag gta cta gcc cta gca tgg gtt ttc tgc atc gtg atg gct Val Leu Gln Val Leu Ala Leu Ala Trp Val Phe Cys Ile Val Met Ala 310 315 320 325			1075
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<210> 28

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 28

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 Pro Pro Lys Asn Leu Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys
 35 40 45
 Gln Trp Val Lys Asn Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly
 50 55 60
 Ala Asp Ala Ile Phe Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala
 65 70 75 80
 Phe Val Val Phe Cys Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp
 85 90 95
 Ala Arg Asp Val Glu Ala Asp Arg Glu His Pro Thr Lys Arg Phe Arg
 100 105 110
 Pro Ile Ala Ala Gly Val Leu Pro Val Gly Met Ala Tyr Gly Met Ala
 115 120 125
 Val Ala Leu Ile Ala Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp
 130 135 140
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 Gly Tyr Cys Phe Gly Trp Lys His Met Pro Val Ile Asp Ile Ala Leu
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 Val Ser Ser Gly Phe Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala
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 Leu Phe Met Ala Ser Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu
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 Tyr Ala Leu Trp Gly Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly
 260 265 270
 Pro Trp Tyr Gln Ile Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg
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Tyr Ala Ala Gly Val Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val
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<211> 2004

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<222> (101)..(1981)

<223> RXA01385

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Lys Ser Leu Gly Tyr Arg Leu Gln Gly Lys Gln Ala Asn His Ala Trp	
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Gly Val Met Asp Ile His Ala Asn Thr Glu Phe Pro Asp Val Arg Lys	
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Lys Cys Thr Ile Lys Ser Asp Ser Gly Arg Thr Ile Leu Leu Ile Pro	
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Pro Asp Asp Gly Ser Lys Ala Val Arg Asp Thr Pro Leu Gln Asp Val	
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gat gca ctt aac ggc gag ggt tct gag cta gac cgc tgg gca gaa tgg Asp Ala Leu Asn Gly Glu Gly Ser Glu Leu Asp Arg Trp Ala Glu Trp 505 510 515			1651
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2004

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<400> 30

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Met	Asp	Val	Leu	Ile	Val	Gly	Ala	Gly	Pro	Ala	Gly	Thr	Ile	Ala	Ala
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Thr	Ile	Glu	Thr	Phe	Gln	Ala	Phe	Gly	Phe	Ala	His	Glu	Ile	Leu	Ala
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Glu	Ala	His	Glu	Ile	Thr	Asp	Met	Ala	Phe	Trp	Lys	Pro	Asp	Pro	Gln
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Pro	Asp	Val	Arg	Lys	Lys	Cys	Thr	Ile	Lys	Ser	Asp	Ser	Gly	Arg	Thr
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 Pro Leu Gln Asp Val Ile Asp Thr Ala Asn Gln Ile Met Ala Pro Phe
 290 295 300
 Thr Leu Asp Val Lys Asn Val Val Trp Asn Ser Ile Tyr Glu Val Gly
 305 310 315 320
 His Arg Val Ala Asp His Phe Asp Asp Arg Val Ser Glu Lys Thr Ser
 325 330 335
 Ser Glu His Pro Arg Ile Phe Ile Ala Gly Asp Ala Cys His Thr His
 340 345 350
 Ser Ala Lys Ala Gly Gln Gly Met Asn Val Ser Met Gln Asp Gly Phe
 355 360 365
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 370 375 380
 Glu Leu Leu Gln Thr Tyr Ala Glu Glu Arg Glu Asp Ile Ala Tyr Lys
 385 390 395 400
 Leu Ile Glu Tyr Asp Lys Asn Trp Ser Thr Leu Met Ala Lys Pro Ser
 405 410 415
 Ser Glu Met Gly Ser Ala Gln Asp Leu Glu Asp Phe Tyr Arg Ala Asn
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 Ser Glu Phe Asn Ala Gly Tyr Met Thr His Tyr Pro Pro Ser Ser Ile
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 Thr Met Asp Gly Ser Asn Gln Asp Leu Ala Lys Gly Tyr Pro Ile Gly
 450 455 460
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 465 470 475 480
 Thr His Leu Gly His Gln Ala Thr Ala Asp Gly Arg Met Arg Ala Tyr
 485 490 495
 Val Phe Ala Gly Ser Asp Ala Leu Asn Gly Glu Gly Ser Glu Leu Asp
 500 505 510
 Arg Trp Ala Glu Trp Ala Glu Ala Asn Leu Asp Pro Thr Leu Val Asp
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 Ala Lys Val Ile Tyr Gln Ser Pro Tyr Thr Glu Leu Asp Thr Arg Gln
 530 535 540
 Val Pro Ser Val Phe Lys Pro Ala Val Gly Ile Phe Glu Leu Thr Asn
 545 550 555 560
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 565 570 575
 Arg Glu Ile Ser Arg Asp Gly Val Val Val Val Val Arg Pro Asp Gln
 580 585 590
 Tyr Val Ser Gly Ile Phe Pro Leu Thr Asp Thr Gln Gly Leu Gly Glu

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600

605

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 Met Gly Phe Arg Ser
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 Gln Ala Ala Gly Glu Ile Val Gly Lys Ala Leu Gln Ala Val Arg Ala
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 Glu Ala Lys Ala Gly Met Ser Thr Trp Asp Leu Asp Gln Ile Ala Glu
 40 45 50
 cag gtt atc cgc gat gct ggc gcc gtt cct aca ttc ctg ggt tac cag 307
 Gln Val Ile Arg Asp Ala Gly Ala Val Pro Thr Phe Leu Gly Tyr Gln
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 Gly Phe Pro Ala Ser Val Cys Ala Ser Val Asn Glu Val Ile Val His
 70 75 80 85
 ggc att cca tcc aag gag acc atc ttg gag gaa ggc gat ctg gtg tcc 403
 Gly Ile Pro Ser Lys Glu Thr Ile Leu Glu Glu Gly Asp Leu Val Ser
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 Ile Asp Cys Gly Ala Thr Phe Asp Gly Trp Val Gly Asp Ser Ala Trp
 105 110 115
 agc ttc ggc atc ggc gag ctg gac gag gac gtc cag ggt ctc aac ttg 499
 Ser Phe Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu
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 gct acc gag tgg gtc ctc atg gaa ggc atg aag gcc atg gtt cca ggc 547
 Ala Thr Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly
 135 140 145

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 Asn Arg Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys
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 gct gag tcc aag ttc ggc gtc gcg ctc ggc atc gtc gat ggc tac ggc 643
 Ala Glu Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly
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 gga cac ggc att ggc cgc cac atg cac gag gag cca tac ttg gct aat 691
 Gly His Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn
 185 190 195
 gag ggc aag gcc ggc aag ggc cct gtg att cag gag ggc tcc gtg ctc 739
 Glu Gly Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu
 200 205 210
 gcc att gag cct atg ctc acc ctc ggc acc gaa gat tcc gca gtg ctg 787
 Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu
 215 220 225
 gaa gat gat tgg act gtc gtg act ctc gac ggt tca tgg gca tca cac 835
 Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His
 230 235 240 245
 tgg gag cac acc gtt gca gcc acc aag ggc ggc ccg cgc atc ctc acg 883
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<212> PRT

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 50 55 60
 Phe Leu Gly Tyr Gln Gly Phe Pro Ala Ser Val Cys Ala Ser Val Asn
 65 70 75 80
 Glu Val Ile Val His Gly Ile Pro Ser Lys Glu Thr Ile Leu Glu Glu
 85 90 95
 Gly Asp Leu Val Ser Ile Asp Cys Gly Ala Thr Phe Asp Gly Trp Val
 100 105 110

Gly Asp Ser Ala Trp Ser Phe Gly Ile Gly Glu Leu Asp Glu Asp Val
 115 120 125
 Gln Gly Leu Asn Leu Ala Thr Glu Trp Val Leu Met Glu Gly Met Lys
 130 135 140
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 165 170 175
 Val Asp Gly Tyr Gly Gly His Gly Ile Gly Arg His Met His Glu Glu
 180 185 190
 Pro Tyr Leu Ala Asn Glu Gly Lys Ala Gly Lys Gly Pro Val Ile Gln
 195 200 205
 Glu Gly Ser Val Leu Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu
 210 215 220
 Asp Ser Ala Val Leu Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly
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 Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly Asn Arg
 35 40 45
 ttg acc gat gtc tcc cac gct ctc gag gtc gca acc cgc aag gct gag 192
 Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys Ala Glu
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 Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly Gly His
 65 70 75 80

ggc att ggc cgc cac atg cac gag gag cca tac ttg gct aat gag ggc 288
 Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn Glu Gly
 85 90 95

 aag gcc ggc aag ggc cct gtg att cag gag ggc tcc gtg ctc gcc att 336
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 100 105 110

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 Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
 115 120 125

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 130 135 140

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 35 40 45

 Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys Ala Glu
 50 55 60

 Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly Gly His
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 Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn Glu Gly
 85 90 95

 Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu Ala Ile
 100 105 110

 Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
 115 120 125

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 130 135 140

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Tyr

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Ala	Pro	Leu	Val	Pro	Gly	Ile	Pro	Thr	Pro	Ile	Arg	Glu	Val	Pro	Ala	20
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His	Ile	Glu	Arg	Pro	Glu	Tyr	Val	Trp	Lys	Asp	Glu	Val	Gln	Glu	Ala	35
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Tyr	Thr	Cys	Asp	Met	Gly	Ala	Tyr	Pro	Ser	Asp	Leu	Gly	Tyr	Arg	Gly	90
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Leu	Ala	Gly	Asp	Val	Ser	Glu	Glu	His	Arg	Leu	Leu	Val	Glu	Arg	Thr	150

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 170 175 180

atc aac gtc att ggg cgt gtc att gag tct tac gcc aag cgt ttt ggc 691
 Ile Asn Val Ile Gly Arg Val Ile Glu Ser Tyr Ala Lys Arg Phe Gly
 185 190 195

tac aac gtg gtc cgc gat ttc acc gga cac ggc atc ggc cca act ttc 739
 Tyr Asn Val Val Arg Asp Phe Thr Gly His Gly Ile Gly Pro Thr Phe
 200 205 210

cac aac ggc ctt gtg gtg ctg cac tac gac aac act cag tac cgc gat 787
 His Asn Gly Leu Val Val Leu His Tyr Asp Asn Thr Gln Tyr Arg Asp
 215 220 225

ctg ctc gtg cca ggc atg acc ttg acc atc gag cca atg atc aac ctt 835
 Leu Leu Val Pro Gly Met Thr Leu Thr Ile Glu Pro Met Ile Asn Leu
 230 235 240 245

ggt tcc ctc gac tac gag atc tgg gaa gat gat tgg act gtc caa aac 883
 Gly Ser Leu Asp Tyr Glu Ile Trp Glu Asp Asp Trp Thr Val Gln Asn
 250 255 260

gtt gac cgt aag ttc agc gcg cag ttc gag cac acc att gtc atc acc 931
 Val Asp Arg Lys Phe Ser Ala Gln Phe Glu His Thr Ile Val Ile Thr
 265 270 275

gaa gac ggc aat gag atc ctc acc ctc cca gac gat tcc gtc 973
 Glu Asp Gly Asn Glu Ile Leu Thr Leu Pro Asp Asp Ser Val
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taaaaacgcc taggccacaa gcc 996

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 Ile Ala Gly Glu Ala Val Lys Pro Gly Val Thr Thr Asp Glu Leu Asp
 65 70 75 80
 Arg Ile Val His Glu Tyr Thr Cys Asp Met Gly Ala Tyr Pro Ser Asp
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 Leu Gly Tyr Arg Gly Phe Thr Lys Ser Ser Cys Ile Ser Leu Asn Glu

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Cys Asn Ala Thr Phe Leu Ala Gly Asp Val Ser Glu Glu His Arg Leu 145 150 155 160		
Leu Val Glu Arg Thr Glu Glu Ala Met Met Arg Ser Ile Arg Ala Ala 165 170 175		
Lys Pro Gly Arg Glu Ile Asn Val Ile Gly Arg Val Ile Glu Ser Tyr 180 185 190		
Ala Lys Arg Phe Gly Tyr Asn Val Val Arg Asp Phe Thr Gly His Gly 195 200 205		
Ile Gly Pro Thr Phe His Asn Gly Leu Val Val Leu His Tyr Asp Asn 210 215 220		
Thr Gln Tyr Arg Asp Leu Leu Val Pro Gly Met Thr Leu Thr Ile Glu 225 230 235 240		
Pro Met Ile Asn Leu Gly Ser Leu Asp Tyr Glu Ile Trp Glu Asp Asp 245 250 255		
Trp Thr Val Gln Asn Val Asp Arg Lys Phe Ser Ala Gln Phe Glu His 260 265 270		
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Asp Ser Val 290		

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 Met Ala Leu Gly Arg
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 Thr Ile Ser Thr Ala Gln Leu Gly Val Gln Ala Lys Ile Val Arg Val
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Glu Ala Asn Val Gly Pro Gly Leu Pro Gly Thr Tyr Ile Val Gly Leu	
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Ala Asp Thr Ala Ile Ser Glu Ser Arg Asp Arg Ile Lys Thr Ala Val	
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Gln Asn Ser Gly Leu Met Trp Pro Lys Thr Lys Val Ile Ile Asn Leu	
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Ser Pro Ala Ser Met Arg Lys Gln Gly Ser Gln Cys Asp Leu Ala Met	
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Thr Val Ala Val Leu Val Ala His Gly Ser Asn Pro Lys Ala Lys Phe	
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His Ala Gln Asn Thr Leu Phe Leu Gly Glu Val Ala Leu Asp Gly Thr	
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Glu Gly Ile Gly Lys Ile Val Ile Pro Glu Gly Asn Ala Gln Glu Ala	
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Gly Leu Val Glu Asp Pro Ser Val Phe Leu Ala His Ser Ile Asp Gln	
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Val Leu Arg Trp Leu Asp Gly Glu Glu Ala Leu Pro Gln Pro Gly Leu	
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Phe Asn Asp Glu Asn Ser Leu Lys Leu Pro Asp Met Arg Asp Val Val	
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Gly Gln Pro Glu Ala Arg Phe Ala Ala Glu Val Ala Ala Ala Gly Gly	
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His His Met Leu Met Ile Gly Pro Pro Gly Ser Gly Lys Ser Met Ile	
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Ile Glu Ala Thr Ala Val His Ser Val Val Gly Arg Thr Phe Ser Gly	
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Pro Val Ser Arg Ala Pro Phe Ile Ser Pro His His Asn Val Ser Lys	

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cca gcg tca atc ctt gat tct ttg agg act cca ttg gaa tac ggc tcg Pro Ala Ser Ile Leu Asp Ser Leu Arg Thr Pro Leu Glu Tyr Gly Ser 310 315 320 325			1075
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ctt tcg ggt ccg ttg agg gat cgc ttg gac atg gtt gtt gcc acc cac Leu Ser Gly Pro Leu Arg Asp Arg Leu Asp Met Val Val Ala Thr His 375 380 385			1267
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ccc aat ctt gac cat att gcg cga gcc atg gag ctt cgg ggc act aca Pro Asn Leu Asp His Ile Ala Arg Ala Met Glu Leu Arg Gly Thr Thr 490 495 500			1603
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 <213> Corynebacterium glutamicum

<400> 38

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Tyr Ile Val Gly Leu Ala Asp Thr Ala Ile Ser Glu Ser Arg Asp Arg
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Ile Lys Thr Ala Val Gln Asn Ser Gly Leu Met Trp Pro Lys Thr Lys
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Val Ile Ile Asn Leu Ser Pro Ala Ser Met Arg Lys Gln Gly Ser Gln
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Cys Asp Leu Ala Met Thr Val Ala Val Leu Val Ala His Gly Ser Asn
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Pro Lys Ala Lys Phe His Ala Gln Asn Thr Leu Phe Leu Gly Glu Val
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Ala Leu Asp Gly Thr Leu Leu Pro Val Thr Gly Val Leu Pro Ala Leu
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Leu Ala Ala Lys Glu Glu Gly Ile Gly Lys Ile Val Ile Pro Glu Gly
          130          135          140

Asn Ala Gln Glu Ala Gly Leu Val Glu Asp Pro Ser Val Phe Leu Ala
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His Ser Ile Asp Gln Val Leu Arg Trp Leu Asp Gly Glu Glu Ala Leu
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Pro Gln Pro Gly Leu Phe Asn Asp Glu Asn Ser Leu Lys Leu Pro Asp
          180          185          190

Met Arg Asp Val Val Gly Gln Pro Glu Ala Arg Phe Ala Ala Glu Val
          195          200          205

Ala Ala Ala Gly Gly His His Met Leu Met Ile Gly Pro Pro Gly Ser
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Gly Lys Ser Met Ile Ala Glu Arg Ile Pro Ser Leu Leu Pro Glu Leu
          225          230          235          240

Ser Pro Gln Gln Met Ile Glu Ala Thr Ala Val His Ser Val Val Gly
          245          250          255

Arg Thr Phe Ser Gly Pro Val Ser Arg Ala Pro Phe Ile Ser Pro His
          260          265          270

His Asn Val Ser Lys Ala Ala Leu Leu Gly Gly Gly Ser Gly Ser Pro
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Leu Pro Gly Ala Ile Ser Leu Ala His His Gly Val Leu Phe Leu Asp
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 Glu Val Ser Glu Ile Pro Ala Ser Ile Leu Asp Ser Leu Arg Thr Pro
 305 310 315 320
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 325 330 335
 Phe Pro Ala Gln Phe Gln Leu Ile Leu Ala Ala Asn Pro Cys Arg Cys
 340 345 350
 Gly Ala Glu Gln Pro Gln Glu Cys Val Cys Ser Gly Ser Ala Arg Ala
 355 360 365
 Thr Tyr Leu Asn Asn Leu Ser Gly Pro Leu Arg Asp Arg Leu Asp Met
 370 375 380
 Val Val Ala Thr His Ser Lys Gly Ala Val Leu Arg Ser Asp Asp Val
 385 390 395 400
 Glu Ala Ser Ala Pro Ile Ala Asp Arg Val Ala Gln Ala Arg Glu Arg
 405 410 415
 Ala Ala Phe Arg Trp Arg Arg Ser Gly Leu Gly Asn Leu Val Asn Ala
 420 425 430
 His Val Asp Pro His Phe Leu Arg Arg Asn Phe Ala Ala Thr Glu Asp
 435 440 445
 Ala Met Val Tyr Leu Gly Ala Phe Leu Ala Glu Gly Thr Ile Ser Gln
 450 455 460
 Arg Gly Cys Asp Arg Ala Ile Lys Leu Gly Trp Thr Leu Cys Asp Leu
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 Val Asn Arg Arg Ile
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Lys Thr Leu Thr Trp Gly Ala Ile Pro Leu Val Leu Leu Ala Ser Leu	
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gta agc att gac cat att ccg gga aca aac atc aac ttg agc gtg cct	211
Val Ser Ile Asp His Ile Pro Gly Thr Asn Ile Asn Leu Ser Val Pro	
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Tyr Ala Ala Glu Gly Pro Gly Pro Thr Ile Asn Thr Leu Gly Gln Val	
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Asp Gly Glu Asp Val Val Ser Ile Ser Ser Ala Asp Leu Asp Glu Thr	
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Glu Gly Asn Leu Asn Met Thr Thr Val Ser Val Arg Ser Gly Met Thr	
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Leu Ser Gln Val Ile Ser Arg Trp Leu Phe Thr Asp Asp Thr Ile Val	
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ccc atc gag cag gtt ttc cct ccc ggc caa tcc acc gag gaa gtc gaa	451
Pro Ile Glu Gln Val Phe Pro Pro Gly Gln Ser Thr Glu Glu Val Glu	
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Glu Ser Asn Arg Thr Ala Phe Ile Ser Ser Glu Ser Ser Ala Thr Ile	
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Ala Ala Met Asn Tyr Leu Asn Ile Pro Val Glu Val Glu Val Ala Glu	
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Val Leu Thr Asp Ser Ala Ala Thr Gly Ile Phe Glu Pro Gly Asp Lys	
150 155 160 165	
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Leu Leu Ser Ile Asp Gly Thr Ala Ile Ser Thr Pro Gly Asp Ala Gln	
170 175 180	
acc atc gtg cga tcg aaa gct ccc ggc gat gag atc acg att tcc tac	691
Thr Ile Val Arg Ser Lys Ala Pro Gly Asp Glu Ile Thr Ile Ser Tyr	
185 190 195	
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Glu Arg Asn Asp Ala Glu Ser Gln Ala Thr Ile Thr Leu Arg Glu His	
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Pro Asp Asp Ser Ser Val Ala Leu Leu Gly Ile Ser Met Leu Ser Val	
215 220 225	
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Pro Ser Ser Ala Ile Glu Val Asp Tyr Asn Leu Glu Asp Ile Gly Gly	
230 235 240 245	
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Pro Ser Ala Gly Met Met Phe Ser Leu Ala Val Val Asp Lys Leu Ser
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 Pro Gly Ala Leu Asn Gly Gly Lys Phe Val Ala Gly Thr Gly Thr Ile
 265 270 275

gcg gag gac ggg tcg gtg ggc ccg att ggc ggt att gcg cac aag gtg 979
 Ala Glu Asp Gly Ser Val Gly Pro Ile Gly Gly Ile Ala His Lys Val
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 Arg Ala Ala Glu Asp Ala Gly Ala Glu Val Phe Leu Ser Pro Ala Asp
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aat tgc gcg gag gcg atg agt gcg aag cct cag gat atg acg atc ttg 1075
 Asn Cys Ala Glu Ala Met Ser Ala Lys Pro Gln Asp Met Thr Ile Leu
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 Lys Val Asp Ser Leu Ser Gln Ala Ile Asp Gln Met Ala Ala Tyr Asn
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Asn Leu Ser Val Pro Tyr Ala Ala Glu Gly Pro Gly Pro Thr Ile Asn
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Thr Leu Gly Gln Val Asp Gly Glu Asp Val Val Ser Ile Ser Ser Ala
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Asp Leu Asp Glu Thr Glu Gly Asn Leu Asn Met Thr Thr Val Ser Val
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Arg Ser Gly Met Thr Leu Ser Gln Val Ile Ser Arg Trp Leu Phe Thr
 85 90 95

Asp Asp Thr Ile Val Pro Ile Glu Gln Val Phe Pro Pro Gly Gln Ser
 100 105 110

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 115 120 125

Ser Ser Ala Thr Ile Ala Ala Met Asn Tyr Leu Asn Ile Pro Val Glu

51

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Gly	Leu	Val	Trp	Thr	Ala	Asp	Glu	Arg	Met	Thr	Met	Ser	Gln	Val	Cys														
			250					255					260																

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 Ala Gly Arg Gly Asp Ser Gly Ala Pro Leu Ile Ala Asp Gly Arg Val
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gtt ggt ctt gta tct ggt ggt gta att cct gat tac aac ctg gca tgc 979
 Val Gly Leu Val Ser Gly Gly Val Ile Pro Asp Tyr Asn Leu Ala Cys
 280 285 290

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 Ala Thr Pro Leu Gln Gly Pro Phe Phe Met Pro Thr Leu Ser Val Asn
 295 300 305

atg gat act gtc cta act gat ttg gat tcg cag gat ctt ccc ggt cga 1075
 Met Asp Thr Val Leu Thr Asp Leu Asp Ser Gln Asp Leu Pro Gly Arg
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 50 55 60

Thr Ser Gly Gly Gln Val Val Glu Gln Ser Leu Gln Val Val Glu Gln
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Glu Val Gln Lys Ala Leu Pro Asn Tyr Glu Ile Arg Thr Asp Leu Gln
 85 90 95

Ser Gln Val Met Gly Ala Thr Leu Gly Glu Val Leu His Arg Val Pro
 100 105 110

Gly Ser Trp Phe Asp Ala Pro Ala Val Pro Glu Glu Ser Arg Ile Val
 115 120 125

Glu Glu Gln Gly Lys Ser Leu Tyr Gly Pro Gly Thr Pro Ile Tyr Leu
 130 135 140

Asn Gly Asn Ser Met Cys Thr Leu Ala Val Thr Gly Thr Asp Ala Asp
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Gly Arg Lys Ile Gly Ile Thr Ala Gly His Cys Gly Lys Ser Gly Asp
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Ala Val Arg Ser Ala Asp Ser Phe Trp Val Gly Asp Thr Gly Thr Val
 180 185 190

Val Tyr Asn Ala Pro Asn Ala Asp Tyr Ser Val Ile Glu Phe Gly Ser
 195 200 205

Asn Ala Glu Leu Ser Asn Thr Tyr Asn Gly Val Thr Ala Asn Ala Val
 210 215 220

Gly Gly Gly Val Thr Asn Gly Gln Glu Val Cys Lys Asn Gly Val Ala
 225 230 235 240

Thr Gly Tyr Thr Cys Gly Leu Val Trp Thr Ala Asp Glu Arg Met Thr
 245 250 255

Met Ser Gln Val Cys Ala Gly Arg Gly Asp Ser Gly Ala Pro Leu Ile
 260 265 270

Ala Asp Gly Arg Val Val Gly Leu Val Ser Gly Gly Val Ile Pro Asp
 275 280 285

Tyr Asn Leu Ala Cys Ala Thr Pro Leu Gln Gly Pro Phe Phe Met Pro
 290 295 300

Thr Leu Ser Val Asn Met Asp Thr Val Leu Thr Asp Leu Asp Ser Gln
 305 310 315 320

Asp Leu Pro Gly Arg Gly Phe Gln Pro Thr Ala Gly
 325 330

<210> 43
 <211> 2049
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2026)
 <223> RXN01868

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ccacaaaccc tgtggcggtta aatcccctag agtaggccac atg aag gat ctt tat 115
 Met Lys Asp Leu Tyr
 1 5

cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat 163
 Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp
 10 15 20

cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa 211
 Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu
 25 30 35

gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt 259
 Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu
 40 45 50

tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca 307

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295	300	305	
cat ttt cct gca agc tcc aag gag cac atg ctt gag ctc gtc gac tac His Phe Pro Ala Ser Ser Lys Glu His Met Leu Glu Leu Val Asp Tyr 310 315 320 325			1075
ctg gtt gcc gcc tac cgt gat cgc att tcc aac ctc gaa tgg atg acg Leu Val Ala Ala Tyr Arg Asp Arg Ile Ser Asn Leu Glu Trp Met Thr 330 335 340			1123
ccc gcc acc cgc gag cgt gcc ctg gaa aag ttg ggc aaa ttc aac gcg Pro Ala Thr Arg Glu Arg Ala Leu Glu Lys Leu Gly Lys Phe Asn Ala 345 350 355			1171
aaa atc ggc tac ccc gac aag tgg cgc tcc tac gaa ggc ctc gaa ttc Lys Ile Gly Tyr Pro Asp Lys Trp Arg Ser Tyr Glu Gly Leu Glu Phe 360 365 370			1219
ggc tcc gac ctg gtg gac aac tcc cgc aag ggc tcc gcg ttc ctc cat Gly Ser Asp Leu Val Asp Asn Ser Arg Lys Gly Ser Ala Phe Leu His 375 380 385			1267
gac tat gag ctg ggc aag atc ggc aaa cca gcc gac cgc gac gaa tgg Asp Tyr Glu Leu Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp 390 395 400 405			1315
gtc acc acc cca caa acc gtc aac gcc ttc tac aac ccc gtg gtc aac Val Thr Thr Pro Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn 410 415 420			1363
gac atc acc ttc ccc gca gcc atc ctg cgc gca cca ttc ttc gac ccc Asp Ile Thr Phe Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro 425 430 435			1411
gaa gca gaa gcc gca gaa aac ttc ggt gca atc ggt gct gtg atc gga Glu Ala Glu Ala Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly 440 445 450			1459
cac gaa atc ggc cac ggc ttt gac gat caa ggc agc caa tac gac ggc His Glu Ile Gly His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly 455 460 465			1507
gac ggc aac ctc aac tcc tgg tgg acc gac gaa gac cgc tcc gca ttc Asp Gly Asn Leu Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe 470 475 480 485			1555
gag cag ctc acc tca cgt ctg gtc acc caa ttc agc gga ctc gtc cct Glu Gln Leu Thr Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro 490 495 500			1603
gcc gtc ctg acc tct gaa gga atc gac acc gac ggc gtc aac ggt gaa Ala Val Leu Thr Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu 505 510 515			1651
ttc act ctc ggc gaa aac atc ggt gac ctc ggc gga ttg ggc atc gct Phe Thr Leu Gly Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala 520 525 530			1699
gtc gtt gcc tac gaa aag tac ctc gca gac cgt ggc caa acc ttt gaa Val Val Ala Tyr Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu 535 540 545			1747

acc tca cca gtc caa aaa ttc gaa gca gaa ggc gcc gag gaa ggc ctg 1795
 Thr Ser Pro Val Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu
 550 555 560 565

gcc gag caa gaa ttc aac ggt ctc caa cgc ctc ttc ctg tcc tgg gct 1843
 Ala Glu Gln Glu Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala
 570 575 580

cgc gtg tgg cgc acc aaa atc cgc cca cag atg gcc gtc caa tac ctg 1891
 Arg Val Trp Arg Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu
 585 590 595

gcc atc gac cca cac tcc cct gca gaa ttc cgc tgc aat gtc atc gcc 1939
 Ala Ile Asp Pro His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala
 600 605 610

gga aac gtc gct gaa ttc tac gaa gca ttc gac gtc ccc gaa gat gca 1987
 Gly Asn Val Ala Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala
 615 620 625

cct gtg tac atc aag cca gaa gag cgc cta gct atc tgg tagttgtag 2036
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 630 635 640

ttggtattga aaa 2049

<210> 44
 <211> 642
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44
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 Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg
 20 25 30
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 35 40 45
 Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn
 50 55 60
 Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val
 65 70 75 80
 Ala Asn Ser Ser Phe Phe Ala Ala Ala Leu Gly Glu Leu Asp Arg Glu
 85 90 95
 Gly Val Gly Ala Pro Val Gly Phe Trp Val Glu Lys Asp Ser Ser Ser
 100 105 110
 Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu Pro Asp
 115 120 125
 Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala Ala Tyr
 130 135 140

Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser Arg Leu
 145 150 155 160
 Phe Gly Leu Ser Ala Ala Ser Ala Ala Arg Ile Val Ala Leu Glu
 165 170 175
 Thr Glu Ile Ala Ala Gly His Trp Asp Val Val Lys Thr Arg Asp Ala
 180 185 190
 Val Ala Thr Tyr Asn Pro Thr Glu Leu Gly Ala Leu Pro Pro Lys Val
 195 200 205
 Arg Thr Leu Leu Ser Ser Ala Gly Leu Pro Asp Gln Arg Leu Val Ser
 210 215 220
 Met Met Pro Ser Tyr Leu Asp His Leu Asn Gly Leu Leu Val Asp Asp
 225 230 235 240
 Arg Leu Pro Asp Trp Gln Leu Trp Ala Thr Trp His Ile Leu Arg Ser
 245 250 255
 Arg Ala Gly Leu Leu Thr Glu Glu Ile Ser Gln Ala Asn Phe Asp Phe
 260 265 270
 Tyr Gly Thr Lys Leu Ser Gly Ala Thr Glu Gln Lys Asp Arg Trp Lys
 275 280 285
 Arg Ala Val Gly Leu Ala Glu Arg Met Val Gly Glu Glu Ile Gly Gln
 290 295 300
 Arg Phe Val Glu Arg His Phe Pro Ala Ser Ser Lys Glu His Met Leu
 305 310 315 320
 Glu Leu Val Asp Tyr Leu Val Ala Ala Tyr Arg Asp Arg Ile Ser Asn
 325 330 335
 Leu Glu Trp Met Thr Pro Ala Thr Arg Glu Arg Ala Leu Glu Lys Leu
 340 345 350
 Gly Lys Phe Asn Ala Lys Ile Gly Tyr Pro Asp Lys Trp Arg Ser Tyr
 355 360 365
 Glu Gly Leu Glu Phe Gly Ser Asp Leu Val Asp Asn Ser Arg Lys Gly
 370 375 380
 Ser Ala Phe Leu His Asp Tyr Glu Leu Gly Lys Ile Gly Lys Pro Ala
 385 390 395 400
 Asp Arg Asp Glu Trp Val Thr Thr Pro Gln Thr Val Asn Ala Phe Tyr
 405 410 415
 Asn Pro Val Val Asn Asp Ile Thr Phe Pro Ala Ala Ile Leu Arg Ala
 420 425 430
 Pro Phe Phe Asp Pro Glu Ala Glu Ala Ala Glu Asn Phe Gly Ala Ile
 435 440 445
 Gly Ala Val Ile Gly His Glu Ile Gly His Gly Phe Asp Asp Gln Gly
 450 455 460
 Ser Gln Tyr Asp Gly Asp Gly Asn Leu Asn Ser Trp Trp Thr Asp Glu

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<210> 45
<211> 1734
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1711)
<223> FRXA01868
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                                     Val Glu Lys Asp Ser
                                     1                               5
tcc tcc aac gaa tcc gtc gcc tat gtc atc cag tcc ggc ctc ggc ctg 163
Ser Ser Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu
                        10                        15                        20
ccc gat gag gct tat tac cgc gag gag gca cac gcc gaa act ctc gcg 211
Pro Asp Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala
                        25                        30                        35

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gcc tac aaa gag cac gtt gag cgc atg ctc ggc tac ttg gat aac agc	259
Ala Tyr Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser	
40 45 50	
cgc ctc ttc ggt ctg tcg gct gct tcc gct gcc gca cga att gtc gcc	307
Arg Leu Phe Gly Leu Ser Ala Ala Ser Ala Ala Arg Ile Val Ala	
55 60 65	
ctg gaa acg gaa atc gct gct ggc cac tgg gat gtc gtg aag acc cgc	355
Leu Glu Thr Glu Ile Ala Ala Gly His Trp Asp Val Val Lys Thr Arg	
70 75 80 85	
gac gcc gta gcc acc tac aac ccc acc gaa ctc ggc gcg ctg cca cca	403
Asp Ala Val Ala Thr Tyr Asn Pro Thr Glu Leu Gly Ala Leu Pro Pro	
90 95 100	
aag gtc cgc acg ctg ctc agt tcc gca ggc ctc ccg gac cag cgc ctg	451
Lys Val Arg Thr Leu Leu Ser Ser Ala Gly Leu Pro Asp Gln Arg Leu	
105 110 115	
gta tcg atg atg ccg tca tac ctc gac cac ctc aac ggc ttg ctt gtc	499
Val Ser Met Met Pro Ser Tyr Leu Asp His Leu Asn Gly Leu Leu Val	
120 125 130	
gac gac cgc ctc ccc gat tgg cag cta tgg gca acc tgg cac atc ttg	547
Asp Asp Arg Leu Pro Asp Trp Gln Leu Trp Ala Thr Trp His Ile Leu	
135 140 145	
agg tct cga gca gga ctg ttg acc gag gaa att agc caa gca aac ttc	595
Arg Ser Arg Ala Gly Leu Leu Thr Glu Glu Ile Ser Gln Ala Asn Phe	
150 155 160 165	
gac ttc tat ggc acc aaa ctg tcc ggc gcc acc gag caa aaa gat cga	643
Asp Phe Tyr Gly Thr Lys Leu Ser Gly Ala Thr Glu Gln Lys Asp Arg	
170 175 180	
tgg aag cgt gct gtc ggc ctg gca gag cgc atg gtg ggc gag gaa atc	691
Trp Lys Arg Ala Val Gly Leu Ala Glu Arg Met Val Gly Glu Glu Ile	
185 190 195	
ggg caa cga ttc gtc gaa agg cat ttt cct gca agc tcc aag gag cac	739
Gly Gln Arg Phe Val Glu Arg His Phe Pro Ala Ser Ser Lys Glu His	
200 205 210	
atg ctt gag ctc gtc gac tac ctg gtt gcc gcc tac cgt gat cgc att	787
Met Leu Glu Leu Val Asp Tyr Leu Val Ala Ala Tyr Arg Asp Arg Ile	
215 220 225	
tcc aac ctc gaa tgg atg acg ccc gcc acc cgc gag cgt gcc ctg gaa	835
Ser Asn Leu Glu Trp Met Thr Pro Ala Thr Arg Glu Arg Ala Leu Glu	
230 235 240 245	
aag ttg ggc aaa ttc aac gcg aaa atc ggc tac ccc gac aag tgg cgc	883
Lys Leu Gly Lys Phe Asn Ala Lys Ile Gly Tyr Pro Asp Lys Trp Arg	
250 255 260	
tcc tac gaa ggc ctc gaa ttc ggc tcc gac ctg gtg gac aac tcc cgc	931
Ser Tyr Glu Gly Leu Glu Phe Gly Ser Asp Leu Val Asp Asn Ser Arg	
265 270 275	
aag ggc tcc gcg ttc ctc cat gac tat gag ctg ggc aag atc ggc aaa	979

Lys	Gly	Ser	Ala	Phe	Leu	His	Asp	Tyr	Glu	Leu	Gly	Lys	Ile	Gly	Lys	
	280						285					290				
cca	gcc	gac	cgc	gac	gaa	tgg	gtc	acc	acc	cca	caa	acc	gtc	aac	gcc	1027
Pro	Ala	Asp	Arg	Asp	Glu	Trp	Val	Thr	Thr	Pro	Gln	Thr	Val	Asn	Ala	
	295					300					305					
ttc	tac	aac	ccc	gtg	gtc	aac	gac	atc	acc	ttc	ccc	gca	gcc	atc	ctg	1075
Phe	Tyr	Asn	Pro	Val	Val	Asn	Asp	Ile	Thr	Phe	Pro	Ala	Ala	Ile	Leu	
310					315					320					325	
cgc	gca	cca	ttc	ttc	gac	ccc	gaa	gca	gaa	gcc	gca	gaa	aac	ttc	ggt	1123
Arg	Ala	Pro	Phe	Phe	Asp	Pro	Glu	Ala	Glu	Ala	Ala	Glu	Asn	Phe	Gly	
				330					335					340		
gca	atc	ggt	gct	gtg	atc	gga	cac	gaa	atc	ggc	cac	ggc	ttt	gac	gat	1171
Ala	Ile	Gly	Ala	Val	Ile	Gly	His	Glu	Ile	Gly	His	Gly	Phe	Asp	Asp	
			345					350					355			
caa	ggc	agc	caa	tac	gac	ggc	gac	ggc	aac	ctc	aac	tcc	tgg	tgg	acc	1219
Gln	Gly	Ser	Gln	Tyr	Asp	Gly	Asp	Gly	Asn	Leu	Asn	Ser	Trp	Trp	Thr	
		360					365					370				
gac	gaa	gac	cgc	tcc	gca	ttc	gag	cag	ctc	acc	tca	cgt	ctg	gtc	acc	1267
Asp	Glu	Asp	Arg	Ser	Ala	Phe	Glu	Gln	Leu	Thr	Ser	Arg	Leu	Val	Thr	
	375					380					385					
caa	ttc	agc	gga	ctc	gtc	cct	gcc	gtc	ctg	acc	tct	gaa	gga	atc	gac	1315
Gln	Phe	Ser	Gly	Leu	Val	Pro	Ala	Val	Leu	Thr	Ser	Glu	Gly	Ile	Asp	
390					395				400						405	
acc	gac	ggc	gtc	aac	ggt	gaa	ttc	act	ctc	ggc	gaa	aac	atc	ggt	gac	1363
Thr	Asp	Gly	Val	Asn	Gly	Glu	Phe	Thr	Leu	Gly	Glu	Asn	Ile	Gly	Asp	
				410					415					420		
ctc	ggc	gga	ttg	ggc	atc	gct	gtc	ggt	gcc	tac	gaa	aag	tac	ctc	gca	1411
Leu	Gly	Gly	Leu	Gly	Ile	Ala	Val	Val	Ala	Tyr	Glu	Lys	Tyr	Leu	Ala	
			425					430					435			
gac	cgt	ggc	caa	acc	ttt	gaa	acc	tca	cca	gtc	caa	aaa	ttc	gaa	gca	1459
Asp	Arg	Gly	Gln	Thr	Phe	Glu	Thr	Ser	Pro	Val	Gln	Lys	Phe	Glu	Ala	
	440						445					450				
gaa	ggc	gcc	gag	gaa	ggc	ctg	gcc	gag	caa	gaa	ttc	aac	ggt	ctc	caa	1507
Glu	Gly	Ala	Glu	Glu	Gly	Leu	Ala	Glu	Gln	Glu	Phe	Asn	Gly	Leu	Gln	
	455					460				465						
cgc	ctc	ttc	ctg	tcc	tgg	gct	cgc	gtg	tgg	cgc	acc	aaa	atc	cgc	cca	1555
Arg	Leu	Phe	Leu	Ser	Trp	Ala	Arg	Val	Trp	Arg	Thr	Lys	Ile	Arg	Pro	
470					475					480					485	
cag	atg	gcc	gtc	caa	tac	ctg	gcc	atc	gac	cca	cac	tcc	cct	gca	gaa	1603
Gln	Met	Ala	Val	Gln	Tyr	Leu	Ala	Ile	Asp	Pro	His	Ser	Pro	Ala	Glu	
				490					495					500		
ttc	cgc	tgc	aac	gtc	atc	gcc	gga	aac	gtc	gct	gaa	ttc	tac	gaa	gca	1651
Phe	Arg	Cys	Asn	Val	Ile	Ala	Gly	Asn	Val	Ala	Glu	Phe	Tyr	Glu	Ala	
			505					510					515			
ttc	gac	gtc	ccc	gaa	gat	gca	cct	gtg	tac	atc	aag	cca	gaa	gag	cgc	1699
Phe	Asp	Val	Pro	Glu	Asp	Ala	Pro	Val	Tyr	Ile	Lys	Pro	Glu	Glu	Arg	

520

525

530

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 Leu Ala Ile Trp
 535

1734

<210> 46

<211> 537

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

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Ala Glu Thr Leu Ala Ala Tyr Lys Glu His Val Glu Arg Met Leu Gly
 35 40 45

Tyr Leu Asp Asn Ser Arg Leu Phe Gly Leu Ser Ala Ala Ser Ala Ala
 50 55 60

Ala Arg Ile Val Ala Leu Glu Thr Glu Ile Ala Ala Gly His Trp Asp
 65 70 75 80

Val Val Lys Thr Arg Asp Ala Val Ala Thr Tyr Asn Pro Thr Glu Leu
 85 90 95

Gly Ala Leu Pro Pro Lys Val Arg Thr Leu Leu Ser Ser Ala Gly Leu
 100 105 110

Pro Asp Gln Arg Leu Val Ser Met Met Pro Ser Tyr Leu Asp His Leu
 115 120 125

Asn Gly Leu Leu Val Asp Asp Arg Leu Pro Asp Trp Gln Leu Trp Ala
 130 135 140

Thr Trp His Ile Leu Arg Ser Arg Ala Gly Leu Leu Thr Glu Glu Ile
 145 150 155 160

Ser Gln Ala Asn Phe Asp Phe Tyr Gly Thr Lys Leu Ser Gly Ala Thr
 165 170 175

Glu Gln Lys Asp Arg Trp Lys Arg Ala Val Gly Leu Ala Glu Arg Met
 180 185 190

Val Gly Glu Glu Ile Gly Gln Arg Phe Val Glu Arg His Phe Pro Ala
 195 200 205

Ser Ser Lys Glu His Met Leu Glu Leu Val Asp Tyr Leu Val Ala Ala
 210 215 220

Tyr Arg Asp Arg Ile Ser Asn Leu Glu Trp Met Thr Pro Ala Thr Arg
 225 230 235 240

Glu Arg Ala Leu Glu Lys Leu Gly Lys Phe Asn Ala Lys Ile Gly Tyr
 245 250 255

Pro Asp Lys Trp Arg Ser Tyr Glu Gly Leu Glu Phe Gly Ser Asp Leu
 260 265 270
 Val Asp Asn Ser Arg Lys Gly Ser Ala Phe Leu His Asp Tyr Glu Leu
 275 280 285
 Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp Val Thr Thr Pro
 290 295 300
 Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn Asp Ile Thr Phe
 305 310 315 320
 Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro Glu Ala Glu Ala
 325 330 335
 Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly His Glu Ile Gly
 340 345 350
 His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly Asp Gly Asn Leu
 355 360 365
 Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe Glu Gln Leu Thr
 370 375 380
 Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro Ala Val Leu Thr
 385 390 395 400
 Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu Phe Thr Leu Gly
 405 410 415
 Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala Val Val Ala Tyr
 420 425 430
 Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu Thr Ser Pro Val
 435 440 445
 Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu Ala Glu Gln Glu
 450 455 460
 Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala Arg Val Trp Arg
 465 470 475 480
 Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu Ala Ile Asp Pro
 485 490 495
 His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala Gly Asn Val Ala
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 Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala Pro Val Tyr Ile
 515 520 525
 Lys Pro Glu Glu Arg Leu Ala Ile Trp
 530 535

<210> 47

<211> 426

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(403)

<223> FRXA01869

<400> 47

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Met Lys Asp Leu Tyr
1 5

cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat 163
Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp
10 15 20

cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa 211
Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu
25 30 35

gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt 259
Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu
40 45 50

tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca 307
Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn Ala Ala Gly Val Ala
55 60 65

ccg ctc gat gcg gat ctg aac agg ctg tct gtt gct aac tca tcg ttt 355
Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val Ala Asn Ser Ser Phe
70 75 80 85

tcg cag ctg ctc tcg gcg aac tgg acc gtg aag gcg ttg gcg cgc cag 403
Ser Gln Leu Leu Ser Ala Asn Trp Thr Val Lys Ala Leu Ala Arg Gln
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<210> 48

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

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Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg
20 25 30

Asp Asp Ala Glu Glu Asp Val His Glu Ile Val Lys Glu Asp Thr Gly
35 40 45

Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn
50 55 60

Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val
65 70 75 80

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85 90 95

Ala Leu Ala Arg Gln
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<210> 49
<211> 2898
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(2875)
<223> RXN03028

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Met Phe Glu Arg Phe
1 5
acc gat cgt gca cgc cgc gtg att gtg ctc gcg cag gaa gag gcg cgc 163
Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala Gln Glu Glu Ala Arg
10 15 20
atg ctc aac cac aat tac atc ggc acg gag cac att ctc ctc ggc ctc 211
Met Leu Asn His Asn Tyr Ile Gly Thr Glu His Ile Leu Leu Gly Leu
25 30 35
att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga 259
Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly
40 45 50
att tcc ctg gac gcc gtc cgc cag gaa gtc gaa gag att atc ggc cag 307
Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu Glu Ile Ile Gly Gln
55 60 65
ggc tcc cag ccc acc acc ggc cac att cct ttt act cca cgt gcc aag 355
Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys
70 75 80 85
aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag 403
Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys
90 95 100
tac atc ggt act gag ttc ctg ctt ctc ggt ttg atc cgt gag ggc gag 451
Tyr Ile Gly Thr Glu Phe Leu Leu Gly Leu Ile Arg Glu Gly Glu
105 110 115
ggc gtt gct gcc cag gtc ctg gtc aag ctt ggt gct gat ctg cca cgc 499
Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg
120 125 130
gtg cgt cag caa gtt att cag ctt ctc tcc ggc tac gaa ggt ggc cag 547
Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly Tyr Glu Gly Gly Gln
135 140 145
ggc gga tcc cca gag ggc ggc cag ggc gcc cct act ggc ggt gac gct 595
Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro Thr Gly Gly Asp Ala
150 155 160 165

gtt ggt gca gga gct gct cct ggc ggt cgt cca tct tcg ggc agc cca	643
Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro Ser Ser Gly Ser Pro	
170 175 180	
ggc gag cgt tct acc tct ttg gtc ctt gac cag ttc ggc cgc aac ctc	691
Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln Phe Gly Arg Asn Leu	
185 190 195	
acc cag gct gca aag gac ggc aag ctg gat cca gtt gtt ggt cgc gat	739
Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp	
200 205 210	
aag gaa atc gag cgc atc atg cag gtg ctc tcc cgt cgt acc aag aac	787
Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser Arg Arg Thr Lys Asn	
215 220 225	
aac cca gtt ctt att ggt gag cca ggt gtt ggt aag acc gca gtt gtt	835
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Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys Val Pro Glu Thr Leu	
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Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly Ser Leu Val Ala Gly	
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Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu Lys Lys Val Leu Lys	
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Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Ser	
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Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu Gln Thr Ile Gly Ala	
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Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu	
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Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu Pro Ser Val Asp Leu	
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acc gtt gag atc ttg aag ggt ctg cgc gac cgc tac gaa gct cac cac	1267
Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg Tyr Glu Ala His His	
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cgc gta tcc atc acc gat ggt gct ctt act gca gca gct cag ctt gct	1315
Arg Val Ser Ile Thr Asp Gly Ala Leu Thr Ala Ala Ala Gln Leu Ala	
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Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro Asp Lys Ala Val Asp Leu	
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Ile Asp Glu Ala Gly Ala Arg Met Arg Ile Lys Arg Met Thr Ala Pro	
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Ser Ser Leu Arg Glu Val Asp Glu Arg Ile Ala Asp Val Arg Arg Glu	
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Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe Glu Lys Ala Ala Gly Leu	
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Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu Arg Ser Glu Lys Glu Lys	
470 475 480 485	
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Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile Ala Glu Val Gly Glu Glu	
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Gln Ile Ala Glu Val Leu Ala Asn Trp Thr Gly Ile Pro Val Phe Lys	
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Leu Thr Ala Glu Ser Ser Arg Leu Leu Asn Met Glu Glu Glu Leu	
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His Lys Arg Ile Ile Gly Gln Asp Glu Ala Val Lys Ala Val Ser Arg	
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Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly Val Gly Lys Thr Glu Leu	
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Ser Lys Ala Leu Ala Gly Phe Leu Phe Gly Asp Asp Asp Ser Leu Ile	
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Gln Ile Asp Met Gly Glu Phe His Asp Arg Phe Thr Ala Ser Arg Leu	
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ttc ggt gcc cct ccg gga tac gtt ggc tac gaa gaa ggt ggc cag ctg	1987
Phe Gly Ala Pro Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu	
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acc gag aag gtt cgc cgt aag cca ttc tcc gtt gtg ctt ttc gac gaa	2035
Thr Glu Lys Val Arg Arg Lys Pro Phe Ser Val Val Leu Phe Asp Glu	
630 635 640 645	
atc gag aag gcc cac aag gag atc tac aac acc ttg ctg cag gtg ttg	2083

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Glu	Asp	Gly	Arg	Leu	Thr	Asp	Gly	Gln	Gly	Arg	Ile	Val	Asp	Phe	Lys			
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aac	acc	gtc	ctg	atc	ttc	acc	tcc	aac	ctg	ggc	acc	gct	gac	atc	tcc	2179		
Asn	Thr	Val	Leu	Ile	Phe	Thr	Ser	Asn	Leu	Gly	Thr	Ala	Asp	Ile	Ser			
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aag	gct	gtt	ggc	ctg	ggc	ttc	tcc	gga	tcc	tcc	gag	act	gac	agc	gat	2227		
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cac	ttc	cgc	cct	gag	ttc	ctg	aac	cgt	att	gat	gag	atc	gtg	gtc	ttc	2323		
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cac	cag	ctc	acc	aag	gat	cag	atc	gtt	cag	atg	gtc	gac	ctt	ctt	atc	2371		
His	Gln	Leu	Thr	Lys	Asp	Gln	Ile	Val	Gln	Met	Val	Asp	Leu	Leu	Ile			
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Gly	Arg	Val	Ser	Asn	Ala	Leu	Ala	Glu	Lys	Asp	Met	Ser	Ile	Glu	Leu			
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cag	atg	tcc	gag	aag	atc	ctc	ttc	ggt	gaa	atc	ggc	gca	ggc	gag	atc	2563		
Gln	Met	Ser	Glu	Lys	Ile	Leu	Phe	Gly	Glu	Ile	Gly	Ala	Gly	Glu	Ile			
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gtc	acc	gtt	gac	gtc	gaa	ggc	tgg	gac	ggc	gag	tcc	aag	gac	acc	gac	2611		
Val	Thr	Val	Asp	Val	Glu	Gly	Trp	Asp	Gly	Glu	Ser	Lys	Asp	Thr	Asp			
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cgt	gcg	aag	ttc	acc	ttc	aca	cca	cgt	cca	aag	cca	atg	cca	gaa	ggt	2659		
Arg	Ala	Lys	Phe	Thr	Phe	Thr	Pro	Arg	Pro	Lys	Pro	Met	Pro	Glu	Gly			
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Lys	Phe	Ser	Glu	Ile	Ser	Val	Glu	Ala	Ala	Glu	Ala	Ile	Gln	Asp	Val			
				855						860						865		
gat	tct	gca	gct	gac	ggc	gat	gtc	cca	gaa	acc	gat	tca	ctt	tcc	gac	2755		
Asp	Ser	Ala	Ala	Asp	Gly	Asp	Val											

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 Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr Tyr Gly Thr Asp Asp Gln
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 gga ggc act gct cca agc aag gag tagcaacctt ttgaaaaagg gcc 2898
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 35 40 45
 Leu Glu Ser Met Gly Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu
 50 55 60
 Glu Ile Ile Gly Gln Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe
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 Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu
 85 90 95
 Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu
 100 105 110
 Ile Arg Glu Gly Glu Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly
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 Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro
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 Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln
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 Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro
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 Val Val Gly Arg Asp Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser
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 Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly
 225 230 235 240

Lys Thr Ala Val Val Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys
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 Val Pro Glu Thr Leu Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly
 260 265 270
 Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
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 Lys Lys Val Leu Lys Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe
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 Ile Asp Glu Ile His Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala
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 Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu
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 Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu
 340 345 350
 Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu
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 Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg
 370 375 380
 Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr Ala
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 Ala Ala Gln Leu Ala Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro Asp
 405 410 415
 Lys Ala Val Asp Leu Ile Asp Glu Ala Gly Ala Arg Met Arg Ile Lys
 420 425 430
 Arg Met Thr Ala Pro Ser Ser Leu Arg Glu Val Asp Glu Arg Ile Ala
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 Asp Val Arg Arg Glu Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe Glu
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 Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu Arg
 465 470 475 480
 Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile Ala
 485 490 495
 Glu Val Gly Glu Glu Gln Ile Ala Glu Val Leu Ala Asn Trp Thr Gly
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 Ile Pro Val Phe Lys Leu Thr Glu Ala Glu Ser Ser Arg Leu Leu Asn
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Pro Lys Arg Pro Ser Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly Val
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 755 760 765
 Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn Arg
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 Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile Gln
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 Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro Lys
 835 840 845
 Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala Glu
 850 855 860
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 Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu Glu

885

890

895

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<212> DNA

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<223> FRXA02470

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att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga 259
 Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly
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att tcc ctg gac gcc gtc cgc cag gaa gtc gaa gag att atc ggc cag 307
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 Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys
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aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag 403
 Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys
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 Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu Ile Arg Glu Gly Glu
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 Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg
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 135 140 145

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 Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp
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 gaa ggt ctt gca cta gac att gtt aac ggc aag gtt cca gag acc ctc 883
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 gag att aac cag cgc ggc gac atc atc ctg ttt atc gat gag atc cac 1027
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 295 300 305
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<213> Corynebacterium glutamicum

<400> 52

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 Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu
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 Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu
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 115 120 125
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 Tyr Glu Gly Gly Gln Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro
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 Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro
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 Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln
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 Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro
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 260 265 270
 Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
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<222> (101)..(1933)

<223> FRXA02471

<400> 53

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Leu Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile
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Glu Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp
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Arg Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr
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Ala Asp Val Arg Arg Glu Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe
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Glu Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu
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cgt tca gag aag gaa aag cag tgg cgc tcc ggc gac ctc gag gac atc 643
Arg Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile
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Ala Glu Val Gly Glu Glu Gln Ile Ala Glu Val Leu Ala Asn Trp Thr

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gat cct aag cgt cct tcc ggc tcc ttc atc ttc gct ggt cca tcc ggc Asp Pro Lys Arg Pro Ser Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly 250 255 260			883
gtt ggt aag acc gag ctg tcc aag gct ctc gca gga ttc ctc ttc ggt Val Gly Lys Thr Glu Leu Ser Lys Ala Leu Ala Gly Phe Leu Phe Gly 265 270 275			931
gac gat gat tcc ctc atc caa atc gac atg ggt gag ttc cac gac cgc Asp Asp Asp Ser Leu Ile Gln Ile Asp Met Gly Glu Phe His Asp Arg 280 285 290			979
ttc acc gcg tcc cga ctt ttc ggt gcc cct ccg gga tac gtt ggc tac Phe Thr Ala Ser Arg Leu Phe Gly Ala Pro Pro Gly Tyr Val Gly Tyr 295 300 305			1027
gaa gaa ggt ggc cag ctg acc gag aag gtt cgc cgt aag cca ttc tcc Glu Glu Gly Gly Gln Leu Thr Glu Lys Val Arg Arg Lys Pro Phe Ser 310 315 320 325			1075
gtt gtg ctt ttc gac gaa atc gag aag gcc cac aag gag atc tac aac Val Val Leu Phe Asp Glu Ile Glu Lys Ala His Lys Glu Ile Tyr Asn 330 335 340			1123
acc ttg ctg cag gtg ttg gaa gat ggt cgc ctt acc gat ggt cag gga Thr Leu Leu Gln Val Leu Glu Asp Gly Arg Leu Thr Asp Gly Gln Gly 345 350 355			1171
cgc atc gtg gac ttc aag aac acc gtc ctg atc ttc acc tcc aac ctg Arg Ile Val Asp Phe Lys Asn Thr Val Leu Ile Phe Thr Ser Asn Leu 360 365 370			1219
ggc acc gct gac atc tcc aag gct gtt ggc ctg ggc ttc tcc gga tcc Gly Thr Ala Asp Ile Ser Lys Ala Val Gly Leu Gly Phe Ser Gly Ser 375 380 385			1267
tcc gag act gac agc gat gct cag tac gac cgc atg aag aac aag gtc Ser Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg Met Lys Asn Lys Val 390 395 400 405			1315
cac gac gag ctg aag aag cac ttc cgc cct gag ttc ctg aac cgt att His Asp Glu Leu Lys Lys His Phe Arg Pro Glu Phe Leu Asn Arg Ile 410 415 420			1363
gat gag atc gtg gtc ttc cac cag ctc acc aag gat cag atc gtt cag Asp Glu Ile Val Val Phe His Gln Leu Thr Lys Asp Gln Ile Val Gln 425 430 435			1411

atg gtc gac ctt ctt atc ggt cgc gtt tcc aac gca ctg gct gag aag 1459
 Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn Ala Leu Ala Glu Lys
 440 445 450
 gac atg agc atc gaa ctg act gag aag gcc aag gac ctc ctg gct aac 1507
 Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn
 455 460 465
 cga ggc ttc gat cca gtt ctg ggt gca cga cca ttg cgt cgc acc atc 1555
 Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile
 470 475 480 485
 cag cgc gaa att gaa gac cag atg tcc gag aag atc ctc ttc ggt gaa 1603
 Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys Ile Leu Phe Gly Glu
 490 495 500
 atc ggc gca ggc gag atc gtc acc gtt gac gtc gaa ggc tgg gag ggc 1651
 Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val Glu Gly Trp Asp Gly
 505 510 515
 gag tcc aag gac acc gac cgt gcg aag ttc acc ttc aca cca cgt cca 1699
 Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro
 520 525 530
 aag cca atg cca gaa ggt aag ttc tct gag atc tct gtc gag gct gcg 1747
 Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala
 535 540 545
 gaa gca att caa gat gta gat tct gca gct gac ggc gat gtc cca gaa 1795
 Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp Gly Asp Val Pro Glu
 550 555 560 565
 acc gat tca ctt tcc gac att gac ctt gaa acc ctt gaa aag ttt gag 1843
 Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu
 570 575 580
 gaa gat gta gaa aac ggc acc gac att gat cag gtg tcc ggt gac tac 1891
 Glu Asp Val Glu Asn Gly Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr
 585 590 595
 tac ggc acc gat gat cag gga ggc act gct cca agc aag gag 1933
 Tyr Gly Thr Asp Asp Gln Gly Gly Thr Ala Pro Ser Lys Glu
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 tagcaacctt ttgaaaaagg gcc 1956

<210> 54

<211> 611

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 54

Val Gln His Glu Gly Ala Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys
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 20 25 30

Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln

35					40					45					
Pro	Val	Gln	Val	Pro	Glu	Pro	Ser	Val	Asp	Leu	Thr	Val	Glu	Ile	Leu
50					55					60					
Lys	Gly	Leu	Arg	Asp	Arg	Tyr	Glu	Ala	His	His	Arg	Val	Ser	Ile	Thr
65					70					75					80
Asp	Gly	Ala	Leu	Thr	Ala	Ala	Ala	Gln	Leu	Ala	Asp	Arg	Tyr	Ile	Asn
				85					90					95	
Asp	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Val	Asp	Leu	Ile	Asp	Glu	Ala	Gly
			100					105					110		
Ala	Arg	Met	Arg	Ile	Lys	Arg	Met	Thr	Ala	Pro	Ser	Ser	Leu	Arg	Glu
			115					120					125		
Val	Asp	Glu	Arg	Ile	Ala	Asp	Val	Arg	Arg	Glu	Lys	Glu	Ala	Ala	Ile
			130					135					140		
Asp	Ala	Gln	Asp	Phe	Glu	Lys	Ala	Ala	Gly	Leu	Arg	Asp	Lys	Glu	Arg
145															160
Lys	Leu	Gly	Glu	Glu	Arg	Ser	Glu	Lys	Glu	Lys	Gln	Trp	Arg	Ser	Gly
				165					170						175
Asp	Leu	Glu	Asp	Ile	Ala	Glu	Val	Gly	Glu	Glu	Gln	Ile	Ala	Glu	Val
			180						185					190	
Leu	Ala	Asn	Trp	Thr	Gly	Ile	Pro	Val	Phe	Lys	Leu	Thr	Glu	Ala	Glu
			195					200					205		
Ser	Ser	Arg	Leu	Leu	Asn	Met	Glu	Glu	Glu	Leu	His	Lys	Arg	Ile	Ile
			210						215						
Gly	Gln	Asp	Glu	Ala	Val	Lys	Ala	Val	Ser	Arg	Ala	Ile	Arg	Arg	Thr
225															240
Arg	Ala	Gly	Leu	Lys	Asp	Pro	Lys	Arg	Pro	Ser	Gly	Ser	Phe	Ile	Phe
				245					250						255
Ala	Gly	Pro	Ser	Gly	Val	Gly	Lys	Thr	Glu	Leu	Ser	Lys	Ala	Leu	Ala
				260					265					270	
Gly	Phe	Leu	Phe	Gly	Asp	Asp	Asp	Ser	Leu	Ile	Gln	Ile	Asp	Met	Gly
				275					280					285	
Glu	Phe	His	Asp	Arg	Phe	Thr	Ala	Ser	Arg	Leu	Phe	Gly	Ala	Pro	Pro
				290					295					300	
Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu	Lys	Val	Arg
305															320
Arg	Lys	Pro	Phe	Ser	Val	Val	Leu	Phe	Asp	Glu	Ile	Glu	Lys	Ala	His
				325					330						335
Lys	Glu	Ile	Tyr	Asn	Thr	Leu	Leu	Gln	Val	Leu	Glu	Asp	Gly	Arg	Leu
				340					345					350	
Thr	Asp	Gly	Gln	Gly	Arg	Ile	Val	Asp	Phe	Lys	Asn	Thr	Val	Leu	Ile
				355					360					365	

Phe Thr Ser Asn Leu Gly Thr Ala Asp Ile Ser Lys Ala Val Gly Leu
 370 375 380
 Gly Phe Ser Gly Ser Ser Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg
 385 390 395 400
 Met Lys Asn Lys Val His Asp Glu Leu Lys Lys His Phe Arg Pro Glu
 405 410 415
 Phe Leu Asn Arg Ile Asp Glu Ile Val Val Phe His Gln Leu Thr Lys
 420 425 430
 Asp Gln Ile Val Gln Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn
 435 440 445
 Ala Leu Ala Glu Lys Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys
 450 455 460
 Asp Leu Leu Ala Asn Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro
 465 470 475 480
 Leu Arg Arg Thr Ile Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys
 485 490 495
 Ile Leu Phe Gly Glu Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val
 500 505 510
 Glu Gly Trp Asp Gly Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr
 515 520 525
 Phe Thr Pro Arg Pro Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile
 530 535 540
 Ser Val Glu Ala Ala Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp
 545 550 555 560
 Gly Asp Val Pro Glu Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr
 565 570 575
 Leu Glu Lys Phe Glu Glu Asp Val Glu Asn Gly Thr Asp Ile Asp Gln
 580 585 590
 Val Ser Gly Asp Tyr Tyr Gly Thr Asp Asp Gln Gly Gly Thr Ala Pro
 595 600 605
 Ser Lys Glu .
 610

<210> 55
 <211> 1446
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1423)
 <223> RXA02630

<400> 55

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cttagagtga cgccccagcc acagggttca taatcaaatac atg aca aat caa ttc 115
Met Thr Asn Gln Phe
1 5

ccc aca aac aac ggt gag aac ccg gac cgt gca tcg gaa act cca tca 163
Pro Thr Asn Asn Gly Glu Asn Pro Asp Arg Ala Ser Glu Thr Pro Ser
10 15 20

gaa acc aac tcc ttc gaa cat gtg cgt agt tca tat ccg cag tgg ggt 211
Glu Thr Asn Ser Phe Glu His Val Arg Ser Ser Tyr Pro Gln Trp Gly
25 30 35

aac act gct tcc aat caa aac ccc tat cct ggt gcg ggc ttc ggc tct 259
Asn Thr Ala Ser Asn Gln Asn Pro Tyr Pro Gly Ala Gly Phe Gly Ser
40 45 50

gaa caa aac act caa caa gga aat gag caa caa gct cca gcc tgg acc 307
Glu Gln Asn Thr Gln Gln Gly Asn Glu Gln Gln Ala Pro Ala Trp Thr
55 60 65

agt tgg gat aat cag cct cta agc aca gat gta aag cca gct aaa gaa 355
Ser Trp Asp Asn Gln Pro Leu Ser Thr Asp Val Lys Pro Ala Lys Glu
70 75 80 85

aag cga aaa gtt ggc atc gga acg gca ctc gcg tta atg ctt gtt ggt 403
Lys Arg Lys Val Gly Ile Gly Thr Ala Leu Ala Leu Met Leu Val Gly
90 95 100

tct att gct acc ggt agc gtt gtg ggt gtt gca gca acc cag ctt ggt 451
Ser Ile Ala Thr Gly Ser Val Val Gly Val Ala Ala Thr Gln Leu Gly
105 110 115

tcg gac tct tca acc cca gtt aat gct ctt gag cag ccc agc gtg cag 499
Ser Asp Ser Ser Thr Pro Val Asn Ala Leu Glu Gln Pro Ser Val Gln
120 125 130

cgc acc act aat gct gaa cca ggt tca gcg gaa cag gtt gct gcc gca 547
Arg Thr Thr Asn Ala Glu Pro Gly Ser Ala Glu Gln Val Ala Ala Ala
135 140 145

gtt ttg cct tct gtc gtc tct att cag gcc att act agg acg tct gct 595
Val Leu Pro Ser Val Val Ser Ile Gln Ala Ile Thr Arg Thr Ser Ala
150 155 160 165

tct gag ggc tct gga tcc att att tcc tct gat ggt tac gtc atg acc 643
Ser Glu Gly Ser Gly Ser Ile Ile Ser Ser Asp Gly Tyr Val Met Thr
170 175 180

aat aat cac gtc gtg gca ggc att gaa caa tct ggt gtg tta gaa gta 691
Asn Asn His Val Val Ala Gly Ile Glu Gln Ser Gly Val Leu Glu Val
185 190 195

agt ttc tcc gat gga act aca gcg caa gct gat ttt att gct ggt gat 739
Ser Phe Ser Asp Gly Thr Thr Ala Gln Ala Asp Phe Ile Ala Gly Asp
200 205 210

cct tcc aca gat att gct gtg atc aag att agg gat gtg tcc aac ctt 787
Pro Ser Thr Asp Ile Ala Val Ile Lys Ile Arg Asp Val Ser Asn Leu
215 220 225

cca gtt atg agc ttt gga gat tcg gac gca tta ggc gtt gga caa agt	835
Pro Val Met Ser Phe Gly Asp Ser Asp Ala Leu Gly Val Gly Gln Ser	
230 235 240 245	
gtg atg gct gtt ggt tct cca ctg ggt ctg agc tcc act gtg acc acc	883
Val Met Ala Val Gly Ser Pro Leu Gly Leu Ser Ser Thr Val Thr Thr	
250 255 260	
ggt att gtg tcg gcc gtg aac cgt cct gtg cga gct tct ggt gat ggc	931
Gly Ile Val Ser Ala Val Asn Arg Pro Val Arg Ala Ser Gly Asp Gly	
265 270 275	
gga gag tcg tcc ctc atc gat gct atc cag acc gat gct gcg atc aac	979
Gly Glu Ser Ser Leu Ile Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn	
280 285 290	
cct ggt aac tct ggt ggt ccg ctg gtt gat atg gat ggc aac ctc att	1027
Pro Gly Asn Ser Gly Gly Pro Leu Val Asp Met Asp Gly Asn Leu Ile	
295 300 305	
ggc atg aat tcg gta att gca tcg att tcg agc acc agc gat tcc gca	1075
Gly Met Asn Ser Val Ile Ala Ser Ile Ser Ser Thr Ser Asp Ser Ala	
310 315 320 325	
ggt tcc att ggt ctt ggt ttt tct atc cca tcc aac ttt gcc aag cgc	1123
Gly Ser Ile Gly Leu Gly Phe Ser Ile Pro Ser Asn Phe Ala Lys Arg	
330 335 340	
gtg gcc gat caa ttg atc agc acc ggc cag gta act cag ccg atg atc	1171
Val Ala Asp Gln Leu Ile Ser Thr Gly Gln Val Thr Gln Pro Met Ile	
345 350 355	
ggt gtg cag gtt ggc act gac aac tca gtg aca ggc gct gtg att gcc	1219
Gly Val Gln Val Gly Thr Asp Asn Ser Val Thr Gly Ala Val Ile Ala	
360 365 370	
agt gtt caa gat ggt gga ccg gcc gca gat gct gga ctt cag cca ggc	1267
Ser Val Gln Asp Gly Gly Pro Ala Ala Asp Ala Gly Leu Gln Pro Gly	
375 380 385	
gat atc gtg acc aag ctc aat gat cga gtt att gat agc cca gac tcc	1315
Asp Ile Val Thr Lys Leu Asn Asp Arg Val Ile Asp Ser Pro Asp Ser	
390 395 400 405	
ttg atc gct gct gtt cgt tcg cat gat ttt ggc gaa acc gtc act tta	1363
Leu Ile Ala Ala Val Arg Ser His Asp Phe Gly Glu Thr Val Thr Leu	
410 415 420	
aca att aca cag cca gat acc tcg cag agc cgg gag gta gag gtt act	1411
Thr Ile Thr Gln Pro Asp Thr Ser Gln Ser Arg Glu Val Glu Val Thr	
425 430 435	
ctg acg agt gag taggtttaaa agagttaatc tgc	1446
Leu Thr Ser Glu	
440	

<210> 56
 <211> 441
 <212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Thr Asn Gln Phe Pro Thr Asn Asn Gly Glu Asn Pro Asp Arg Ala
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 Ser Glu Thr Pro Ser Glu Thr Asn Ser Phe Glu His Val Arg Ser Ser
 20 25 30
 Tyr Pro Gln Trp Gly Asn Thr Ala Ser Asn Gln Asn Pro Tyr Pro Gly
 35 40 45
 Ala Gly Phe Gly Ser Glu Gln Asn Thr Gln Gln Gly Asn Glu Gln Gln
 50 55 60
 Ala Pro Ala Trp Thr Ser Trp Asp Asn Gln Pro Leu Ser Thr Asp Val
 65 70 75 80
 Lys Pro Ala Lys Glu Lys Arg Lys Val Gly Ile Gly Thr Ala Leu Ala
 85 90 95
 Leu Met Leu Val Gly Ser Ile Ala Thr Gly Ser Val Val Gly Val Ala
 100 105 110
 Ala Thr Gln Leu Gly Ser Asp Ser Ser Thr Pro Val Asn Ala Leu Glu
 115 120 125
 Gln Pro Ser Val Gln Arg Thr Thr Asn Ala Glu Pro Gly Ser Ala Glu
 130 135 140
 Gln Val Ala Ala Ala Val Leu Pro Ser Val Val Ser Ile Gln Ala Ile
 145 150 155 160
 Thr Arg Thr Ser Ala Ser Glu Gly Ser Gly Ser Ile Ile Ser Ser Asp
 165 170 175
 Gly Tyr Val Met Thr Asn Asn His Val Val Ala Gly Ile Glu Gln Ser
 180 185 190
 Gly Val Leu Glu Val Ser Phe Ser Asp Gly Thr Thr Ala Gln Ala Asp
 195 200 205
 Phe Ile Ala Gly Asp Pro Ser Thr Asp Ile Ala Val Ile Lys Ile Arg
 210 215 220
 Asp Val Ser Asn Leu Pro Val Met Ser Phe Gly Asp Ser Asp Ala Leu
 225 230 235 240
 Gly Val Gly Gln Ser Val Met Ala Val Gly Ser Pro Leu Gly Leu Ser
 245 250 255
 Ser Thr Val Thr Thr Gly Ile Val Ser Ala Val Asn Arg Pro Val Arg
 260 265 270
 Ala Ser Gly Asp Gly Gly Glu Ser Ser Leu Ile Asp Ala Ile Gln Thr
 275 280 285
 Asp Ala Ala Ile Asn Pro Gly Asn Ser Gly Gly Pro Leu Val Asp Met
 290 295 300
 Asp Gly Asn Leu Ile Gly Met Asn Ser Val Ile Ala Ser Ile Ser Ser

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Asp	Ser	Lys	Gly	Arg	Ser	Val	Asp	Phe	Lys	Asn	Thr	Ile	Ile	Ile	Met	
1				5					10					15		
act	agt	aat	att	ggt	tca	caa	gta	tta	ctt	gaa	aat	gta	aaa	gat	gct	96
Thr	Ser	Asn	Ile	Gly	Ser	Gln	Val	Leu	Leu	Glu	Asn	Val	Lys	Asp	Ala	
			20					25					30			
ggt	gaa	att	agt	gat	gat	aca	gag	aaa	gca	ggt	atg	gac	agt	cta	cat	144
Gly	Glu	Ile	Ser	Asp	Asp	Thr	Glu	Lys	Ala	Val	Met	Asp	Ser	Leu	His	
		35					40					45				
gca	tac	ttc	aaa	cct	gaa	ata	tta	aat	cgt	atg	gat	gac	atc	gtg	tta	192
Ala	Tyr	Phe	Lys	Pro	Glu	Ile	Leu	Asn	Arg	Met	Asp	Asp	Ile	Val	Leu	
50						55					60					
ttt	aaa	cca	tta	tca	ggt	aat	gat	atg	agt	atg	att	gta	gat	aaa	att	240
Phe	Lys	Pro	Leu	Ser	Val	Asn	Asp	Met	Ser	Met	Ile	Val	Asp	Lys	Ile	
65					70					75					80	
tta	aca	caa	tta	aat	atg	aga	tta	tta	gat	caa	cat	atc	tca	att	gaa	288
Leu	Thr	Gln	Leu	Asn	Met	Arg	Leu	Leu	Asp	Gln	His	Ile	Ser	Ile	Glu	
				85					90					95		

gtg aca gaa gaa gcg aaa aaa tgg cta ggt gaa gaa gcg tat gaa cca 336
Val Thr Glu Glu Ala Lys Lys Trp Leu Gly Glu Glu Ala Tyr Glu Pro
100 105 110

caa ttt ggt gca aga cca tta aaa cgc ttt gtt caa cga caa ata gaa 384
Gln Phe Gly Ala Arg Pro Leu Lys Arg Phe Val Gln Arg Gln Ile Glu
115 120 125

act cca att gca cgt atg atg att aaa gaa agt cta cct gaa ggt aca 432
Thr Pro Ile Ala Arg Met Met Ile Lys Glu Ser Leu Pro Glu Gly Thr
130 135 140

ata att aaa gta gat tta aat gac aat aaa gaa ctt gat ttt aag gtt 480
Ile Ile Lys Val Asp Leu Asn Asp Asn Lys Glu Leu Asp Phe Lys Val
145 150 155 160

gtt aaa cct acg tct taatctagca aaatattaat ttg 518
Val Lys Pro Thr Ser
165

<210> 58

<211> 165

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 58

Asp Ser Lys Gly Arg Ser Val Asp Phe Lys Asn Thr Ile Ile Ile Met
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Thr Ser Asn Ile Gly Ser Gln Val Leu Leu Glu Asn Val Lys Asp Ala
20 25 30

Gly Glu Ile Ser Asp Asp Thr Glu Lys Ala Val Met Asp Ser Leu His
35 40 45

Ala Tyr Phe Lys Pro Glu Ile Leu Asn Arg Met Asp Asp Ile Val Leu
50 55 60

Phe Lys Pro Leu Ser Val Asn Asp Met Ser Met Ile Val Asp Lys Ile
65 70 75 80

Leu Thr Gln Leu Asn Met Arg Leu Leu Asp Gln His Ile Ser Ile Glu
85 90 95

Val Thr Glu Glu Ala Lys Lys Trp Leu Gly Glu Glu Ala Tyr Glu Pro
100 105 110

Gln Phe Gly Ala Arg Pro Leu Lys Arg Phe Val Gln Arg Gln Ile Glu
115 120 125

Thr Pro Ile Ala Arg Met Met Ile Lys Glu Ser Leu Pro Glu Gly Thr
130 135 140

Ile Ile Lys Val Asp Leu Asn Asp Asn Lys Glu Leu Asp Phe Lys Val
145 150 155 160

Val Lys Pro Thr Ser
165

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<210> 59
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1291)
<223> BXA00112
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atattatcga ttttcgaaag cgtagaacac caaaccattg ttg agc ccc agc ctg 115
Leu Ser Pro Ser Leu
1 5

gtc gtc gat gcc gtc atc gtc ctc gtt atg gca ttc gcc ctg tgg ggt 163
Val Val Asp Ala Val Ile Val Leu Val Met Ala Phe Ala Leu Trp Gly
10 15 20

ggt tgg cgt caa ggc gcc ttc acc tcg ctg ctg tcc acc gtc ggc gtc 211
Gly Trp Arg Gln Gly Ala Phe Thr Ser Leu Leu Ser Thr Val Gly Val
25 30 35

gtt tct ggc ctg gta gtt ggc gca gca gca gct cca ttt gtc atg ggt 259
Val Ser Gly Leu Val Val Gly Ala Ala Ala Ala Pro Phe Val Met Gly
40 45 50

ctc acc gat tcc acc gcg ctt cgc ttc ctc ctg gcg atc ggc acc gtg 307
Leu Thr Asp Ser Thr Ala Leu Arg Phe Leu Leu Ala Ile Gly Thr Val
55 60 65

gtg ctg ctg gtt ggt ttg gga aat ctc atc ggc gcc cac ttg ggt gct 355
Val Leu Leu Val Gly Leu Gly Asn Leu Ile Gly Ala His Leu Gly Ala
70 75 80 85

gcg att aga gac aac atc aaa ttc cga agt tcc agg acc tta gat tct 403
Ala Ile Arg Asp Asn Ile Lys Phe Arg Ser Ser Arg Thr Leu Asp Ser
90 95 100

ggg ctc ggc gcc att ttc caa gta ttg gcc acc ttg atc gtg gtg tgg 451
Gly Leu Gly Ala Ile Phe Gln Val Leu Ala Thr Leu Ile Val Val Trp
105 110 115

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ctc gtc gca att ccc ctg gcc aca ggc ctc ccc gga act gtc gcc agc    499
Leu Val Ala Ile Pro Leu Ala Thr Gly Leu Pro Gly Thr Val Ala Ser
      120                      125                      130

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gga att aga gac tcc cgc atc ctg ggc ttt gta gac aaa tac acc ccg 547
Gly Ile Arg Asp Ser Arg Ile Leu Gly Phe Val Asp Lys Tyr Thr Pro
135 140 145

caa ggc cta gat acc ctg ccc tcc aaa atc gct gcg atg ctc agc gaa 595
Gln Gly Leu Asp Thr Leu Pro Ser Lys Ile Ala Ala Met Leu Ser Glu
150 155 160 165

tcc ggc ctc cca cca ctg att tcc ccc ttc acc ggc gga tcc tcg gtg 643
Ser Gly Leu Pro Pro Leu Ile Ser Pro Phe Thr Gly Gly Ser Ser Val
170 175 180

gaa gtg gac gcc ccc gaa atc aac gtc acc aac gtt gac cta gtc gaa 691
 Glu Val Asp Ala Pro Glu Ile Asn Val Thr Asn Val Asp Leu Val Glu
 185 190 195

gca atg cgc ccg tcc gtc atc cac gtg atg ggt gac gcc caa gaa tgc 739
 Ala Met Arg Pro Ser Val Ile His Val Met Gly Asp Ala Gln Glu Cys
 200 205 210

agc cgc cga ctc atg ggt tct ggc ttt gtg gca tcc ccc gac tac gtt 787
 Ser Arg Arg Leu Met Gly Ser Gly Phe Val Ala Ser Pro Asp Tyr Val
 215 220 225

gtg acc aac gcc cac gtt gtt gca ggt acc tcc acc gtc agc ctg gat 835
 Val Thr Asn Ala His Val Val Ala Gly Thr Ser Thr Val Ser Leu Asp
 230 235 240 245

acc atg atc gga acc cgc tcc gca gag gta gtg ttc tac gac ccg aac 883
 Thr Met Ile Gly Thr Arg Ser Ala Glu Val Val Phe Tyr Asp Pro Asn
 250 255 260

ctg gac atc gca gtc ctt tac agc cct gac ctc ggc ttg gat cca ctg 931
 Leu Asp Ile Ala Val Leu Tyr Ser Pro Asp Leu Gly Leu Asp Pro Leu
 265 270 275

ccg tgg gca tcc act ccg cta gac act ggc gat gaa gca atc gtc atg 979
 Pro Trp Ala Ser Thr Pro Leu Asp Thr Gly Asp Glu Ala Ile Val Met
 280 285 290

gga ttc cca cag tcc gga cct ttc aac gcc tcc cca gcc agg gtc cgc 1027
 Gly Phe Pro Gln Ser Gly Pro Phe Asn Ala Ser Pro Ala Arg Val Arg
 295 300 305

gaa cgc atc atg atc acc ggc agc aac att tac gcc aac ggc cag cac 1075
 Glu Arg Ile Met Ile Thr Gly Ser Asn Ile Tyr Ala Asn Gly Gln His
 310 315 320 325

gaa cgc gaa gcc tat tca gtc cgc gga tcc atc caa tct gga aac tcc 1123
 Glu Arg Glu Ala Tyr Ser Val Arg Gly Ser Ile Gln Ser Gly Asn Ser
 330 335 340

ggc ggc cca atg acc aac gaa atg ggt gaa gtg gtt ggt gtt gtc ttc 1171
 Gly Gly Pro Met Thr Asn Glu Met Gly Glu Val Val Gly Val Val Phe
 345 350 355

ggc gca gcg atc gac ggc tcc gat acc ggt tac gtt ctc act gcc gaa 1219
 Gly Ala Ala Ile Asp Gly Ser Asp Thr Gly Tyr Val Leu Thr Ala Glu
 360 365 370

gag gta cag gag cgg atc ggc gac atc acc gcg ctg act cag cct gtc 1267
 Glu Val Gln Glu Arg Ile Gly Asp Ile Thr Ala Leu Thr Gln Pro Val
 375 380 385

gat acg atg cag tgc gcg gtt tct tagtcgtcgg gagctaggac cag 1314
 Asp Thr Met Gln Cys Ala Val Ser
 390 395

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<213> Corynebacterium glutamicum

<400> 60

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Phe Ala Leu Trp Gly Gly Trp Arg Gln Gly Ala Phe Thr Ser Leu Leu
      20              25              30

Ser Thr Val Gly Val Val Ser Gly Leu Val Val Gly Ala Ala Ala Ala
      35              40              45

Pro Phe Val Met Gly Leu Thr Asp Ser Thr Ala Leu Arg Phe Leu Leu
      50              55              60

Ala Ile Gly Thr Val Val Leu Leu Val Gly Leu Gly Asn Leu Ile Gly
      65              70              75              80

Ala His Leu Gly Ala Ala Ile Arg Asp Asn Ile Lys Phe Arg Ser Ser
      85              90              95

Arg Thr Leu Asp Ser Gly Leu Gly Ala Ile Phe Gln Val Leu Ala Thr
      100             105             110

Leu Ile Val Val Trp Leu Val Ala Ile Pro Leu Ala Thr Gly Leu Pro
      115             120             125

Gly Thr Val Ala Ser Gly Ile Arg Asp Ser Arg Ile Leu Gly Phe Val
      130             135             140

Asp Lys Tyr Thr Pro Gln Gly Leu Asp Thr Leu Pro Ser Lys Ile Ala
      145             150             155             160

Ala Met Leu Ser Glu Ser Gly Leu Pro Pro Leu Ile Ser Pro Phe Thr
      165             170             175

Gly Gly Ser Ser Val Glu Val Asp Ala Pro Glu Ile Asn Val Thr Asn
      180             185             190

Val Asp Leu Val Glu Ala Met Arg Pro Ser Val Ile His Val Met Gly
      195             200             205

Asp Ala Gln Glu Cys Ser Arg Arg Leu Met Gly Ser Gly Phe Val Ala
      210             215             220

Ser Pro Asp Tyr Val Val Thr Asn Ala His Val Val Ala Gly Thr Ser
      225             230             235             240

Thr Val Ser Leu Asp Thr Met Ile Gly Thr Arg Ser Ala Glu Val Val
      245             250             255

Phe Tyr Asp Pro Asn Leu Asp Ile Ala Val Leu Tyr Ser Pro Asp Leu
      260             265             270

Gly Leu Asp Pro Leu Pro Trp Ala Ser Thr Pro Leu Asp Thr Gly Asp
      275             280             285

Glu Ala Ile Val Met Gly Phe Pro Gln Ser Gly Pro Phe Asn Ala Ser
      290             295             300

Pro Ala Arg Val Arg Glu Arg Ile Met Ile Thr Gly Ser Asn Ile Tyr

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305					310					315					320
Ala	Asn	Gly	Gln	His	Glu	Arg	Glu	Ala	Tyr	Ser	Val	Arg	Gly	Ser	Ile
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Gln	Ser	Gly	Asn	Ser	Gly	Gly	Pro	Met	Thr	Asn	Glu	Met	Gly	Glu	Val
			340					345					350		
Val	Gly	Val	Val	Phe	Gly	Ala	Ala	Ile	Asp	Gly	Ser	Asp	Thr	Gly	Tyr
		355					360					365			
Val	Leu	Thr	Ala	Glu	Glu	Val	Gln	Glu	Arg	Ile	Gly	Asp	Ile	Thr	Ala
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<213> Corynebacterium glutamicum
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<223> RXA00566
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								Met	Pro	Thr	Ser	Arg				
								1				5				
tac	gtg	ctg	cct	tcc	ttc	att	gag	cag	tcc	gca	tac	ggc	acc	aaa	gag	163
Tyr	Val	Leu	Pro	Ser	Phe	Ile	Glu	Gln	Ser	Ala	Tyr	Gly	Thr	Lys	Glu	
				10				15						20		
acc	aac	cct	tac	gca	aaa	ctc	ttt	gaa	gag	cgc	atc	atc	ttc	ctg	ggc	211
Thr	Asn	Pro	Tyr	Ala	Lys	Leu	Phe	Glu	Glu	Arg	Ile	Ile	Phe	Leu	Gly	
			25					30					35			
acc	cag	gtc	gac	gac	acc	tct	gca	aac	gac	atc	atg	gcg	cag	ctc	ctt	259
Thr	Gln	Val	Asp	Asp	Thr	Ser	Ala	Asn	Asp	Ile	Met	Ala	Gln	Leu	Leu	
		40					45					50				
gtc	ctc	gaa	ggc	atg	gac	cca	gac	cgc	gat	atc	acc	ctg	tac	atc	aac	307
Val	Leu	Glu	Gly	Met	Asp	Pro	Asp	Arg	Asp	Ile	Thr	Leu	Tyr	Ile	Asn	
	55					60					65					
tca	cct	ggt	gga	tcc	ttc	acc	gcg	ttg	atg	gca	att	tac	gac	acc	atg	355
Ser	Pro	Gly	Gly	Ser	Phe	Thr	Ala	Leu	Met	Ala	Ile	Tyr	Asp	Thr	Met	
70					75					80					85	
cag	tac	gtc	cgc	cca	gac	gtt	cag	acc	gtc	tgc	ctt	ggt	cag	gca	gca	403
Gln	Tyr	Val	Arg	Pro	Asp	Val	Gln	Thr	Val	Cys	Leu	Gly	Gln	Ala	Ala	
				90					95					100		
tcc	gca	gcc	gca	gtt	ctt	ctt	gca	gcc	ggt	gca	cca	ggt	aag	cgc	gct	451
Ser	Ala	Ala	Ala	Val	Leu	Leu	Ala	Ala	Gly	Ala	Pro	Gly	Lys	Arg	Ala	

105 110 115
 gtt ctt cct aac tcc cgc gtg ctg atc cac cag cca gca acc cag ggc 499
 Val Leu Pro Asn Ser Arg Val Leu Ile His Gln Pro Ala Thr Gln Gly
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 acc cag ggt cag gtt tct gac ctc gag atc cag gca gct gaa atc gag 547
 Thr Gln Gly Gln Val Ser Asp Leu Glu Ile Gln Ala Ala Glu Ile Glu
 135 140 145
 cgc atg cgt cgt ttg atg gaa acc acc ttg gct gag cac acc ggc aag 595
 Arg Met Arg Arg Leu Met Glu Thr Thr Leu Ala Glu His Thr Gly Lys
 150 155 160 165
 acc gcg gag cag atc cgc atc gat acc gac cgt gac aag atc ctc acc 643
 Thr Ala Glu Gln Ile Arg Ile Asp Thr Asp Arg Asp Lys Ile Leu Thr
 170 175 180
 gct gag gaa gca ctc gag tat ggc atc gtt gac cag gtc ttc gat tac 691
 Ala Glu Glu Ala Leu Glu Tyr Gly Ile Val Asp Gln Val Phe Asp Tyr
 185 190 195
 cgc aag ctc aag cgc tagagttttt taaagattcg ggt 729
 Arg Lys Leu Lys Arg
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 <213> Corynebacterium glutamicum
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 Ile Ile Phe Leu Gly Thr Gln Val Asp Asp Thr Ser Ala Asn Asp Ile
 35 40 45
 Met Ala Gln Leu Leu Val Leu Glu Gly Met Asp Pro Asp Arg Asp Ile
 50 55 60
 Thr Leu Tyr Ile Asn Ser Pro Gly Gly Ser Phe Thr Ala Leu Met Ala
 65 70 75 80
 Ile Tyr Asp Thr Met Gln Tyr Val Arg Pro Asp Val Gln Thr Val Cys
 85 90 95
 Leu Gly Gln Ala Ala Ser Ala Ala Ala Val Leu Leu Ala Ala Gly Ala
 100 105 110
 Pro Gly Lys Arg Ala Val Leu Pro Asn Ser Arg Val Leu Ile His Gln
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 Pro Ala Thr Gln Gly Thr Gln Gly Gln Val Ser Asp Leu Glu Ile Gln
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 Ala Ala Glu Ile Glu Arg Met Arg Arg Leu Met Glu Thr Thr Leu Ala

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<213> Corynebacterium glutamicum
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Met Ser Asp Ile Arg																	5
atg gca gcc cag ggt ggg cct ggt ttc gga aat gac gtc ttt gat cgc																	163
Met Ala Ala Gln Gly Gly Pro Gly Phe Gly Asn Asp Val Phe Asp Arg																	20
ctc atg agt gag cgc atc att ttc ctg gga agc cag gta gac gat gag																	211
Leu Met Ser Glu Arg Ile Ile Phe Leu Gly Ser Gln Val Asp Asp Glu																	35
att gca aac aag cta tgc gct cag atc ctg ctg ctg tcc gct gag gat																	259
Ile Ala Asn Lys Leu Cys Ala Gln Ile Leu Leu Leu Ser Ala Glu Asp																	50
cca acc agg gac atc tcc ctg tac att aac tcc cca ggt ggc tcc gtc																	307
Pro Thr Arg Asp Ile Ser Leu Tyr Ile Asn Ser Pro Gly Gly Ser Val																	65
acc gca ggc atg gca att tat gac acc atg aaa tac tcc cca tgc gac																	355
Thr Ala Gly Met Ala Ile Tyr Asp Thr Met Lys Tyr Ser Pro Cys Asp																	85
atc gca acc tac ggc atg ggc ctg gca gca tcc atg ggc cag ttc ctg																	403
Ile Ala Thr Tyr Gly Met Gly Leu Ala Ala Ser Met Gly Gln Phe Leu																	100
ctt tcc ggt ggc act aag ggc aag cgt ttc gca ttg cca cac gca cgt																	451
Leu Ser Gly Gly Thr Lys Gly Lys Arg Phe Ala Leu Pro His Ala Arg																	115
atc atg atg cac cag cct tcc gct ggt gtt ggt ggt acc gca gct gat																	499
Ile Met Met His Gln Pro Ser Ala Gly Val Gly Gly Thr Ala Ala Asp																	120

atc gct atc cag gct gag cag ttc gca gcc acc aag cgt gaa atg gcc 547
 Ile Ala Ile Gln Ala Glu Gln Phe Ala Ala Thr Lys Arg Glu Met Ala
 135 140 145

cag ctg atc gct gag cac acc ggc cag acc ttt gag cag atc tcc aag 595
 Gln Leu Ile Ala Glu His Thr Gly Gln Thr Phe Glu Gln Ile Ser Lys
 150 155 160 165

gat tcc gat cgt gac cgc tgg ttc act gca cag gaa gct aag gat tac 643
 Asp Ser Asp Arg Asp Arg Trp Phe Thr Ala Gln Glu Ala Lys Asp Tyr
 170 175 180

gga ctt gtt gac cac gtg att acc ttg gct gaa ggc cca atc agc aac 691
 Gly Leu Val Asp His Val Ile Thr Leu Ala Glu Gly Pro Ile Ser Asn
 185 190 195

taggcgcacg gaaaacttta aag 714

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 64
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Gln Val Asp Asp Glu Ile Ala Asn Lys Leu Cys Ala Gln Ile Leu Leu
 35 40 45

Leu Ser Ala Glu Asp Pro Thr Arg Asp Ile Ser Leu Tyr Ile Asn Ser
 50 55 60

Pro Gly Gly Ser Val Thr Ala Gly Met Ala Ile Tyr Asp Thr Met Lys
 65 70 75 80

Tyr Ser Pro Cys Asp Ile Ala Thr Tyr Gly Met Gly Leu Ala Ala Ser
 85 90 95

Met Gly Gln Phe Leu Leu Ser Gly Gly Thr Lys Gly Lys Arg Phe Ala
 100 105 110

Leu Pro His Ala Arg Ile Met Met His Gln Pro Ser Ala Gly Val Gly
 115 120 125

Gly Thr Ala Ala Asp Ile Ala Ile Gln Ala Glu Gln Phe Ala Ala Thr
 130 135 140

Lys Arg Glu Met Ala Gln Leu Ile Ala Glu His Thr Gly Gln Thr Phe
 145 150 155 160

Glu Gln Ile Ser Lys Asp Ser Asp Arg Asp Arg Trp Phe Thr Ala Gln
 165 170 175

Glu Ala Lys Asp Tyr Gly Leu Val Asp His Val Ile Thr Leu Ala Glu
 180 185 190

Gly Pro Ile Ser Asn
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1852)
<223> RXN03094

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Met Ser Ser Phe Asn
1 5

cca act acc aaa acc aat gaa gcc atg cag gct gct ctt cag cag gca 163
Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala Ala Leu Gln Gln Ala
10 15 20

tcc tcg gct ggc aac cct gat att cgt cca gct cac ctg ttg gct gcc 211
Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala His Leu Leu Ala Ala
25 30 35

atc ttg gag caa act gat ggc gta gca gcg cca gtc ctc atg gct act 259
Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro Val Leu Met Ala Thr
40 45 50

ggg gtg gat cct aag gag atc ctc gca gag gcc aag aag ttg gtt gct 307
Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Val Ala
55 60 65

tct tac ccc aag gct tct ggc gcc aat atg gct aat cca aac ttc aac 355
Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala Asn Pro Asn Phe Asn
70 75 80 85

cgg gat gcc ctc aat gcg ttc act gca gct cag gag ctt gcc ggt gag 403
Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln Glu Leu Ala Gly Glu
90 95 100

ttg ggc gat gag tac gtc tca acc gaa gta ctt ctt gcc ggt atc gct 451
Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu Leu Ala Gly Ile Ala
105 110 115

cgc gga aag tct gat gct gcg gat ctg ttg acc aac aag ggt gca acc 499
Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr Asn Lys Gly Ala Thr
120 125 130

tat gac gcc atc aaa gag gct ttc cct tcg gtt cgt gga tct cag cgt 547
Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val Arg Gly Ser Gln Arg
135 140 145

gtc acc act cag gat cca gag gga cag ttc cag gct ttg gaa aag tac 595
Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln Ala Leu Glu Lys Tyr
150 155 160 165

tcc act gac ctg acc aag ctt gct cgt gaa ggc aag att gat cct gtt Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly Lys Ile Asp Pro Val 170 175 180	643
att ggc cgt gac cag gaa att cgt cgc gtc gtt cag gtg ctt agc cgt Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val Gln Val Leu Ser Arg 185 190 195	691
cgt acc aag aac aac cct gtt ctg atc ggt gag cca ggt gtc ggt aaa Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys 200 205 210	739
acc gcc atc gtg gaa ggc ctt gca cgc cgc atc gtt gct ggt gac gtt Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile Val Ala Gly Asp Val 215 220 225	787
cca gaa tcc ctc aag ggc aaa act ctg atc agt ctt gat ctt ggt tcc Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser Leu Asp Leu Gly Ser 230 235 240 245	835
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gct gtt ctg gat gag atc aag gga gct aac ggc gaa gtc gtt acc ttc Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly Glu Val Val Thr Phe 265 270 275	931
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ctg cgc ttg gtt ggt gcc acc acg ctg aat gag tac cgc aag tac atc Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu Tyr Arg Lys Tyr Ile 310 315 320 325	1075
gaa aag gac gct gcc ctg gag cgt agg ttc cag cag gtt tat gtc ggt Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Gln Val Tyr Val Gly 330 335 340	1123
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gcc gca gct gaa ctc tca aac cgc tat atc acc agc cgt ttc ctt cct Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr Ser Arg Phe Leu Pro 375 380 385	1267
gat aag gct att gac tta gtt gat gag gca gca tca cgc ctg cgc atg Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala Ser Arg Leu Arg Met 390 395 400 405	1315
gag att gat tct tca cct cag gaa atc gat gag ctg gag cgt atc gtc	1363

Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu Leu Glu Arg Ile Val
 410 415 420
 cgc cgc ctc gag atc gaa gag atg gcg ctg tcc aag gaa tcc gat gca 1411
 Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser Lys Glu Ser Asp Ala
 425 430 435
 gct tcc aag gaa cgt cta gaa aag ctg cgc tcg gaa ctt gct gat gaa 1459
 Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser Glu Leu Ala Asp Glu
 440 445 450
 cgc gaa aag ctc tct gag ttg aag gct cgt tgg cag aat gag aaa act 1507
 Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp Gln Asn Glu Lys Thr
 455 460 465
 gct att gac gat gtc cgg gag atg aaa gaa gag ctg gaa gcg ctg cgt 1555
 Ala Ile Asp Asp Val Arg Glu Met Lys Glu Leu Glu Ala Leu Arg
 470 475 480 485
 tct gag tcg gat att gca aaa cgt gac ggc aat tat tgt cgt gtc gca 1603
 Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn Tyr Cys Arg Val Ala
 490 495 500
 aag ctt cgc tac ggc cga atc cct gag ctg gaa aag cag atc gag gat 1651
 Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu Lys Gln Ile Glu Asp
 505 510 515
 gca gaa tcc aag gtc gag gtc aat gaa aat gcc atg ctc act gag gag 1699
 Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala Met Leu Thr Glu Glu
 520 525 530
 gtc acg cca gac acg atc gcc gat gtg gtt tcc gca tgg acg ggc att 1747
 Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser Ala Trp Thr Gly Ile
 535 540 545
 cct gca ggc aag atg atg cag ggt gag acc gag aag ctg ctc aac atg 1795
 Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu Lys Leu Leu Asn Met
 550 555 560 565
 gag cgc gtc ttg ggc aac cgt gtg gtc ggt cag cta gaa agc ggt aac 1843
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 Cys Ser Val

<210> 66

<211> 584

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 66

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 20 25 30

His Leu Leu Ala Ala Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro

35	40	45
Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala 50 55 60		
Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala 65 70 75 80		
Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln 85 90 95		
Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu 100 105 110		
Leu Ala Gly Ile Ala Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr 115 120 125		
Asn Lys Gly Ala Thr Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val 130 135 140		
Arg Gly Ser Gln Arg Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln 145 150 155 160		
Ala Leu Glu Lys Tyr Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly 165 170 175		
Lys Ile Asp Pro Val Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val 180 185 190		
Gln Val Leu Ser Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu 195 200 205		
Pro Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile 210 215 220		
Val Ala Gly Asp Val Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser 225 230 235 240		
Leu Asp Leu Gly Ser Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe 245 250 255		
Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly 260 265 270		
Glu Val Val Thr Phe Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly 275 280 285		
Ala Ser Gly Glu Ser Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu 290 295 300		
Leu Ala Arg Gly Glu Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu 305 310 315 320		
Tyr Arg Lys Tyr Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln 325 330 335		
Gln Val Tyr Val Gly Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu 340 345 350		
Arg Gly Leu Lys Glu Arg Tyr Glu Val His His Gly Val Arg Ile Gln 355 360 365		

Asp Ser Ala Leu Val Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr
 370 375 380
 Ser Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala
 385 390 395 400
 Ser Arg Leu Arg Met Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu
 405 410 415
 Leu Glu Arg Ile Val Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser
 420 425 430
 Lys Glu Ser Asp Ala Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser
 435 440 445
 Glu Leu Ala Asp Glu Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp
 450 455 460
 Gln Asn Glu Lys Thr Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu
 465 470 475 480
 Leu Glu Ala Leu Arg Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn
 485 490 495
 Tyr Cys Arg Val Ala Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu
 500 505 510
 Lys Gln Ile Glu Asp Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala
 515 520 525
 Met Leu Thr Glu Glu Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser
 530 535 540
 Ala Trp Thr Gly Ile Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu
 545 550 555 560
 Lys Leu Leu Asn Met Glu Arg Val Leu Gly Asn Arg Val Val Gly Gln
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
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 <223> FRXA01668

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 Met Ser Ser Phe Asn
 1 5

cca act acc aaa acc aat gaa gcc atg cag gct gct ctt cag cag gca	163
Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala Ala Leu Gln Gln Ala	
10 15 20	
tcc tcg gct ggc aac cct gat att cgt cca gct cac ctg ttg gct gcc	211
Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala His Leu Leu Ala Ala	
25 30 35	
atc ttg gag caa act gat ggc gta gca gcg cca gtc ctc atg gct act	259
Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro Val Leu Met Ala Thr	
40 45 50	
ggc gtg gat cct aag gag atc ctc gca gag gcc aag aag ttg gtt gct	307
Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Val Ala	
55 60 65	
tct tac ccc aag gct tct ggc gcc aat atg gct aat cca aac ttc aac	355
Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala Asn Pro Asn Phe Asn	
70 75 80 85	
cgg gat gcc ctc aat gcg ttc act gca gct cag gag ctt gcc ggt gag	403
Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln Glu Leu Ala Gly Glu	
90 95 100	
ttg ggc gat gag tac gtc tca acc gaa gta ctt ctt gcc ggt atc gct	451
Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu Leu Ala Gly Ile Ala	
105 110 115	
cgc gga aag tct gat gct gcg gat ctg ttg acc aac aag ggt gca acc	499
Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr Asn Lys Gly Ala Thr	
120 125 130	
tat gac gcc atc aaa gag gct ttc cct tcg gtt cgt gga tct cag cgt	547
Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val Arg Gly Ser Gln Arg	
135 140 145	
gtc acc act cag gat cca gag gga cag ttc cag gct ttg gaa aag tac	595
Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln Ala Leu Glu Lys Tyr	
150 155 160 165	
tcc act gac ctg acc aag ctt gct cgt gaa ggc aag att gat cct gtt	643
Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly Lys Ile Asp Pro Val	
170 175 180	
att ggc cgt gac cag gaa att cgt cgc gtc gtt cag gtg ctt agc cgt	691
Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val Gln Val Leu Ser Arg	
185 190 195	
cgt acc aag aac aac cct gtt ctg atc ggt gag cca ggt gtc ggt aaa	739
Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys	
200 205 210	
acc gcc atc gtg gaa ggc ctt gca cgc cgc atc gtt gct ggt gac gtt	787
Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile Val Ala Gly Asp Val	
215 220 225	
cca gaa tcc ctc aag ggc aaa act ctg atc agt ctt gat ctt ggt tcc	835
Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser Leu Asp Leu Gly Ser	
230 235 240 245	
atg gtt gcc ggc gct aag tat cgc ggt gaa ttc gag gag cga ctg aag	883

Met	Val	Ala	Gly	Ala	Lys	Tyr	Arg	Gly	Glu	Phe	Glu	Glu	Arg	Leu	Lys		
				250					255					260			
gct	gtt	ctg	gat	gag	atc	aag	gga	gct	aac	ggc	gaa	gtc	gtt	acc	ttc	931	
Ala	Val	Leu	Asp	Glu	Ile	Lys	Gly	Ala	Asn	Gly	Glu	Val	Val	Thr	Phe		
			265					270					275				
atc	gat	gag	ctg	cac	acc	atc	gtc	ggc	gct	ggt	gct	tcg	ggt	gaa	tcc	979	
Ile	Asp	Glu	Leu	His	Thr	Ile	Val	Gly	Ala	Gly	Ala	Ser	Gly	Glu	Ser		
			280					285					290				
gcc	atg	gat	gcc	gga	aac	atg	att	aag	cca	ctg	ctt	gcc	cgc	ggt	gag	1027	
Ala	Met	Asp	Ala	Gly	Asn	Met	Ile	Lys	Pro	Leu	Leu	Ala	Arg	Gly	Glu		
			295				300					305					
ctg	cgc	ttg	gtt	ggt	gcc	acc	acg	ctg	aat	gag	tac	cgc	aag	tac	atc	1075	
Leu	Arg	Leu	Val	Gly	Ala	Thr	Thr	Leu	Asn	Glu	Tyr	Arg	Lys	Tyr	Ile		
310						315				320					325		
gaa	aag	gac	gct	gcc	ctg	gag	cgt	agg	ttc	cag	cag	gtt	tat	gtc	ggt	1123	
Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Phe	Gln	Gln	Val	Tyr	Val	Gly		
				330					335					340			
gag	cca	acg	gta	gaa	gat	gcc	atc	ggt	att	ctt	cgt	gga	ttg	aag	gaa	1171	
Glu	Pro	Thr	Val	Glu	Asp	Ala	Ile	Gly	Ile	Leu	Arg	Gly	Leu	Lys	Glu		
			345					350					355				
cgc	tac	gag	gtc	cat	cac	ggt	gtc	cgc	atc	cag	gac	tcc	gca	ctg	gtc	1219	
Arg	Tyr	Glu	Val	His	His	Gly	Val	Arg	Ile	Gln	Asp	Ser	Ala	Leu	Val		
			360				365					370					
gcc	gca	gct	gaa	ctc	tca	aac	cgc	tat	atc	acc	agc	cgt	ttc	ctt	cct	1267	
Ala	Ala	Ala	Glu	Leu	Ser	Asn	Arg	Tyr	Ile	Thr	Ser	Arg	Phe	Leu	Pro		
			375				380				385						
gat	aag	gct	att	gac	tta	gtt	gat	gag	gca	gca	tca	cgc	ctg	cgc	atg	1315	
Asp	Lys	Ala	Ile	Asp	Leu	Val	Asp	Glu	Ala	Ala	Ser	Arg	Leu	Arg	Met		
390						395				400					405		
gag	att	gat	tct	tca	cct	cag	gaa	atc	gat	gag	ctg	gag	cgt	atc	gtc	1363	
Glu	Ile	Asp	Ser	Ser	Pro	Gln	Glu	Ile	Asp	Glu	Leu	Glu	Arg	Ile	Val		
				410					415					420			
cgc	cgc	ctc	gag	atc	gaa	gag	atg	gcg	ctg	tcc	aag	gaa	tcc	gat	gca	1411	
Arg	Arg	Leu	Glu	Ile	Glu	Glu	Met	Ala	Leu	Ser	Lys	Glu	Ser	Asp	Ala		
			425					430					435				
gct	tcc	aag	gaa	cgt	cta	gaa	aag	ctg	cgc	tcg	gaa	ctt	gct	gat	gaa	1459	
Ala	Ser	Lys	Glu	Arg	Leu	Glu	Lys	Leu	Arg	Ser	Glu	Leu	Ala	Asp	Glu		
			440				445					450					
cgc	gaa	aag	ctc	tct	gag	ttg	aag	gct	cgt	tg	cag	aat	gag	aaa	act	1507	
Arg	Glu	Lys	Leu	Ser	Glu	Leu	Lys	Ala	Arg	Trp	Gln	Asn	Glu	Lys	Thr		
			455				460				465						
gct	att	gac	gat	gtc	cgg	gag	atg	aaa	gaa	gag	ctg	gaa	gcg	ctg	cgt	1555	
Ala	Ile	Asp	Asp	Val	Arg	Glu	Met	Lys	Glu	Glu	Leu	Glu	Ala	Leu	Arg		
470						475				480					485		
tct	gag	tcg	gat	att	gca	aaa	cgt	gac	ggc	aat	tat	tgt	cgt	gtc	gca	1603	
Ser	Glu	Ser	Asp	Ile	Ala	Lys	Arg	Asp	Gly	Asn	Tyr	Cys	Arg	Val	Ala		

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Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu Lys Gln Ile Glu Asp			
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gca gaa tcc aag gtc gag gtc aat gaa aat gcc atg ctc act gag gag			1699
Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala Met Leu Thr Glu Glu			
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gtc acg cca gac acg atc gcc gat gtg gtt tcc gca tgg acg ggc att			1747
Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser Ala Trp Thr Gly Ile			
535	540	545	
cct gca ggc aag atg atg cag ggt gag acc gag aag ctg ctc aac atg			1795
Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu Lys Leu Leu Asn Met			
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gag cgc gtc ttg ggc aac ccg			1816
Glu Arg Val Leu Gly Asn Pro			
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His Leu Leu Ala Ala Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro			
35	40	45	
Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala			
50	55	60	
Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala			
65	70	75	80
Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln			
85	90	95	
Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu			
100	105	110	
Leu Ala Gly Ile Ala Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr			
115	120	125	
Asn Lys Gly Ala Thr Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val			
130	135	140	
Arg Gly Ser Gln Arg Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln			
145	150	155	160
Ala Leu Glu Lys Tyr Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly			
165	170	175	

Lys Ile Asp Pro Val Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val
 180 185 190
 Gln Val Leu Ser Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu
 195 200 205
 Pro Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile
 210 215 220
 Val Ala Gly Asp Val Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser
 225 230 235 240
 Leu Asp Leu Gly Ser Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe
 245 250 255
 Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly
 260 265 270
 Glu Val Val Thr Phe Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly
 275 280 285
 Ala Ser Gly Glu Ser Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu
 290 295 300
 Leu Ala Arg Gly Glu Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu
 305 310 315 320
 Tyr Arg Lys Tyr Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln
 325 330 335
 Gln Val Tyr Val Gly Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu
 340 345 350
 Arg Gly Leu Lys Glu Arg Tyr Glu Val His His Gly Val Arg Ile Gln
 355 360 365
 Asp Ser Ala Leu Val Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr
 370 375 380
 Ser Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala
 385 390 395 400
 Ser Arg Leu Arg Met Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu
 405 410 415
 Leu Glu Arg Ile Val Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser
 420 425 430
 Lys Glu Ser Asp Ala Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser
 435 440 445
 Glu Leu Ala Asp Glu Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp
 450 455 460
 Gln Asn Glu Lys Thr Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu
 465 470 475 480
 Leu Glu Ala Leu Arg Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn
 485 490 495

Lys Leu Leu Asn Met Glu Arg Val Leu Gly Asn Pro
565 570

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Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val
105 110 115

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Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe	
120 125 130	
ctt gcc cag act ttg gca aag ctg ctg gat gtt cct ttt gct atc gcg	547
Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala	
135 140 145	
gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa	595
Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu	
150 155 160 165	
aac atc ttg ctc aag ctg ctt cag gct gct gat ttt gat gtg gaa cgt	643
Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg	
170 175 180	
gca cag cgc ggc atc att tac atc gat gaa gtg gac aag att tcc cgc	691
Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val Asp Lys Ile Ser Arg	
185 190 195	
aag tct gaa aac cca tcg atc act cgc gat gtt tcc ggt gaa ggc gtg	739
Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val	
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cag cag gca ctg ctg aaa att ttg gaa ggc act gtc gcc gca atc cca	787
Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr Val Ala Ala Ile Pro	
215 220 225	
ccg cag gga gga cgc aag cac ccc aac cag gat ttc atc cag ctg gat	835
Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp Phe Ile Gln Leu Asp	
230 235 240 245	
acc acc aac att ttg ttc atc gtt gct ggt gcg ttc tct ggt ctg gag	883
Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala Phe Ser Gly Leu Glu	
250 255 260	
aag gtc atc gcg gac cgc aat ggc aag aaa ggc ttg ggc ttc ggt gtg	931
Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly Leu Gly Phe Gly Val	
265 270 275	
gag gtc tct tcc aag aag gaa gaa gcc aac att gtg gat atc ttc aag	979
Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile Val Asp Ile Phe Lys	
280 285 290	
gat gtc ctc cct gag gac ctg gtg aag ttt ggt ctc atc cca gaa ttc	1027
Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly Leu Ile Pro Glu Phe	
295 300 305	
att ggg cgt ctg cca gtc gtt gcc acc gta tcc aac ctg gat cag aaa	1075
Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser Asn Leu Asp Gln Lys	
310 315 320 325	
tct ctg gtc aag gtt ctc acg gag cct cgt aac tca ttg gtg aag cag	1123
Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn Ser Leu Val Lys Gln	
330 335 340	
tat cga cgt ctg ttt gaa atg gat gac gct gtg ttg acc ttt act gat	1171
Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val Leu Thr Phe Thr Asp	
345 350 355	
gat gct ttg gag gag atc gct aat cag gca ctc gag cgc aaa act ggc	1219

Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu Glu Arg Lys Thr Gly
 360 365 370
 gcc cgt ggc ctg cgc gcg atc atg gaa gag atc ctg gtt ccg atc atg 1267
 Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile Leu Val Pro Ile Met
 375 380 385
 tat gac ctc cca gac cgt aaa gac gtt ggc gaa gtc atc atc aac ggt 1315
 Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu Val Ile Ile Asn Gly
 390 395 400 405
 gcc gtt gcc cgt ggc gaa gcc gaa cca gag atg ttg gaa gct gtc gca 1363
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 35 40 45
 Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro
 50 55 60
 Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln
 65 70 75 80
 Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys
 85 90 95
 Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro
 100 105 110
 Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly
 115 120 125
 Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val
 130 135 140
 Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val
 145 150 155 160
 Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp
 165 170 175
 Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val
 180 185 190

Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val
 195 200 205
 Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr
 210 215 220
 Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp
 225 230 235 240
 Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala
 245 250 255
 Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly
 260 265 270
 Leu Gly Phe Gly Val Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile
 275 280 285
 Val Asp Ile Phe Lys Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly
 290 295 300
 Leu Ile Pro Glu Phe Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser
 305 310 315 320
 Asn Leu Asp Gln Lys Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn
 325 330 335
 Ser Leu Val Lys Gln Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val
 340 345 350
 Leu Thr Phe Thr Asp Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu
 355 360 365
 Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile
 370 375 380
 Leu Val Pro Ile Met Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu
 385 390 395 400
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 Leu Glu Ala Val Ala Glu Glu Lys Thr Ala
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<210> 71

<211> 1401

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1378)

<223> FRXA01120

<400> 71

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gaa agc gcc gat ctg ctc aaa tgt tcc ttc tgc gga aag agc caa aag						163
Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys Gly Lys Ser Gln Lys						
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cag gta aaa aaa ctc atc gcg ggt ggc gcc gta tat atc tgt gat gag						211
Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val Tyr Ile Cys Asp Glu						
	25		30		35	
tgc att gag ctg tgc aac gag att att gaa gaa gaa ctc ggt caa gct						259
Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu Glu Leu Gly Gln Ala						
	40		45		50	
caa cac gac gag cag gag cgc aac gag ctc ccc aag ccg tcg gag att						307
Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro Lys Pro Ser Glu Ile						
	55		60		65	
tca gcc ttc ctt gat act tat gtc atc ggg cag gac cca gca aaa cgt						355
Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln Asp Pro Ala Lys Arg						
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atc ctg tcg gtt gcg gtg tac aac cat tac aag cgt ctc cgc gca tcg						403
Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Leu Arg Ala Ser						
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gaa acc atc ggt cgt cgc agg aat gac gag cct gaa acc gaa ctg gtt						451
Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val						
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aag tcc aat att ttg atg ctc ggc ccc act ggc tcc ggc aag act ttc						499
Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe						
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ctt gcc cag act ttg gca aag ctg ctg gat gtt cct ttt gct atc gcg						547
Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala						
	135		140		145	
gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa						595
Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu						
	150		155		160	165
aac atc ttg ctc aag ctg ctt cag gct gct gat ttt gat gtg gaa cgt						643
Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg						
	170		175		180	
gca cag cgc ggc atc att tac atc gat gaa gtg gac aag att tcc cgc						691
Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val Asp Lys Ile Ser Arg						
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aag tct gaa aac cca tcg atc act cgc gat gtt tcc ggt gaa ggc gtg						739
Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val						
	200		205		210	
cag cag gca ctg ctg aaa att ttg gaa ggc act gtc gcc gca atc cca						787
Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr Val Ala Ala Ile Pro						
	215		220		225	
ccg cag gga gga cgc aag cac ccc aac cag gat ttc atc cag ctg gat						835
Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp Phe Ile Gln Leu Asp						

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acc acc aac att ttg ttc atc gtt gct ggt gcg ttc tct ggt ctg gag	883			
Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala Phe Ser Gly Leu Glu				
250	255	260		
aag gtc atc gcg gac cgc aat ggc aag aaa ggc ttg ggc ttc ggt gtg	931			
Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly Leu Gly Phe Gly Val				
265	270	275		
gag gtc tct tcc aag aag gaa gaa gcc aac att gtg gat atc ttc aag	979			
Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile Val Asp Ile Phe Lys				
280	285	290		
gat gtc ctg cct gag gac ctg gtg aag ttt ggt ctg atc cca gaa ttc	1027			
Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly Leu Ile Pro Glu Phe				
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Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser Asn Leu Asp Gln Lys				
310	315	320	325	
tct ctg gtc aag gtt ctg acg gag cct cgt aac tca ttg gtg aag cag	1123			
Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn Ser Leu Val Lys Gln				
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Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val Leu Thr Phe Thr Asp				
345	350	355		
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Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu Glu Arg Lys Thr Gly				
360	365	370		
gcc cgt ggc ctg cgc gcg atc atg gaa gag atc ctg gtt ccg atc atg	1267			
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375	380	385		
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Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu Val Ile Ile Asn Gly				
390	395	400	405	
gcc gtt gcc cgt ggc gaa gcc gaa cca gag atg ttg gaa gct gtc gca	1363			
Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met Leu Glu Ala Val Ala				
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Glu Glu Lys Thr Ala				
425				

<210> 72

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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Tyr Ile Cys Asp Glu Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu 35 40 45		
Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro 50 55 60		
Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln 65 70 75 80		
Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys 85 90 95		
Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro 100 105 110		
Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly 115 120 125		
Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val 130 135 140		
Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val 145 150 155 160		
Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp 165 170 175		
Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val 180 185 190		
Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val 195 200 205		
Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr 210 215 220		
Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp 225 230 235 240		
Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala 245 250 255		
Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly 260 265 270		
Leu Gly Phe Gly Val Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile 275 280 285		
Val Asp Ile Phe Lys Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly 290 295 300		
Leu Ile Pro Glu Phe Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser 305 310 315 320		
Asn Leu Asp Gln Lys Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn 325 330 335		
Ser Leu Val Lys Gln Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val 340 345 350		

Leu Thr Phe Thr Asp Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu
355 360 365

Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile
370 375 380

Leu Val Pro Ile Met Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu
385 390 395 400

Val Ile Ile Asn Gly Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met
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Leu Glu Ala Val Ala Glu Glu Lys Thr Ala
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<210> 73

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA00744

<400> 73

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Met Gly Asn Trp Ala
1 5

gag att act gat gaa att tct aag att tac caa gat aat cag tac aag 163
Glu Ile Thr Asp Glu Ile Ser Lys Ile Tyr Gln Asp Asn Gln Tyr Lys
10 15 20

att aga caa ata aat gat gtt gac gca gta agc gat aaa cgt aga gaa 211
Ile Arg Gln Ile Asn Asp Val Asp Ala Val Ser Asp Lys Arg Arg Glu
25 30 35

gcg cta caa gca ctg ttt gaa cat act ggt cga aat gta atc gtc tat 259
Ala Leu Gln Ala Leu Phe Glu His Thr Gly Arg Asn Val Ile Val Tyr
40 45 50

tat tca gcg tgg tta gaa aat ggt cga cga ttt tcc ggg caa tct acg 307
Tyr Ser Ala Trp Leu Glu Asn Gly Arg Arg Phe Ser Gly Gln Ser Thr
55 60 65

gat ttt tcg gta aat gat act gat aaa aac agt ttt atg act gcg ctc 355
Asp Phe Ser Val Asn Asp Thr Asp Lys Asn Ser Phe Met Thr Ala Leu
70 75 80 85

cat aag ttg gat cag agt aaa ggt ctc gat ctt atc ctc cac act ccg 403
His Lys Leu Asp Gln Ser Lys Gly Leu Asp Leu Ile Leu His Thr Pro
90 95 100

ggg gga gat gtt gct gcg aca gag tcg tta gta gat tac att cac gca 451
Gly Gly Asp Val Ala Ala Thr Glu Ser Leu Val Asp Tyr Ile His Ala
105 110 115

ctc ttt ggt caa gat ttc aga gtc att gtc ccc caa ctc gca atg tca 499
 Leu Phe Gly Gln Asp Phe Arg Val Ile Val Pro Gln Leu Ala Met Ser
 120 125 130

gca gga aca atg atc gca ctt tcg tcc aaa gag att gtt atg ggg aag 547
 Ala Gly Thr Met Ile Ala Leu Ser Ser Lys Glu Ile Val Met Gly Lys
 135 140 145

cat tct agt ctt ggc ccc att gat cct cag ttt aac ggc cta ccg gca 595
 His Ser Ser Leu Gly Pro Ile Asp Pro Gln Phe Asn Gly Leu Pro Ala
 150 155 160 165

cac ggg tta ttg gaa gaa ttt gag caa gcg aag aaa gag gtc tct gag 643
 His Gly Leu Leu Glu Glu Phe Glu Gln Ala Lys Lys Glu Val Ser Glu
 170 175 180

aat ccg cag act gct cat ata tgg cag gtg atc ttg aat aaa tac aac 691
 Asn Pro Gln Thr Ala His Ile Trp Gln Val Ile Leu Asn Lys Tyr Asn
 185 190 195

ccc acg atg ttg ggt gaa gct aaa aaa gct att cag tgg tcc aac tcg 739
 Pro Thr Met Leu Gly Glu Ala Lys Lys Ala Ile Gln Trp Ser Asn Ser
 200 205 210

atg gtt aag cag tgg ctt gaa aag ggt atg ttt tta gac gag cct gac 787
 Met Val Lys Gln Trp Leu Glu Lys Gly Met Phe Leu Asp Glu Pro Asp
 215 220 225

aaa gaa gaa aaa gcc act cgc gct atc aaa gag ctc gct gat cat tcc 835
 Lys Glu Glu Lys Ala Thr Arg Ala Ile Lys Glu Leu Ala Asp His Ser
 230 235 240 245

gtt act ctt gcg cat aat cga cac att tcg gtc agt aaa gca ctt gag 883
 Val Thr Leu Ala His Asn Arg His Ile Ser Val Ser Lys Ala Leu Glu
 250 255 260

ctg gga ttg aat atc aaa gaa ctt gag agc gat cca aag ctt caa gat 931
 Leu Gly Leu Asn Ile Lys Glu Leu Glu Ser Asp Pro Lys Leu Gln Asp
 265 270 275

tta gtt ctt act ctt cac cac ctg tcc gtt att gct gcg caa cga gga 979
 Leu Val Leu Thr Leu His His Leu Ser Val Ile Ala Ala Gln Arg Gly
 280 285 290

cca tta att aag ttt gtc gtc aat cat gac aac cgt ggc act ttt ctg 1027
 Pro Leu Ile Lys Phe Val Val Asn His Asp Asn Arg Gly Thr Phe Leu
 295 300 305

cag ggg cat gaa aac taattaagt atgcaatagt cta 1065
 Gln Gly His Glu Asn
 310

<210> 74

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

Met Gly Asn Trp Ala Glu Ile Thr Asp Glu Ile Ser Lys Ile Tyr Gln

1	5	10	15
Asp Asn Gln Tyr	Lys Ile Arg Gln	Ile Asn Asp Val	Asp Ala Val Ser
20	25	30	
Asp Lys Arg Arg	Glu Ala Leu Gln	Ala Leu Phe Glu	His Thr Gly Arg
35	40	45	
Asn Val Ile Val	Tyr Tyr Ser Ala	Trp Leu Glu Asn	Gly Arg Arg Phe
50	55	60	
Ser Gly Gln Ser	Thr Asp Phe Ser	Val Asn Asp Thr	Asp Lys Asn Ser
65	70	75	80
Phe Met Thr Ala	Leu His Lys Leu	Asp Gln Ser Lys	Gly Leu Asp Leu
85	90	95	
Ile Leu His Thr	Pro Gly Gly Asp	Val Ala Ala Thr	Glu Ser Leu Val
100	105	110	
Asp Tyr Ile His	Ala Leu Phe Gly	Gln Asp Phe Arg	Val Ile Val Pro
115	120	125	
Gln Leu Ala Met	Ser Ala Gly Thr	Met Ile Ala Leu	Ser Ser Lys Glu
130	135	140	
Ile Val Met Gly	Lys His Ser Ser	Leu Gly Pro Ile	Asp Pro Gln Phe
145	150	155	160
Asn Gly Leu Pro	Ala His Gly Leu	Leu Glu Glu Phe	Glu Gln Ala Lys
165	170	175	
Lys Glu Val Ser	Glu Asn Pro Gln	Thr Ala His Ile	Trp Gln Val Ile
180	185	190	
Leu Asn Lys Tyr	Asn Pro Thr Met	Leu Gly Glu Ala	Lys Lys Ala Ile
195	200	205	
Gln Trp Ser Asn	Ser Met Val Lys	Gln Trp Leu Glu	Lys Gly Met Phe
210	215	220	
Leu Asp Glu Pro	Asp Lys Glu Glu	Lys Ala Thr Arg	Ala Ile Lys Glu
225	230	235	240
Leu Ala Asp His	Ser Val Thr Leu	Ala His Asn Arg	His Ile Ser Val
245	250	255	
Ser Lys Ala Leu	Glu Leu Gly Leu	Asn Ile Lys Glu	Leu Glu Ser Asp
260	265	270	
Pro Lys Leu Gln	Asp Leu Val Leu	Thr Leu His His	Leu Ser Val Ile
275	280	285	
Ala Ala Gln Arg	Gly Pro Leu Ile	Lys Phe Val Val	Asn His Asp Asn
290	295	300	
Arg Gly Thr Phe	Leu Gln Gly His	Glu Asn	
305	310		

<210> 75

<211> 957
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(934)
 <223> RXA00844

<400> 75
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gtgacaacat tttgtagagc aaccatctag actgttcttt atg tct tct gcg tca 115
 Met Ser Ser Ala Ser
 1 5

ttt acc acc aaa gca ctg tcc gta ctc gca gct tta acg gct gcg tct 163
 Phe Thr Thr Lys Ala Leu Ser Val Leu Ala Ala Leu Thr Ala Ala Ser
 10 15 20

gcc ccc tta gtg gcg gcg tca cct gca cat gct ttg gca aat gct cgc 211
 Ala Pro Leu Val Ala Ala Ser Pro Ala His Ala Leu Ala Asn Ala Arg
 25 30 35

aac gtt acg ggt tca agc acc act tca gat tca att gtt cgt ctg cac 259
 Asn Val Thr Gly Ser Ser Thr Thr Ser Asp Ser Ile Val Arg Leu His
 40 45 50

atc ggt aac act gca tgt aca gga acc atg atc acc cca acg tgg gcg 307
 Ile Gly Asn Thr Ala Cys Thr Gly Thr Met Ile Thr Pro Thr Trp Ala
 55 60 65

atc acc gcc cgc cac tgt atc cct gag ggc ggt att gcc ggt gca gct 355
 Ile Thr Ala Arg His Cys Ile Pro Glu Gly Gly Ile Ala Gly Ala Ala
 70 75 80 85

att ggt tca agc act ttg agc caa ttt cag cag gtg tcc caa gcg atc 403
 Ile Gly Ser Ser Thr Leu Ser Gln Phe Gln Gln Val Ser Gln Ala Ile
 90 95 100

ttg cac cct act gcg gac tta gct ctc gtt gag ctt ccc aat cag gca 451
 Leu His Pro Thr Ala Asp Leu Ala Leu Val Glu Leu Pro Asn Gln Ala
 105 110 115

agt tcc aac acg gtt gat ctc tac ggt gca cac gtg cag cct ggt gaa 499
 Ser Ser Asn Thr Val Asp Leu Tyr Gly Ala His Val Gln Pro Gly Glu
 120 125 130

aat ggt caa gca gcc ggc tgg ggt ggg tac tct gcc ttt ggc caa aat 547
 Asn Gly Gln Ala Ala Gly Trp Gly Gly Tyr Ser Ala Phe Gly Gln Asn
 135 140 145

ggt gca cag caa gcc gat gtg caa att caa cgc agg gta gtc aat gtg 595
 Val Ala Gln Gln Ala Asp Val Gln Ile Gln Arg Arg Val Val Asn Val
 150 155 160 165

cca agc ccc gac cgc acc gct gtg ctg ctt gaa ggc act gtt tct aac 643
 Pro Ser Pro Asp Arg Thr Ala Val Leu Leu Glu Gly Thr Val Ser Asn
 170 175 180

ggt cgt ctc gta cca ggc gat tcc ggc gga cct ttg tac atc aat ggt 691

Gly Arg Leu Val Pro Gly Asp Ser Gly Gly Pro Leu Tyr Ile Asn Gly
 185 190 195

caa ctg gct ggt gtg ctc agc atg tcc act gac gta gaa aac gat gca 739
 Gln Leu Ala Gly Val Leu Ser Met Ser Thr Asp Val Glu Asn Asp Ala
 200 205 210

cta gac ggc acc gtc ggc tgg tac atc ccc gtt gct gaa cac gcc gag 787
 Leu Asp Gly Thr Val Gly Trp Tyr Ile Pro Val Ala Glu His Ala Glu
 215 220 225

tgg atc gcc tac tac acc ggc aag cac att gcc ccc att gct ggt gcg 835
 Trp Ile Ala Tyr Tyr Thr Gly Lys His Ile Ala Pro Ile Ala Gly Ala
 230 235 240 245

ccc gca gaa ctt gtt gac gcc acc gcc aac ccc acc ttc atc cct gct 883
 Pro Ala Glu Leu Val Asp Ala Thr Ala Asn Pro Thr Phe Ile Pro Ala
 250 255 260

cca cag cct ttc acc ggt tca tcc atc ggt ggt tgg gcg ctg ggc agc 931
 Pro Gln Pro Phe Thr Gly Ser Ser Ile Gly Gly Trp Ala Leu Gly Ser
 265 270 275

tcc tagaatatgc tgatctccct gct 957
 Ser

<210> 76

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

Met Ser Ser Ala Ser Phe Thr Thr Lys Ala Leu Ser Val Leu Ala Ala
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Leu Thr Ala Ala Ser Ala Pro Leu Val Ala Ala Ser Pro Ala His Ala
 20 25 30

Leu Ala Asn Ala Arg Asn Val Thr Gly Ser Ser Thr Thr Ser Asp Ser
 35 40 45

Ile Val Arg Leu His Ile Gly Asn Thr Ala Cys Thr Gly Thr Met Ile
 50 55 60

Thr Pro Thr Trp Ala Ile Thr Ala Arg His Cys Ile Pro Glu Gly Gly
 65 70 75 80

Ile Ala Gly Ala Ala Ile Gly Ser Ser Thr Leu Ser Gln Phe Gln Gln
 85 90 95

Val Ser Gln Ala Ile Leu His Pro Thr Ala Asp Leu Ala Leu Val Glu
 100 105 110

Leu Pro Asn Gln Ala Ser Ser Asn Thr Val Asp Leu Tyr Gly Ala His
 115 120 125

Val Gln Pro Gly Glu Asn Gly Gln Ala Ala Gly Trp Gly Gly Tyr Ser
 130 135 140

Ala Phe Gly Gln Asn Val Ala Gln Gln Ala Asp Val Gln Ile Gln Arg
 145 150 155 160

Arg Val Val Asn Val Pro Ser Pro Asp Arg Thr Ala Val Leu Leu Glu
 165 170 175

Gly Thr Val Ser Asn Gly Arg Leu Val Pro Gly Asp Ser Gly Gly Pro
 180 185 190

Leu Tyr Ile Asn Gly Gln Leu Ala Gly Val Leu Ser Met Ser Thr Asp
 195 200 205

Val Glu Asn Asp Ala Leu Asp Gly Thr Val Gly Trp Tyr Ile Pro Val
 210 215 220

Ala Glu His Ala Glu Trp Ile Ala Tyr Tyr Thr Gly Lys His Ile Ala
 225 230 235 240

Pro Ile Ala Gly Ala Pro Ala Glu Leu Val Asp Ala Thr Ala Asn Pro
 245 250 255

Thr Phe Ile Pro Ala Pro Gln Pro Phe Thr Gly Ser Ser Ile Gly Gly
 260 265 270

Trp Ala Leu Gly Ser Ser
 275

<210> 77
 <211> 958
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(958)
 <223> RXA01151

<400> 77
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aagacctagt tggagggcgt aaagggttag agtggtgacc atg agt tca cca act 115
 Met Ser Ser Pro Thr
 1 5

gat tct tcg ccg tct aat tct ttt agc gac ttc aac cgg gag gaa cag 163
 Asp Ser Ser Pro Ser Asn Ser Phe Ser Asp Phe Asn Arg Glu Glu Gln
 10 15 20

tcc cgg tta tct gat gag gtg cgc cag ctc aag cgc acc aac tct gat 211
 Ser Arg Leu Ser Asp Glu Val Arg Gln Leu Lys Arg Thr Asn Ser Asp
 25 30 35

ctt ggg gca cgt aat gcc aag ctc gcg gag atg ctg aag tcg tct cgg 259
 Leu Gly Ala Arg Asn Ala Lys Leu Ala Glu Met Leu Lys Ser Ser Arg
 40 45 50

gat aaa ttg tct gtg ctg ttt tct cag ttg gag gat atg gct cag ccg 307
 Asp Lys Leu Ser Val Leu Phe Ser Gln Leu Glu Asp Met Ala Gln Pro
 55 60 65

cca tcg gtg tat ggc act ttc ttg gaa acc gcg aaa gac ggt tct aat	355
Pro Ser Val Tyr Gly Thr Phe Leu Glu Thr Ala Lys Asp Gly Ser Asn	
70 75 80 85	
gcg gag atc ttt gct ggt gga cgt cgc atg cgt gtg gct gtt tct cct	403
Ala Glu Ile Phe Ala Gly Gly Arg Arg Met Arg Val Ala Val Ser Pro	
90 95 100	
atg ctg tgt gcc gcg gat ttg atg ccg ggt gtg cag gtt cgt ttg ggt	451
Met Leu Cys Ala Ala Asp Leu Met Pro Gly Val Gln Val Arg Leu Gly	
105 110 115	
gaa ggc aat caa gtt ctt gag gcc tgt gat ttt gaa caa acc ggt gaa	499
Glu Gly Asn Gln Val Leu Glu Ala Cys Asp Phe Glu Gln Thr Gly Glu	
120 125 130	
tta gcc acg ttg atg gaa atg att ggc cgg gat cgt gct ttg gtt tca	547
Leu Ala Thr Leu Met Glu Met Ile Gly Arg Asp Arg Ala Leu Val Ser	
135 140 145	
gat cgc tcg ggg gag gag cgc gtc gtc aag ctt gct ggt ccg ttg atg	595
Asp Arg Ser Gly Glu Arg Val Val Lys Leu Ala Gly Pro Leu Met	
150 155 160 165	
gat cgc acc gca aag ctg ccg cgc ccc ggt gac acc ctg ctt gtt gac	643
Asp Arg Thr Ala Lys Leu Pro Arg Pro Gly Asp Thr Leu Leu Val Asp	
170 175 180	
cgc aaa gcg ggc tac gct ttt gag gcg att gcc aag acg gaa att tcg	691
Arg Lys Ala Gly Tyr Ala Phe Glu Ala Ile Ala Lys Thr Glu Ile Ser	
185 190 195	
agg ctt gcg ctg gaa gag gcg cca gat gtg tct tat cag gat att ggt	739
Arg Leu Ala Leu Glu Glu Ala Pro Asp Val Ser Tyr Gln Asp Ile Gly	
200 205 210	
ggc ttg gat gat cag att gaa ttg att caa gat gcc gtt gag ctg cca	787
Gly Leu Asp Asp Gln Ile Glu Leu Ile Gln Asp Ala Val Glu Leu Pro	
215 220 225	
ttt ttg cac ccg gag atg tac cgc gcc tac aac ctg cat cca cca aag	835
Phe Leu His Pro Glu Met Tyr Arg Ala Tyr Asn Leu His Pro Pro Lys	
230 235 240 245	
ggc gtg ctg ctg tac ggc cct ccc gcc tgt gga aag acg ctg att gct	883
Gly Val Leu Leu Tyr Gly Pro Pro Gly Cys Gly Lys Thr Leu Ile Ala	
250 255 260	
aag gct gtg gct aat tct ttg gcc aac cgc atc ggt gag act ggc acc	931
Lys Ala Val Ala Asn Ser Leu Ala Asn Arg Ile Gly Glu Thr Gly Thr	
265 270 275	
tcg tac ttc atc aac gtc aag ggg cca	958
Ser Tyr Phe Ile Asn Val Lys Gly Pro	
280 285	

<210> 78

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

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Met Ser Ser Pro Thr Asp Ser Ser Pro Ser Asn Ser Phe Ser Asp Phe
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Asn Arg Glu Glu Gln Ser Arg Leu Ser Asp Glu Val Arg Gln Leu Lys
      20           25           30

Arg Thr Asn Ser Asp Leu Gly Ala Arg Asn Ala Lys Leu Ala Glu Met
      35           40           45

Leu Lys Ser Ser Arg Asp Lys Leu Ser Val Leu Phe Ser Gln Leu Glu
 50           55           60

Asp Met Ala Gln Pro Pro Ser Val Tyr Gly Thr Phe Leu Glu Thr Ala
 65           70           75           80

Lys Asp Gly Ser Asn Ala Glu Ile Phe Ala Gly Gly Arg Arg Met Arg
      85           90           95

Val Ala Val Ser Pro Met Leu Cys Ala Asp Leu Met Pro Gly Val
      100           105           110

Gln Val Arg Leu Gly Glu Gly Asn Gln Val Leu Glu Ala Cys Asp Phe
 115           120           125

Glu Gln Thr Gly Glu Leu Ala Thr Leu Met Glu Met Ile Gly Arg Asp
 130           135           140

Arg Ala Leu Val Ser Asp Arg Ser Gly Glu Glu Arg Val Val Lys Leu
 145           150           155           160

Ala Gly Pro Leu Met Asp Arg Thr Ala Lys Leu Pro Arg Pro Gly Asp
      165           170           175

Thr Leu Leu Val Asp Arg Lys Ala Gly Tyr Ala Phe Glu Ala Ile Ala
 180           185           190

Lys Thr Glu Ile Ser Arg Leu Ala Leu Glu Glu Ala Pro Asp Val Ser
 195           200           205

Tyr Gln Asp Ile Gly Gly Leu Asp Asp Gln Ile Glu Leu Ile Gln Asp
 210           215           220

Ala Val Glu Leu Pro Phe Leu His Pro Glu Met Tyr Arg Ala Tyr Asn
 225           230           235           240

Leu His Pro Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Cys Gly
      245           250           255

Lys Thr Leu Ile Ala Lys Ala Val Ala Asn Ser Leu Ala Asn Arg Ile
 260           265           270

Gly Glu Thr Gly Thr Ser Tyr Phe Ile Asn Val Lys Gly Pro
 275           280           285

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<210> 79

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(712)

<223> RXA02317

<400> 79

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gacgtcgaaa agcgaattca tggcccccac ttgccttaaa atg gcg cac atg cgc 115
                                   Met Ala His Met Arg
                                   1 5

tta ctg ctg acc tcc ttt ggc cat gat cat att cgg gat ttt gta cgc 163
Leu Leu Leu Thr Ser Phe Gly His Asp His Ile Arg Asp Phe Val Arg
          10          15          20

ggt acc gtg gcg tat atc cct gat gcg acc agg ctt ttt gct gat agt 211
Gly Thr Val Ala Tyr Ile Pro Asp Ala Thr Arg Leu Phe Ala Asp Ser
          25          30          35

ccc gag gct gct cct ttt atg gag acg gag cga aat atg ctg cgc gag 259
Pro Glu Ala Ala Pro Phe Met Glu Thr Glu Arg Asn Met Leu Arg Glu
          40          45          50

cac ggc ttg agc att cgt gag ctg ccg att tcc acg tcg act ccg gag 307
His Gly Leu Ser Ile Arg Glu Leu Pro Ile Ser Thr Ser Thr Pro Glu
          55          60          65

gaa gtg gat cgg gtg ctt ggt gag gtt gat ggg gtg tat gtg gcg ggc 355
Glu Val Asp Arg Val Leu Gly Glu Val Asp Gly Val Tyr Val Ala Gly
          70          75          80          85

ggt gag act ttt gat ctg atg tgg ctg ctg cgt tcc aca ggc aat gat 403
Gly Glu Thr Phe Asp Leu Met Trp Leu Leu Arg Ser Thr Gly Asn Asp
          90          95          100

gag gtg ttg att aag cat gtt cgc gct ggt cta ccg tat att gga acg 451
Glu Val Leu Ile Lys His Val Arg Ala Gly Leu Pro Tyr Ile Gly Thr
          105          110          115

agc gcc ggc gcg gta att gca ggt cct tcg att gaa ccg atc agc ttt 499
Ser Ala Gly Ala Val Ile Ala Gly Pro Ser Ile Glu Pro Ile Ser Phe
          120          125          130

ttg gat agc ccc gat gtc gcg ccg aat tta agc gac tat tca ggt cta 547
Leu Asp Ser Pro Asp Val Ala Pro Asn Leu Ser Asp Tyr Ser Gly Leu
          135          140          145

ggc ctg tgc gag cat gtc gtg gtg ccc cat gct ggt ggc acg atc ccg 595
Gly Leu Cys Glu His Val Val Val Pro His Ala Gly Gly Thr Ile Pro
          150          155          160          165

caa ttt ccc atc gat gtg ttt gcg gaa acc gtg cgc acc tac ggc gcc 643
Gln Phe Pro Ile Asp Val Phe Ala Glu Thr Val Arg Thr Tyr Gly Ala
          170          175          180

gaa ttc ccg ctg gtc ctg ctt aaa gat gga cag gca ctg ctt atc gac 691
Glu Phe Pro Leu Val Leu Leu Lys Asp Gly Gln Ala Leu Leu Ile Asp
          185          190          195

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gac cac ggc gtc cac cta att taggatgggt ccccatgagc acc
 Asp His Gly Val His Leu Ile
 200

735

<210> 80

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Ala His Met Arg Leu Leu Leu Thr Ser Phe Gly His Asp His Ile
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 20 25 30

Leu Phe Ala Asp Ser Pro Glu Ala Ala Pro Phe Met Glu Thr Glu Arg
 35 40 45

Asn Met Leu Arg Glu His Gly Leu Ser Ile Arg Glu Leu Pro Ile Ser
 50 55 60

Thr Ser Thr Pro Glu Glu Val Asp Arg Val Leu Gly Glu Val Asp Gly
 65 70 75 80

Val Tyr Val Ala Gly Gly Glu Thr Phe Asp Leu Met Trp Leu Leu Arg
 85 90 95

Ser Thr Gly Asn Asp Glu Val Leu Ile Lys His Val Arg Ala Gly Leu
 100 105 110

Pro Tyr Ile Gly Thr Ser Ala Gly Ala Val Ile Ala Gly Pro Ser Ile
 115 120 125

Glu Pro Ile Ser Phe Leu Asp Ser Pro Asp Val Ala Pro Asn Leu Ser
 130 135 140

Asp Tyr Ser Gly Leu Gly Leu Cys Glu His Val Val Val Pro His Ala
 145 150 155 160

Gly Gly Thr Ile Pro Gln Phe Pro Ile Asp Val Phe Ala Glu Thr Val
 165 170 175

Arg Thr Tyr Gly Ala Glu Phe Pro Leu Val Leu Leu Lys Asp Gly Gln
 180 185 190

Ala Leu Leu Ile Asp Asp His Gly Val His Leu Ile
 195 200

<210> 81

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA02644

<400> 81
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tgaaaaatgct gccggttggc gagctaagat gtgagatgct atg gca cat ctc acg 115
Met Ala His Leu Thr
1 5
caa tac caa ctc cct cag gcc ggt caa gtc ttt gag cat gaa cta gag 163
Gln Tyr Gln Leu Pro Gln Ala Gly Gln Val Phe Glu His Glu Leu Glu
10 15 20
atc aag cgc tcg cga ttt ctg acc tat atc acg cgt gtg caa gat cag 211
Ile Lys Arg Ser Arg Phe Leu Thr Tyr Ile Thr Arg Val Gln Asp Gln
25 30 35
gag cag gct cgc gaa ttt att cac tcc atc aag gag ctg tat ccg gat 259
Glu Gln Ala Arg Glu Phe Ile His Ser Ile Lys Glu Leu Tyr Pro Asp
40 45 50
gcg cgt cat cat tgc agt gcc ttt att ttc cat gtg gat ggc tca aat 307
Ala Arg His His Cys Ser Ala Phe Ile Phe His Val Asp Gly Ser Asn
55 60 65
gat gtg gag cgt tcc tct gat gat ggc gaa cct tcc ggt acc gcg gga 355
Asp Val Glu Arg Ser Ser Asp Asp Gly Glu Pro Ser Gly Thr Ala Gly
70 75 80 85
aaa ccc atg cta gag gcg ttg cgt ggc tcg gga atg aaa gat att gcc 403
Lys Pro Met Leu Glu Ala Leu Arg Gly Ser Gly Met Lys Asp Ile Ala
90 95 100
gct gtg gtg gtg cgt tat ttc ggt ggc gta aaa ctg ggc act ggc gga 451
Ala Val Val Val Arg Tyr Phe Gly Gly Val Lys Leu Gly Thr Gly Gly
105 110 115
tta gtt aat gcc tac acc aac gcg gtg acg gag ctt cta cct gag gtt 499
Leu Val Asn Ala Tyr Thr Asn Ala Val Thr Glu Leu Leu Pro Glu Val
120 125 130
ttg caa gtc acc cgc tct gtt cgg gag att ttc aag att gac ctt ccg 547
Leu Gln Val Thr Arg Ser Val Arg Glu Ile Phe Lys Ile Asp Leu Pro
135 140 145
cat tct gat gcg ggg cgc att gaa gcg aat ctg cgc ggc atg ggc atc 595
His Ser Asp Ala Gly Arg Ile Glu Ala Asn Leu Arg Gly Met Gly Ile
150 155 160 165
atc att act gac act gaa tat ggt gca gaa gtc aca tac acc ttg gct 643
Ile Ile Thr Asp Thr Glu Tyr Gly Ala Glu Val Thr Tyr Thr Leu Ala
170 175 180
tta ttg cct ggt gaa cag gct gcg gtg gaa tct caa ttg tca tcc atg 691
Leu Leu Pro Gly Glu Gln Ala Ala Val Glu Ser Gln Leu Ser Ser Met
185 190 195
atg ggt gca gaa att gaa ttg aaa gaa tcc ggg cac atg tgg gtg gaa 739
Met Gly Ala Glu Ile Glu Leu Lys Glu Ser Gly His Met Trp Val Glu
200 205 210
tcc ccg agt gac tagtgcggtg taagagcact aga 774
Ser Pro Ser Asp

215

<210> 82

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Ala His Leu Thr Gln Tyr Gln Leu Pro Gln Ala Gly Gln Val Phe
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Glu His Glu Leu Glu Ile Lys Arg Ser Arg Phe Leu Thr Tyr Ile Thr
 20 25 30

Arg Val Gln Asp Gln Glu Gln Ala Arg Glu Phe Ile His Ser Ile Lys
 35 40 45

Glu Leu Tyr Pro Asp Ala Arg His His Cys Ser Ala Phe Ile Phe His
 50 55 60

Val Asp Gly Ser Asn Asp Val Glu Arg Ser Ser Asp Asp Gly Glu Pro
 65 70 75 80

Ser Gly Thr Ala Gly Lys Pro Met Leu Glu Ala Leu Arg Gly Ser Gly
 85 90 95

Met Lys Asp Ile Ala Ala Val Val Val Arg Tyr Phe Gly Gly Val Lys
 100 105 110

Leu Gly Thr Gly Gly Leu Val Asn Ala Tyr Thr Asn Ala Val Thr Glu
 115 120 125

Leu Leu Pro Glu Val Leu Gln Val Thr Arg Ser Val Arg Glu Ile Phe
 130 135 140

Lys Ile Asp Leu Pro His Ser Asp Ala Gly Arg Ile Glu Ala Asn Leu
 145 150 155 160

Arg Gly Met Gly Ile Ile Ile Thr Asp Thr Glu Tyr Gly Ala Glu Val
 165 170 175

Thr Tyr Thr Leu Ala Leu Leu Pro Gly Glu Gln Ala Ala Val Glu Ser
 180 185 190

Gln Leu Ser Ser Met Met Gly Ala Glu Ile Glu Leu Lys Glu Ser Gly
 195 200 205

His Met Trp Val Glu Ser Pro Ser Asp
 210 215

<210> 83

<211> 1411

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1411)

<223> RXN02820

<400> 83

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aatatctccc cacataaaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
                               Met Lys Val Thr Gln
                               1           5

agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc 163
Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
                10                15                20

ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc 211
Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
                25                30                35

acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt 259
Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala Ala Ser Pro Pro Leu
                40                45                50

gcg cct tgt gaa ctt ccc gcc gac gct tct gct gaa gag gaa gta gaa 307
Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala Glu Glu Glu Val Glu
                55                60                65

ggc act cac aca ggt gaa gat att tct gtt gcc ccg gaa atc ggt acc 355
Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala Pro Glu Ile Gly Thr
                70                75                80                85

ggc tac cgc gag ggc atg acc cct gtt caa acc caa ggt tat gcg gtg 403
Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr Gln Gly Tyr Ala Val
                90                95                100

gca act gca aac ccc atc gct tct gaa gca gcc tgc gcg gtg tta aga 451
Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala Cys Ala Val Leu Arg
                105                110                115

gaa ggc ggc act gca gct gat gct ctt gtc acc gcg cag ttt gtt ttg 499
Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr Ala Gln Phe Val Leu
                120                125                130

gga ctg acg gaa ccg cag tcg tct ggc ctt ggt ggt ggc gga tac att 547
Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly Gly Gly Gly Tyr Ile
                135                140                145

ctg tac tac gac gcc gaa gcc aat gcg gtg aca gcc att gat ggc cgt 595
Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr Ala Ile Asp Gly Arg
                150                155                160                165

gaa aca gcg cca gtt gct gct gat gaa aac tat ctc att cat gtt tct 643
Glu Thr Ala Pro Val Ala Ala Asp Glu Asn Tyr Leu Ile His Val Ser
                170                175                180

gca gag gat caa acg gca cct gtt cct gat gcc cga cgt tcc ggc agg 691
Ala Glu Asp Gln Thr Ala Pro Val Pro Asp Ala Arg Arg Ser Gly Arg
                185                190                195

tca att ggt gtg cca gga atc gtg gca gcc ctt gga cag ctg cat gat 739
Ser Ile Gly Val Pro Gly Ile Val Ala Ala Leu Gly Gln Leu His Asp
                200                205                210

tca ttc gga aag acc tcc tgg cag gac gtg ctg aca act ccg cag cag 787

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Ser	Phe	Gly	Lys	Thr	Ser	Trp	Gln	Asp	Val	Leu	Thr	Thr	Pro	Gln	Gln		
215						220					225						
ctc	gca	act	gat	ggg	ttt	tcc	atc	agc	cct	cgc	atg	tca	gca	tca	att	835	
Leu	Ala	Thr	Asp	Gly	Phe	Ser	Ile	Ser	Pro	Arg	Met	Ser	Ala	Ser	Ile		
230					235					240					245		
gct	aac	tcc	gct	gag	gat	ctc	tcc	cac	gat	ccg	gaa	gct	gcc	gca	tat	883	
Ala	Asn	Ser	Ala	Glu	Asp	Leu	Ser	His	Asp	Pro	Glu	Ala	Ala	Ala	Tyr		
				250					255					260			
ttc	ctt	gat	gaa	aac	ggg	gat	gcg	aag	gca	ccc	ggc	aca	ctt	tta	caa	931	
Phe	Leu	Asp	Glu	Asn	Gly	Asp	Ala	Lys	Ala	Pro	Gly	Thr	Leu	Leu	Gln		
			265					270					275				
aac	cct	gac	tat	gca	gaa	acg	att	cgt	ctc	atc	tct	gaa	ggg	ggc	ccc	979	
Asn	Pro	Asp	Tyr	Ala	Glu	Thr	Ile	Arg	Leu	Ile	Ser	Glu	Gly	Gly	Pro		
		280						285				290					
gat	gcg	ttc	tac	acg	ggg	gag	att	gca	gca	gac	atc	gtg	gaa	cgc	gcc	1027	
Asp	Ala	Phe	Tyr	Thr	Gly	Glu	Ile	Ala	Ala	Asp	Ile	Val	Glu	Arg	Ala		
		295				300					305						
acc	cgt	gag	gtt	gac	ggg	ttc	aca	cca	tca	ctg	atg	agc	acg	gca	gat	1075	
Thr	Arg	Glu	Val	Asp	Gly	Phe	Thr	Pro	Ser	Leu	Met	Ser	Thr	Ala	Asp		
310					315					320					325		
ttg	gct	gcc	tac	act	ccg	gaa	act	cgt	gaa	gct	ttg	tgt	gct	ccc	tac	1123	
Leu	Ala	Ala	Tyr	Thr	Pro	Glu	Thr	Arg	Glu	Ala	Leu	Cys	Ala	Pro	Tyr		
				330					335					340			
cgc	gac	aag	att	gtt	tgt	ggc	atg	cca	ccg	tca	tca	tcg	ggg	ggc	gtc	1171	
Arg	Asp	Lys	Ile	Val	Cys	Gly	Met	Pro	Pro	Ser	Ser	Ser	Gly	Gly	Val		
			345					350					355				
aca	gtg	atg	gaa	acc	ctg	ggg	atc	ttg	aac	aac	ttt	gat	ctc	gcc	caa	1219	
Thr	Val	Met	Glu	Thr	Leu	Gly	Ile	Leu	Asn	Asn	Phe	Asp	Leu	Ala	Gln		
			360					365				370					
tac	cca	ccc	act	gag	gtt	ggg	ttg	gat	ggc	gga	ttg	cca	aat	gcg	gaa	1267	
Tyr	Pro	Pro	Thr	Glu	Val	Gly	Leu	Asp	Gly	Gly	Leu	Pro	Asn	Ala	Glu		
		375				380					385						
gct	gtt	cac	ctg	att	tca	gag	gct	gag	cgc	ctg	gct	tat	gct	gat	cgc	1315	
Ala	Val	His	Leu	Ile	Ser	Glu	Ala	Glu	Arg	Leu	Ala	Tyr	Ala	Asp	Arg		
390					395					400					405		
gat	gct	tac	atc	ggg	gat	cct	gct	ttc	gtg	gaa	gtt	cca	gca	ggg	ggg	1363	
Asp	Ala	Tyr	Ile	Gly	Asp	Pro	Ala	Phe	Val	Glu	Val	Pro	Ala	Gly	Gly		
				410					415					420			
gtc	caa	cag	tgg	atc	aac	cat	gtc	cac	acg	ggc	gaa	cac	tcc	aaa	ctt	1411	
Val	Gln	Gln	Trp	Ile	Asn	His	Val	His	Thr	Gly	Glu	His	Ser	Lys	Leu		
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<210> 84

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

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 Val Ala Ala Leu Thr Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp
 20 25 30
 Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala
 35 40 45
 Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala
 50 55 60
 Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala
 65 70 75 80
 Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr
 85 90 95
 Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala
 100 105 110
 Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr
 115 120 125
 Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly
 130 135 140
 Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr
 145 150 155 160
 Ala Ile Asp Gly Arg Glu Thr Ala Pro Val Ala Ala Asp Glu Asn Tyr
 165 170 175
 Leu Ile His Val Ser Ala Glu Asp Gln Thr Ala Pro Val Pro Asp Ala
 180 185 190
 Arg Arg Ser Gly Arg Ser Ile Gly Val Pro Gly Ile Val Ala Ala Leu
 195 200 205
 Gly Gln Leu His Asp Ser Phe Gly Lys Thr Ser Trp Gln Asp Val Leu
 210 215 220
 Thr Thr Pro Gln Gln Leu Ala Thr Asp Gly Phe Ser Ile Ser Pro Arg
 225 230 235 240
 Met Ser Ala Ser Ile Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro
 245 250 255
 Glu Ala Ala Ala Tyr Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro
 260 265 270
 Gly Thr Leu Leu Gln Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile
 275 280 285
 Ser Glu Gly Gly Pro Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp
 290 295 300
 Ile Val Glu Arg Ala Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu
 305 310 315 320

<400> 85																
gct	aac	tcc	gct	gag	gat	ctc	tcc	cac	gat	ccg	gaa	gct	gcc	gca	tat	48
Ala	Asn	Ser	Ala	Glu	Asp	Leu	Ser	His	Asp	Pro	Glu	Ala	Ala	Ala	Tyr	
1				5					10					15		
ttc	ctt	gat	gaa	aac	ggg	gat	gcg	aag	gca	ccc	ggc	aca	ctt	tta	caa	96
Phe	Leu	Asp	Glu	Asn	Gly	Asp	Ala	Lys	Ala	Pro	Gly	Thr	Leu	Leu	Gln	
			20					25					30			
aac	cct	gac	tat	gca	gaa	acg	att	cgt	ctc	atc	tct	gaa	ggg	ggc	ccc	144
Asn	Pro	Asp	Tyr	Ala	Glu	Thr	Ile	Arg	Leu	Ile	Ser	Glu	Gly	Gly	Pro	
		35					40					45				
gat	gcg	ttc	tac	acg	ggg	gag	att	gca	gca	gac	atc	gtg	gaa	cgc	gcc	192
Asp	Ala	Phe	Tyr	Thr	Gly	Glu	Ile	Ala	Ala	Asp	Ile	Val	Glu	Arg	Ala	
	50					55					60					
acc	cgt	gag	gtt	gac	ggg	ttc	aca	cca	tca	ctg	atg	agc	acg	gca	gat	240
Thr	Arg	Glu	Val	Asp	Gly	Phe	Thr	Pro	Ser	Leu	Met	Ser	Thr	Ala	Asp	
65				70						75					80	
ttg	gct	gcc	tac	act	ccg	gaa	act	cgt	gaa	gct	ttg	tgt	gct	ccc	tac	288
Leu	Ala	Ala	Tyr	Thr	Pro	Glu	Thr	Arg	Glu	Ala	Leu	Cys	Ala	Pro	Tyr	
				85					90					95		
cgc	gac	aag	att	gtt	tgt	ggc	atg	cca	ccg	tca	tca	tcg	ggg	ggc	gtc	336

Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
 100 105 110

aca gtg atg gaa acc ctg ggt atc ttg aac aac ttt gat ctc gcc caa 384
 Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
 115 120 125

tac cca ccc act gag gtt ggt ttg gat ggc gga ttg cca aat gcg gaa 432
 Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
 130 135 140

gct gtt cac ctg att tca gag gct gag cgc ctg gct tat gct gat cgc 480
 Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
 145 150 155 160

gat gct tac atc ggt gat cct gct ttc 507
 Asp Ala Tyr Ile Gly Asp Pro Ala Phe
 165

<210> 86

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr
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Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln
 20 25 30

Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
 35 40 45

Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
 50 55 60

Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
 65 70 75 80

Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
 85 90 95

Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
 100 105 110

Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
 115 120 125

Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
 130 135 140

Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
 145 150 155 160

Asp Ala Tyr Ile Gly Asp Pro Ala Phe
 165

<210> 87

<211> 604
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(604)
 <223> FRXA02000

<400> 87

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aatatctccc cacataaaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
                                     Met Lys Val Thr Gln
                                     1 5

agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc 163
Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
                10                15                20

ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc 211
Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
                25                30                35

acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt 259
Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala Ala Ser Pro Pro Leu
                40                45                50

gcg cct tgt gaa ctt ccc gcc gac gct tct gct gaa gag gaa gta gaa 307
Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala Glu Glu Glu Val Glu
                55                60                65

ggc act cac aca ggt gaa gat att tct gtt gcc ccg gaa atc ggt acc 355
Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala Pro Glu Ile Gly Thr
                70                75                80                85

ggc tac cgc gag ggc atg acc cct gtt caa acc caa ggt tat gcg gtg 403
Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr Gln Gly Tyr Ala Val
                90                95                100

gca act gca aac ccc atc gct tct gaa gca gcc tgc gcg gtg tta aga 451
Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala Cys Ala Val Leu Arg
                105                110                115

gaa ggc ggc act gca gct gat gct ctt gtc acc gcg cag ttt gtt ttg 499
Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr Ala Gln Phe Val Leu
                120                125                130

gga ctg acg gaa ccg cag tcg tct ggc ctt ggt ggt ggc gga tac att 547
Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly Gly Gly Tyr Ile
                135                140                145

ctg tac tac gac gcc gaa gcc aat gcg gtg aca gcc att gat ggc cgt 595
Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr Ala Ile Asp Gly Arg
                150                155                160                165

gaa aca gcg
Glu Thr Ala 604

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<210> 88
 <211> 168
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 88
 Met Lys Val Thr Gln Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr
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 Val Ala Ala Leu Thr Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp
 20 25 30
 Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala
 35 40 45
 Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala
 50 55 60
 Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala
 65 70 75 80
 Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr
 85 90 95
 Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala
 100 105 110
 Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr
 115 120 125
 Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly
 130 135 140
 Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr
 145 150 155 160
 Ala Ile Asp Gly Arg Glu Thr Ala
 165

<210> 89
 <211> 824
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(801)
 <223> RXN03178

<400> 89
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 Pro Thr Thr Val Val Thr Gly Thr Met Glu Ala Ala Asn Ile Glu Gly
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 Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
 20 25 30
 ctg cac ggt ctt ctt tta gcc agc ggt aac gat gcg gcg tat atg ttg 144
 Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu

35	40	45	
gct cag gaa ctt ggt ggg gat caa gca acc ctg gag aaa gta aac gcg Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala 50 55 60			192
ctg gcc aag gag ttg ggc act caa gac acc ttc gtt gcc act tat tcc Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser 65 70 75 80			240
ggt ttg gat gcg ccg gga atg tcg acc tcc gca tac gac atg tca ttg Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu 85 90 95			288
att tat cag cat gcg tgg cag aac ccg gtt ttc gag tcg att atc tcc Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser 100 105 110			336
acc gat cac att gat ttc cct ggt tgg ggc gac aat gag ggt ttc caa Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln 115 120 125			384
gtc tgg aac gat aac gcc ttg ttc atg aac gat cct gat ggc atc ggc Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly 130 135 140			432
ggc aag acc ggc tac acc gac gac gcg aac cac acc ttt gtc ggc ggt Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly 145 150 155 160			480
ctc gat cgg ggt ggt cgc cgc ctc gcc gcc gta ctc ttg gat tcc acc Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr 165 170 175			528
gtc agc gac att cgt ccg tgg gaa caa gca cga ttg ctt atc gac gcc Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala 180 185 190			576
tcc ctc ccc atc acg ccg ggg tcc ggc gtg ggc cag ctg ggc tcc ggc Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly 195 200 205			624
agc gcg aac gat gtg gca ccg gcg acc cca gaa tta cca gaa ccc acc Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr 210 215 220			672
gac aac ctg act tca ggt gag ggt ggg tcg cag aac acg ctt ctt aag Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys 225 230 235 240			720
ctc gtg gtg ccc atc gga atc atc gtg ctg ttg cta atc gcc gca cta Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu 245 250 255			768
gcg tgg aca ttc aga tct ccc aag aaa aag aac taggtgttct tcttcacgac Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn 260 265			821
ctc			824

<210> 90
 <211> 267
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 90

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Pro Thr Thr Val Val Thr Gly Thr Met Glu Ala Ala Asn Ile Glu Gly
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Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
          20          25          30

Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu
      35          40          45

Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala
 50          55          60

Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser
65          70          75          80

Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu
          85          90          95

Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser
      100          105          110

Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln
      115          120          125

Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly
      130          135          140

Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly
      145          150          155          160

Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr
      165          170          175

Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala
      180          185          190

Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly
      195          200          205

Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr
      210          215          220

Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys
      225          230          235          240

Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu
      245          250          255

Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn
      260          265

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<210> 91
 <211> 749
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> FRXA02859

<400> 91

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aac gat gcg gcg tat ctg ttg gct cag gaa ctt ggt ggg gat caa gca	96
Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala	
20 25 30	
acc ctg gag aaa gta aac gcg ctg gcc aag gag ttg ggc act caa gac	144
Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp	
35 40 45	
acc ttc gtt gcc act tat tcc ggt ttg gat gcg ccg gga atg tcg acc	192
Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr	
50 55 60	
tcc gca tac gac atg tca ttg att tat cag cat gcg tgg cag aac ccg	240
Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro	
65 70 75 80	
gtt ttc gag tcg att atc tcc acc gat cac att gat ttc cct ggt tgg	288
Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp	
85 90 95	
ggc gac aat gag ggt ttc caa gtc tgg aac gat aac gcc ttg ttc atg	336
Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met	
100 105 110	
aac gat cct gat ggc atc ggc ggc aag acc ggc tac acc gac gac gcg	384
Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala	
115 120 125	
aac cac acc ttt gtc ggc ggt ctc gat cgg ggt ggt cgc cgc ctc gcc	432
Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala	
130 135 140	
gcc gta ctc ttg gat tcc acc gtc agc gac att cgt ccg tgg gaa caa	480
Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln	
145 150 155 160	
gca cga ttg ctt atc gac gcc tcc ctc ccc atc acg ccg ggg tcc ggc	528
Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly	
165 170 175	
gtg ggc cag ctg ggc tcc ggc agc gcg aac gat gtg gca ccg gcg acc	576
Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr	
180 185 190	
cca gaa tta cca gaa ccc acc gac aac ctg act tca ggt gag ggt ggg	624
Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly	
195 200 205	
tcg cag aac acg ctg ctt aag ctc gtg gtg ccc atc gga atc atc gtg	672

Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
 210 215 220

ctg ttg cta atc gcc gca cta gcg tgg aca ttc aga tct ccc aag aaa 720
 Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
 225 230 235 240

aag aac taggtgttct tcttcacgac ctc 749
 Lys Asn

<210> 92
 <211> 242
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 92
 Gln Tyr Thr Val Asp Gln Leu Leu His Gly Leu Leu Leu Ala Ser Gly
 1 5 10 15

Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
 20 25 30

Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
 35 40 45

Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
 50 55 60

Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65 70 75 80

Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
 85 90 95

Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
 100 105 110

Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
 115 120 125

Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
 130 135 140

Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
 145 150 155 160

Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
 165 170 175

Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
 180 185 190

Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
 195 200 205

Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
 210 215 220

Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys

225

230

235

240

Lys Asn

<210> 93

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00137

<400> 93

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                                         Met Ala Leu Ala Asp
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acc cga ttt gcc act cgt cgt cgc gca ctt gcc gca aaa ctg gca gct 163
Thr Arg Phe Ala Thr Arg Arg Arg Ala Leu Ala Ala Lys Leu Ala Ala
                        10 15 20

caa cgg atc gac tca att ttg gtg aca agc ccg atc cat gtt cgc tat 211
Gln Arg Ile Asp Ser Ile Leu Val Thr Ser Pro Ile His Val Arg Tyr
                        25 30 35

ctc agc gga ttc acc ggc tcc aac ggc gca ctg atc gtg aac aaa gat 259
Leu Ser Gly Phe Thr Gly Ser Asn Gly Ala Leu Ile Val Asn Lys Asp
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ctc tcc gcg cag atc tgc acc gac ggt cgc tac acc acc cag atc gca 307
Leu Ser Ala Gln Ile Cys Thr Asp Gly Arg Tyr Thr Thr Gln Ile Ala
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gaa gaa gtc ccg gac atc gag gcg ctg att gag cgt gcc tcg gca acg 355
Glu Glu Val Pro Asp Ile Glu Ala Leu Ile Glu Arg Ala Ser Ala Thr
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acg ctg cta gcg cag gtc gaa ggg ccg cgt cgt ata gca atc gaa gcc 403
Thr Leu Leu Ala Gln Val Glu Gly Pro Arg Arg Ile Ala Ile Glu Ala
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gca caa acc acc ctg gac cag cta gac agc ctg cgt gaa gca acc cag 451
Ala Gln Thr Thr Leu Asp Gln Leu Asp Ser Leu Arg Glu Ala Thr Gln
                        105 110 115

gaa gac gtc gag ctg atc ccc gtg tca ggt gtt gtg gaa tcc att cgc 499
Glu Asp Val Glu Leu Ile Pro Val Ser Gly Val Val Glu Ser Ile Arg
                        120 125 130

ctg acc aaa gac agc ttc gaa ctc gac cgc ctc cgc gat gtc gca gcg 547
Leu Thr Lys Asp Ser Phe Glu Leu Asp Arg Leu Arg Asp Val Ala Ala
                        135 140 145

ctg gct tcc caa gca ttc gaa gat tta ctc gca gca gga gaa ctc gcc 595
Leu Ala Ser Gln Ala Phe Glu Asp Leu Leu Ala Ala Gly Glu Leu Ala

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150	155	160	165	
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Glu Gly Arg Ser Glu Arg Gln Val Ala Ala Asp Leu Glu Tyr Arg Met				
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cgc ctg ttg gga gca gaa cgc ccc agc ttc gac acc atc gtg gcc tct				691
Arg Leu Leu Gly Ala Glu Arg Pro Ser Phe Asp Thr Ile Val Ala Ser				
	185	190	195	
gga cct aac tcc gcg aaa cca cac cac ggc gca ggc gac cgc atc ctc				739
Gly Pro Asn Ser Ala Lys Pro His His Gly Ala Gly Asp Arg Ile Leu				
	200	205	210	
cag cgc ggc gat cta gtc acc atc gat ttc ggc gca cac gca cgc gga				787
Gln Arg Gly Asp Leu Val Thr Ile Asp Phe Gly Ala His Ala Arg Gly				
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ttc aac tcc gat atg acc cgc acc ctc gtt atg ggc gaa gca ggg gag				835
Phe Asn Ser Asp Met Thr Arg Thr Leu Val Met Gly Glu Ala Gly Glu				
	230	235	240	245
ttc gaa gca gaa atc tac gac atc gtc ctg cgc tcc caa ctc gct ggt				883
Phe Glu Ala Glu Ile Tyr Asp Ile Val Leu Arg Ser Gln Leu Ala Gly				
	250	255	260	
gtt gaa gca gcc tac tca ggc gcc aac ctc ttc gac atc gac gca gca				931
Val Glu Ala Ala Tyr Ser Gly Ala Asn Leu Phe Asp Ile Asp Ala Ala				
	265	270	275	
tgc cgc aaa atc atc gaa gac gca ggc tac ggc gaa tac ttc gtg cac				979
Cys Arg Lys Ile Ile Glu Asp Ala Gly Tyr Gly Glu Tyr Phe Val His				
	280	285	290	
tcc acc ggc cac ggc atc gga ctt gaa gtc cac gaa gcc cca agc gca				1027
Ser Thr Gly His Gly Ile Gly Leu Glu Val His Glu Ala Pro Ser Ala				
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tcc aaa acc tca caa gga gtc cta gaa acc ggc tcc aca ctg acc atc				1075
Ser Lys Thr Ser Gln Gly Val Leu Glu Thr Gly Ser Thr Leu Thr Ile				
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gaa ccc gga att tac gtc ccc gga aag ggc ggc gta cgc atc gaa gac				1123
Glu Pro Gly Ile Tyr Val Pro Gly Lys Gly Gly Val Arg Ile Glu Asp				
	330	335	340	
acc ctg att att acc tca gga gca ccg gaa atc atc acc aag gtg agt				1171
Thr Leu Ile Ile Thr Ser Gly Ala Pro Glu Ile Ile Thr Lys Val Ser				
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Lys Asp Leu Ile Val Val				
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<210> 94

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 94

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 20 25 30
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 35 40 45
 Ile Val Asn Lys Asp Leu Ser Ala Gln Ile Cys Thr Asp Gly Arg Tyr
 50 55 60
 Thr Thr Gln Ile Ala Glu Glu Val Pro Asp Ile Glu Ala Leu Ile Glu
 65 70 75 80
 Arg Ala Ser Ala Thr Thr Leu Leu Ala Gln Val Glu Gly Pro Arg Arg
 85 90 95
 Ile Ala Ile Glu Ala Ala Gln Thr Thr Leu Asp Gln Leu Asp Ser Leu
 100 105 110
 Arg Glu Ala Thr Gln Glu Asp Val Glu Leu Ile Pro Val Ser Gly Val
 115 120 125
 Val Glu Ser Ile Arg Leu Thr Lys Asp Ser Phe Glu Leu Asp Arg Leu
 130 135 140
 Arg Asp Val Ala Ala Leu Ala Ser Gln Ala Phe Glu Asp Leu Leu Ala
 145 150 155 160
 Ala Gly Glu Leu Ala Glu Gly Arg Ser Glu Arg Gln Val Ala Ala Asp
 165 170 175
 Leu Glu Tyr Arg Met Arg Leu Leu Gly Ala Glu Arg Pro Ser Phe Asp
 180 185 190
 Thr Ile Val Ala Ser Gly Pro Asn Ser Ala Lys Pro His His Gly Ala
 195 200 205
 Gly Asp Arg Ile Leu Gln Arg Gly Asp Leu Val Thr Ile Asp Phe Gly
 210 215 220
 Ala His Ala Arg Gly Phe Asn Ser Asp Met Thr Arg Thr Leu Val Met
 225 230 235 240
 Gly Glu Ala Gly Glu Phe Glu Ala Glu Ile Tyr Asp Ile Val Leu Arg
 245 250 255
 Ser Gln Leu Ala Gly Val Glu Ala Ala Tyr Ser Gly Ala Asn Leu Phe
 260 265 270
 Asp Ile Asp Ala Ala Cys Arg Lys Ile Ile Glu Asp Ala Gly Tyr Gly
 275 280 285
 Glu Tyr Phe Val His Ser Thr Gly His Gly Ile Gly Leu Glu Val His
 290 295 300
 Glu Ala Pro Ser Ala Ser Lys Thr Ser Gln Gly Val Leu Glu Thr Gly
 305 310 315 320
 Ser Thr Leu Thr Ile Glu Pro Gly Ile Tyr Val Pro Gly Lys Gly Gly

325 330 335

Val Arg Ile Glu Asp Thr Leu Ile Ile Thr Ser Gly Ala Pro Glu Ile
340 345 350

Ile Thr Lys Val Ser Lys Asp Leu Ile Val Val
355 360

<210> 95
<211> 1404
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1381)
<223> RXN00499

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Val Val Gly Val Val
1 5

tcc acc cct gcg cgt aac ctg gga agc atg act aaa aca ctt ggt tcc 163
Ser Thr Pro Ala Arg Asn Leu Gly Ser Met Thr Lys Thr Leu Gly Ser
10 15 20

ctt cag ctg gaa gaa atc acg ctg acc ctc cct ctg act gaa gat gtg 211
Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu Pro Leu Thr Glu Asp Val
25 30 35

gcc gat gaa cgc acc att gat gtg ttc gca cgc att gcc aca cgc gtc 259
Ala Asp Glu Arg Thr Ile Asp Val Phe Ala Arg Ile Ala Thr Arg Val
40 45 50

ggg ggg gaa gac ctt cca tat tta gta ttc ctg cag ggt ggg cct ggc 307
Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe Leu Gln Gly Gly Pro Gly
55 60 65

aat gaa gct cca cgt cca agc ctt aat ccc ctc aac ccc aat tgg ttg 355
Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro Leu Asn Pro Asn Trp Leu
70 75 80 85

ggc gtg gcc ttg gag gaa tac cgc gtg gtc atg ttg gat caa cgt ggc 403
Gly Val Ala Leu Glu Glu Tyr Arg Val Val Met Leu Asp Gln Arg Gly
90 95 100

acc ggc cgt tcc acc cca gtg ggt aat gat att ttg gaa aaa ccc aca 451
Thr Gly Arg Ser Thr Pro Val Gly Asn Asp Ile Leu Glu Lys Pro Thr
105 110 115

gca gaa gta gtg gag tac tta tcc cac ctg cgc gca gat ggc att gtg 499
Ala Glu Val Val Glu Tyr Leu Ser His Leu Arg Ala Asp Gly Ile Val
120 125 130

cga gat gct gaa gcc ctg cgt aag cat ttg ggt gtg aat cag tgg aac 547
Arg Asp Ala Glu Ala Leu Arg Lys His Leu Gly Val Asn Gln Trp Asn
135 140 145

ctt tta ggc cag tcc ttc gga ggt ttc acc acc ctg cat tac ttg tcc	595
Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr Thr Leu His Tyr Leu Ser	
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cgg cac gcc gat tcc ttg gac aac gtg ttt att acc ggc ggt ctc agc	643
Arg His Ala Asp Ser Leu Asp Asn Val Phe Ile Thr Gly Gly Leu Ser	
170 175 180	
gct att gat cgc cca gca gaa gac gtg tat gcc aac tgt tac aac cgc	691
Ala Ile Asp Arg Pro Ala Glu Asp Val Tyr Ala Asn Cys Tyr Asn Arg	
185 190 195	
atg cgc cga aac tct gag gaa ttc tac cgt cgc ttc ccg caa tta cgg	739
Met Arg Arg Asn Ser Glu Glu Phe Tyr Arg Arg Phe Pro Gln Leu Arg	
200 205 210	
gaa act ttc cga ggg ttg gtt aat cgt gct cgc gcc ggg gag att gtg	787
Glu Thr Phe Arg Gly Leu Val Asn Arg Ala Arg Ala Gly Glu Ile Val	
215 220 225	
ctt ccc acc ggc gaa gtt gtg tca gaa acc agg ctg cga tcc ctt ggt	835
Leu Pro Thr Gly Glu Val Val Ser Glu Thr Arg Leu Arg Ser Leu Gly	
230 235 240 245	
cac ttg ttg ggt agc aat gac ggc tgg ttt gat ctg tac aac ctg ctg	883
His Leu Leu Gly Ser Asn Asp Gly Trp Phe Asp Leu Tyr Asn Leu Leu	
250 255 260	
gaa tta gat ccc acc tcc aac gct ttt gtc cat gac ctg gca gga ctt	931
Glu Leu Asp Pro Thr Ser Asn Ala Phe Val His Asp Leu Ala Gly Leu	
265 270 275	
ttg cct ttc ggc aac cgc aac cca att tat tac gtg ctc cat gag tcc	979
Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr Tyr Val Leu His Glu Ser	
280 285 290	
tct tac gcc gac ggt gtg gtg aca aat tgg gca gca gag cgt gtg ctt	1027
Ser Tyr Ala Asp Gly Val Val Thr Asn Trp Ala Ala Glu Arg Val Leu	
295 300 305	
cca gag gat ttc cgc gag gat cca aca ctg ctc acc ggt gag cac gtg	1075
Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Thr Gly Glu His Val	
310 315 320 325	
ttc cag gag tgg aca gac acc gtg ccg tcg ctc aag ccg tgg aag gac	1123
Phe Gln Glu Trp Thr Asp Thr Val Pro Ser Leu Lys Pro Trp Lys Asp	
330 335 340	
gtt gcc ctg gca ttg gct cag cag gaa tgg ccc aag ctt tat gat gcg	1171
Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro Lys Leu Tyr Asp Ala	
345 350 355	
aag gca ttg gaa aac tca cag gcc aag ggc gct gca gca gtg tat gcc	1219
Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala Ala Ala Val Tyr Ala	
360 365 370	
aat gac gtt ttc gtc cca gtg gat tac tct ctg gaa acc gca caa cac	1267
Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu Glu Thr Ala Gln His	
375 380 385	

ctg ccc ggt gtg cag ctg ttt atc acc agc cag cat gaa cac aat gga 1315
 Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln His Glu His Asn Gly
 390 395 400 405

ctt cgt gcc agc tca ggc gca gta ctg aag cac ctt ttc gat ctg gcc 1363
 Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His Leu Phe Asp Leu Ala
 410 415 420

cac ggc cga gag gta cgc tgattcctcg tgtagtact agc 1404
 His Gly Arg Glu Val Arg
 425

<210> 96

<211> 427

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 96

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Leu Thr Glu Asp Val Ala Asp Glu Arg Thr Ile Asp Val Phe Ala Arg
 35 40 45

Ile Ala Thr Arg Val Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe Leu
 50 55 60

Gln Gly Gly Pro Gly Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro Leu
 65 70 75 80

Asn Pro Asn Trp Leu Gly Val Ala Leu Glu Glu Tyr Arg Val Val Met
 85 90 95

Leu Asp Gln Arg Gly Thr Gly Arg Ser Thr Pro Val Gly Asn Asp Ile
 100 105 110

Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu Ser His Leu Arg
 115 120 125

Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg Lys His Leu Gly
 130 135 140

Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr Thr
 145 150 155 160

Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp Asn Val Phe Ile
 165 170 175

Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu Asp Val Tyr Ala
 180 185 190

Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu Phe Tyr Arg Arg
 195 200 205

Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val Asn Arg Ala Arg
 210 215 220

Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val Ser Glu Thr Arg
 225 230 235 240

Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp Gly Trp Phe Asp
 245 250 255

Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn Ala Phe Val His
 260 265 270

Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr Tyr
 275 280 285

Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val Thr Asn Trp Ala
 290 295 300

Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Leu
 305 310 315 320

Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr Val Pro Ser Leu
 325 330 335

Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro
 340 345 350

Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala
 355 360 365

Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu
 370 375 380

Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln
 385 390 395 400

His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His
 405 410 415

Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
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<210> 97

<211> 980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA00499

<400> 97

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tcc cac ctg cgc gca gat ggc att gtg cga gat gct gaa gcc ctg cgt 96
 Ser His Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg
 20 25 30

aag cat ttg ggt gtg aat cag tgg aac ctt tta ggc cag tcc ttc gga 144
 Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly

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aac gtg ttt att acc ggc ggt ctc agc gct att gat cgc cca gca gaa Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu 65 70 75 80			240
gac gtg tat gcc aac tgt tac aac cgc atg cgc cga aac tct gag gaa Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu 85 90 95			288
ttc tac cgt cgc ttc ccg caa tta cgg gaa act ttc cga ggg ttg gtt Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val 100 105 110			336
aat cgt gct cgc gcc ggg gag att gtg ctt ccc acc ggc gaa gtt gtg Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val 115 120 125			384
tca gaa acc agg ctg cga tcc ctt ggt cac ttg ttg ggt agc aat gac Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp 130 135 140			432
ggc tgg ttt gat ctg tac aac ctg ctg gaa tta gat ccc acc tcc aac Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn 145 150 155 160			480
gct ttt gtc cat gac ctg gca gga ctt ttg cct ttc ggc aac cgc aac Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn 165 170 175			528
cca att tat tac gtg ctc cat gag tcc tct tac gcc gac ggt gtg gtg Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val 180 185 190			576
aca aat tgg gca gca gag cgt gtg ctt cca gag gat ttc cgc gag gat Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp 195 200 205			624
cca aca ctg ctc acc ggt gag cac gtg ttc cag gag tgg aca gac acc Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr 210 215 220			672
gtg ccg tcg ctc aag ccg tgg aag gac gtt gcc ctg gca ttg gct cag Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln 225 230 235 240			720
cag gaa tgg ccc aag ctt tat gat gcg aag gca ttg gaa aac tca cag Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln 245 250 255			768
gcc aag ggc gct gca gca gtg tat gcc aat gac gtt ttc gtc cca gtg Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val 260 265 270			816
gat tac tct ctg gaa acc gca caa cac ctg ccc ggt gtg cag ctg ttt Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe 275 280 285			864

atc acc agc cag cat gaa cac aat gga ctt cgt gcc agc tca ggc gca 912
 Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala
 290 295 300

gta ctg aag cac ctt ttc gat ctg gcc cac ggc cga gag gta cgc 957
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<210> 98

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 98

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 20 25 30

Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly
 35 40 45

Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp
 50 55 60

Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu
 65 70 75 80

Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu
 85 90 95

Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val
 100 105 110

Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val
 115 120 125

Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp
 130 135 140

Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn
 145 150 155 160

Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn
 165 170 175

Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val
 180 185 190

Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp
 195 200 205

Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr
 210 215 220

Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln

225	230	235	240
Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln			
	245	250	255
Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val			
	260	265	270
Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe			
	275	280	285
Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala			
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Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg			
305	310	315	

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 <211> 1788
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1765)
 <223> RXN00877

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 Met Thr Val Glu His
 1 5
 ctg ctc aag ccc agc acc ttg ccc tac cag ctg ccc gat ttc gca gcg 163
 Leu Leu Lys Pro Ser Thr Leu Pro Tyr Gln Leu Pro Asp Phe Ala Ala
 10 15 20
 atc aag gtg gct gat ttc ccg ccc gcc ttc gaa ctc gca tta gct gaa 211
 Ile Lys Val Ala Asp Phe Pro Pro Ala Phe Glu Leu Ala Leu Ala Glu
 25 30 35
 cac gat gct gaa att aca gcg atc gct acc aat gag gac gct cct acc 259
 His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn Glu Asp Ala Pro Thr
 40 45 50
 tgg gag aac acc att gag gcc ctg gaa cgc gca ggc ctg tcc ctc aac 307
 Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala Gly Leu Ser Leu Asn
 55 60 65
 cgc gtc gcc gcc gta ttc ttc aac ttg cag ggc acc gat tcc tcc cct 355
 Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly Thr Asp Ser Ser Pro
 70 75 80 85
 gaa atg gat gaa atc gca gcc act atc gcg ccg aaa ctc tcc gcg cat 403
 Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro Lys Leu Ser Ala His
 90 95 100
 tcg gat gcg att ttc cac aat gct gcg ctt ttc gcg cgc att gag gcc 451
 Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe Ala Arg Ile Glu Ala

105	110	115	
gta gaa gca ccg gcc gac gag gaa tcg caa cgc ctg ttg tcc cac acc Val Glu Ala Pro Ala Asp Glu Glu Ser Gln Arg Leu Leu Ser His Thr 120 125 130			499
aag cgc gct ttt cga cgt cgc ggt gca gca ctc aac gcc gac ggc aag Lys Arg Ala Phe Arg Arg Arg Gly Ala Ala Leu Asn Ala Asp Gly Lys 135 140 145			547
gcc cga ctg agc acc atc aac cag cgc cta tcg gca ctg tcc gaa cag Ala Arg Leu Ser Thr Ile Asn Gln Arg Leu Ser Ala Leu Ser Glu Gln 150 155 160 165			595
ttc ggc cgc aac ctg ctt cag gac acc cgc gat ctg gcg gtc aac ttt Phe Gly Arg Asn Leu Leu Gln Asp Thr Arg Asp Leu Ala Val Asn Phe 170 175 180			643
gaa gaa tct gaa ctt gcc ggt ttt agc gaa gcc cgc ata tcc gcc gcc Glu Glu Ser Glu Leu Ala Gly Phe Ser Glu Ala Arg Ile Ser Ala Ala 185 190 195			691
gct gac tac gca gca gca gtt ggc acc gaa ggc tac gtg gtt cca ctg Ala Asp Tyr Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu 200 205 210			739
gaa ctg ccc acc gtg cag tca gag cag gca gta tta acc gaa tcc gcc Glu Leu Pro Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala 215 220 225			787
tcg cgt gca aag ctt tat gaa gcc tcc cag aag cgt ggc gcc agc ctg Ser Arg Ala Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu 230 235 240 245			835
aac aag gac gtg ctg ctc gaa acc gtg cgt ctg cgt gct gaa cgc gcc Asn Lys Asp Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala 250 255 260			883
aca ctt tta ggc tac gac acc cac gcc gat tac gtc atc gaa gaa gaa Thr Leu Leu Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu 265 270 275			931
acc gcc gat gac gtc gca gcc gtg cgc gcc ttg ctt tat gat ctc gcc Thr Ala Asp Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala 280 285 290			979
cca gcc gcc tct gcc aat gcg aaa gcc gaa tac aaa ctc tcc gca gaa Pro Ala Ala Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu 295 300 305			1027
gaa gca gaa gaa cac ggc caa aaa gtc ggc gca gct gac tgg agc ttc Glu Ala Glu Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe 310 315 320 325			1075
tgg gaa gcc aaa gtc cgc gcc cgc gac tac gcc ctg gac gaa acc gaa Trp Glu Ala Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu 330 335 340			1123
ctg cgc aac tac ttc cca ttg aac caa gta ctc cgt gac ggc gtc ttc Leu Arg Asn Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe 345 350 355			1171

ttc gct gct aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac 1219
 Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp
 360 365 370

ctg cgc ggt tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct 1267
 Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser
 375 380 385

gac ggc tcc ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca 1315
 Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro
 390 395 400 405

tcc aag cgg ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag 1363
 Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu
 410 415 420

ctg cta ggc acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa 1411
 Leu Leu Gly Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys
 425 430 435

cca acc acc ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc 1459
 Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile
 440 445 450

ttc cac gaa ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc 1507
 Phe His Glu Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg
 455 460 465

tac cca agc ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc 1555
 Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe
 470 475 480 485

ccc tcc cag atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc 1603
 Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg
 490 495 500

aac tac gcc cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg 1651
 Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu
 505 510 515

ctt gag gca gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat 1699
 Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His
 520 525 530

gtg agt act tgt ccc cat cta tta tcg acc tgc cct gtc tct ccc tgt 1747
 Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys
 535 540 545

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<210> 100

<211> 555

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

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Leu Ala Leu Ala Glu His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn	35	40	45
Glu Asp Ala Pro Thr Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala	50	55	60
Gly Leu Ser Leu Asn Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly	65	70	75
Thr Asp Ser Ser Pro Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro	85	90	95
Lys Leu Ser Ala His Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe	100	105	110
Ala Arg Ile Glu Ala Val Glu Ala Pro Ala Asp Glu Glu Ser Gln Arg	115	120	125
Leu Leu Ser His Thr Lys Arg Ala Phe Arg Arg Arg Gly Ala Ala Leu	130	135	140
Asn Ala Asp Gly Lys Ala Arg Leu Ser Thr Ile Asn Gln Arg Leu Ser	145	150	155
Ala Leu Ser Glu Gln Phe Gly Arg Asn Leu Leu Gln Asp Thr Arg Asp	165	170	175
Leu Ala Val Asn Phe Glu Glu Ser Glu Leu Ala Gly Phe Ser Glu Ala	180	185	190
Arg Ile Ser Ala Ala Ala Asp Tyr Ala Ala Ala Val Gly Thr Glu Gly	195	200	205
Tyr Val Val Pro Leu Glu Leu Pro Thr Val Gln Ser Glu Gln Ala Val	210	215	220
Leu Thr Glu Ser Ala Ser Arg Ala Lys Leu Tyr Glu Ala Ser Gln Lys	225	230	235
Arg Gly Ala Ser Leu Asn Lys Asp Val Leu Leu Glu Thr Val Arg Leu	245	250	255
Arg Ala Glu Arg Ala Thr Leu Leu Gly Tyr Asp Thr His Ala Asp Tyr	260	265	270
Val Ile Glu Glu Glu Thr Ala Asp Asp Val Ala Ala Val Arg Ala Leu	275	280	285
Leu Tyr Asp Leu Ala Pro Ala Ala Ser Ala Asn Ala Lys Ala Glu Tyr	290	295	300
Lys Leu Ser Ala Glu Glu Ala Glu Glu His Gly Gln Lys Val Gly Ala	305	310	315
Ala Asp Trp Ser Phe Trp Glu Ala Lys Val Arg Ala Arg Asp Tyr Ala	325	330	335

Leu Asp Glu Thr Glu Leu Arg Asn Tyr Phe Pro Leu Asn Gln Val Leu
340 345 350

Arg Asp Gly Val Phe Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val
355 360 365

Glu Pro Arg Pro Asp Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp
370 375 380

Glu Val Leu Asp Ser Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp
385 390 395 400

Tyr Tyr Gly Arg Pro Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe
405 410 415

Val Asp Gln Ser Glu Leu Leu Gly Thr Lys Pro Val Val Val Asn Val
420 425 430

Met Gly Ile Thr Lys Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp
435 440 445

Glu Val Thr Thr Ile Phe His Glu Phe Gly His Gly Leu His Gly Leu
450 455 460

Leu Ser Lys Val Arg Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg
465 470 475 480

Asp Tyr Val Glu Phe Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp
485 490 495

Pro Ala Val Val Arg Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile
500 505 510

Ile Pro Asp Ser Leu Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp
515 520 525

Arg Val Val Glu His Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys
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Pro Val Ser Pro Cys Pro Gln Arg Met Pro His
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<210> 101

<211> 1088

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1065)

<223> FRXA00877

<400> 101

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Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala Ser Arg Ala

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aag ctt tat gaa gcc tcc cag aag cgt ggc gcc agc ctg aac aag gac Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu Asn Lys Asp 35 40 45			144
gtg ctg ctc gaa acc gtg cgt ctg cgt gct gaa cgc gcc aca ctt tta Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala Thr Leu Leu 50 55 60			192
ggc tac gac acc cac gcc gat tac gtc atc gaa gaa gaa acc gcc gat Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu Thr Ala Asp 65 70 75 80			240
gac gtc gca gcc gtg cgc gcc ttg ctt tat gat ctc gcc cca gcc gcc Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala Pro Ala Ala 85 90 95			288
tct gcc aat gcg aaa gcc gaa tac aaa ctc tcc gca gaa gaa gca gaa Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu Glu Ala Glu 100 105 110			336
gaa cac ggc caa aaa gtc ggc gca gct gac tgg agc ttc tgg gaa gcc Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe Trp Glu Ala 115 120 125			384
aaa gtc cgc gcc cgc gac tac gcc ctg gac gaa acc gaa ctg cgc aac Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu Leu Arg Asn 130 135 140			432
tac ttc cca ttg aac caa gta ctc cgt gac ggc gtc ttc ttc gct gct Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe Phe Ala Ala 145 150 155 160			480
aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac ctg cgc ggt Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly 165 170 175			528
tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct gac ggc tcc Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser 180 185 190			576
ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca tcc aag cgg Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg 195 200 205			624
ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag ctg cta ggc Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly 210 215 220			672
acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa cca acc acc Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr 225 230 235 240			720
ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc ttc cac gaa Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu 245 250 255			768
ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc tac cca agc Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser 260 265 270			816

ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc ccc tcc cag 864
 Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln
 275 280 285
 atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc aac tac gcc 912
 Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala
 290 295 300
 cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg ctt gag gca 960
 Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala
 305 310 315 320
 gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat gtg agt act 1008
 Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr
 325 330 335
 tgt ccc cat cta tta tcg acc tgc cct gtc tct ccc tgt cca cag cgg 1056
 Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
 340 345 350
 atg ccg cac tagtcaatga cattgaccaa tta 1088
 Met Pro His
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 <211> 355
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 102
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 35 40 45
 Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala Thr Leu Leu
 50 55 60
 Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu Thr Ala Asp
 65 70 75 80
 Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala Pro Ala Ala
 85 90 95
 Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu Glu Ala Glu
 100 105 110
 Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe Trp Glu Ala
 115 120 125
 Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu Leu Arg Asn
 130 135 140
 Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe Phe Ala Ala
 145 150 155 160

Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly
 165 170 175
 Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser
 180 185 190
 Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg
 195 200 205
 Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly
 210 215 220
 Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr
 225 230 235 240
 Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu
 245 250 255
 Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser
 260 265 270
 Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln
 275 280 285
 Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala
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 Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala
 305 310 315 320
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<220>
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 <222> (101)..(2701)
 <223> RXN01014

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 Leu Thr Ser Thr Asn
 1 5
 ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt	211
Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser	
25 30 35	
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Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe	
40 45 50	
att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg	307
Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val	
55 60 65	
tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag	355
Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu	
70 75 80 85	
acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg	403
Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu	
90 95 100	
cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac	451
Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His	
105 110 115	
cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt	499
Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe	
120 125 130	
gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac	547
Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp	
135 140 145	
ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag	595
Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys	
150 155 160 165	
atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac	643
Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr	
170 175 180	
gat acc cac att tcc cga gtg gac tat ccc ctc tcc acc tac ctg att	691
Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu Ser Thr Tyr Leu Ile	
185 190 195	
gcg gtg tgc gcg ggt cgt tac cac gag gtg tgc gat gtc tgg aag ggt	739
Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys Asp Val Trp Lys Gly	
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acg ctc acc cac cat gca gaa aca cct gcc gat cag cca act gag ctg	787
Thr Leu Thr His His Ala Glu Thr Pro Ala Asp Gln Pro Thr Glu Leu	
215 220 225	
act gtt ccg ctt gct ctc tac tgc cgc agt tct ttg gct aaa gat ctt	835
Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser Leu Ala Lys Asp Leu	
230 235 240 245	
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Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln Gly Phe Asp Trp Tyr	
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His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly Lys Tyr Asp Gln Ile	
265 270 275	
ttc gtc cct gaa ttt aat gct ggc gcg atg gag aac gcc ggc gct gtc	979
Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu Asn Ala Gly Ala Val	
280 285 290	
acc atc cgc gat gag tac gtt ttt gca tcc aag gca acc cgt tac cgc	1027
Thr Ile Arg Asp Glu Tyr Val Phe Ala Ser Lys Ala Thr Arg Tyr Arg	
295 300 305	
tac gag cgc cgc gct gaa acc atc ctt cac gag ctc gct cac atg tgg	1075
Tyr Glu Arg Arg Ala Thr Ile Leu His Glu Leu Ala His Met Trp	
310 315 320 325	
ttc ggt gtg ctg gtg acc atg cag tgg tgg gat gat ctg tgg ctc aac	1123
Phe Gly Val Leu Val Thr Met Gln Trp Trp Asp Asp Leu Trp Leu Asn	
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Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile Ser Gln Ala Glu Glu Thr	
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Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn Val Glu Lys Ser Trp	
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Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His Pro Val Phe Ser Asp	
375 380 385	
gga tac gac att gag act gtc gac cag aac ttc gac ggc atc acc tac	1315
Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe Asp Gly Ile Thr Tyr	
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Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln Ala Tyr Val Gly Arg	
410 415 420	
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Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp Leu Lys Thr Thr Gly	
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atc aac acc ctc ggc gca aag ttc acc acc gac aac ggc aaa tac acc	1555
Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp Asn Gly Lys Tyr Thr	
470 475 480 485	
tcc ttc tcc gtc acc cag acc ggc gcc gcg ccg ggt gcc ggt gag ctg	1603
Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro Gly Ala Gly Glu Leu	
490 495 500	
cgg act cac cgc atc gcg gtg ggt ctt tat aag ctt gtc gac gga tcc	1651

Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys Leu Val Asp Gly Ser	
505 510 515	
ctc aac cgc tac gca cga gta gaa ctt gac tgc agt ggc gcg tcg aca	1699
Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys Ser Gly Ala Ser Thr	
520 525 530	
agc gtt gaa gag atc gtt gga ctt gag cag gct gac ttc gtg ctg gtc	1747
Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala Asp Phe Val Leu Val	
535 540 545	
aac gat gat gat ctg acg tat gcg ctg ctg gat ctg gat gat gat tca	1795
Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp Leu Asp Asp Asp Ser	
550 555 560 565	
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Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe Ser Asp Pro Met Pro	
570 575 580	
cgc acg ctg gtg tgg tcc gct gcg tgg gag atg act cgc gct ggt cag	1891
Arg Thr Leu Val Trp Ser Ala Ala Trp Glu Met Thr Arg Ala Gly Gln	
585 590 595	
atg aag gct cgt gat ttc atc gcg ctg gtt gct cgt ggc gct gct gcg	1939
Met Lys Ala Arg Asp Phe Ile Ala Leu Val Ala Arg Gly Ala Ala Ala	
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Glu Thr Glu Ile Ala Val Leu Glu Arg Ile Leu Ala Gln Ala Thr Ser	
615 620 625	
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Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp Ala Glu Ala Thr Gly Asn	
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gac ctg ctg gcc gat gct ttc ctt gag ggt gct cgc tcc gca gaa cca	2083
Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly Ala Arg Ser Ala Glu Pro	
650 655 660	
gac tcc gac act cag ttg gcg ttc att cag gct ctg gca aaa gca acg	2131
Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln Ala Leu Ala Lys Ala Thr	
665 670 675	
ctc aat gat gct gct gcc gat tac ttc cgc gac att ctt gcc ggc aac	2179
Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg Asp Ile Leu Ala Gly Asn	
680 685 690	
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Val Glu Gly Leu Thr Val Asp Pro Asp Leu Arg Trp Trp Ala Leu Thr	
695 700 705	
gcg ctt atc gcc cgt ggt gac atc gag gct gtc gaa gat gca atc gcc	2275
Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala Val Glu Asp Ala Ile Ala	
710 715 720 725	
gct gaa ctt tcc cgc gac aac tcc agt gcc tcc ttc ctc gca tca ctt	2323
Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala Ser Phe Leu Ala Ser Leu	
730 735 740	
cga gcc ggt gcc gct gtg aac act gaa gaa gtg aag gct gct gca tac	2371
Arg Ala Gly Ala Ala Val Asn Thr Glu Glu Val Lys Ala Ala Ala Tyr	

745	750	755	
aag cat gtc acg gca gtt gat agt ggc cta tcc aac ctg gag ctg cgc Lys His Val Thr Ala Val Asp Ser Gly Leu Ser Asn Leu Glu Leu Arg 760 765 770			2419
cac aag att gaa ggc ctc aca ttc act ggc tct tct gaa ctg ctg caa His Lys Ile Glu Gly Leu Thr Phe Thr Gly Ser Ser Glu Leu Leu Gln 775 780 785			2467
gcc tac aac gag cag tac ttc gaa atc ctt gat gat gtg tgg gcg aac Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu Asp Asp Val Trp Ala Asn 790 795 800 805			2515
ttc tcc ggc gaa atg gca cag cag atc gtc ctc gga ctg ttc cct tca Phe Ser Gly Glu Met Ala Gln Gln Ile Val Leu Gly Leu Phe Pro Ser 810 815 820			2563
tgg aac gtt tcc gaa gag ggt ctc aag cgt acc gac gag ttt ctt gat Trp Asn Val Ser Glu Glu Gly Leu Lys Arg Thr Asp Glu Phe Leu Asp 825 830 835			2611
ggc gaa cat gtc gca ggc atc aag cga att gtt tcc gaa tcc ctc gac Gly Glu His Val Ala Gly Ile Lys Arg Ile Val Ser Glu Ser Leu Asp 840 845 850			2659
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Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys 35 40 45			
Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val 50 55 60			
Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys 65 70 75 80			
Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro 85 90 95			
Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr 100 105 110			
Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr			

115	120	125
Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys		
130	135	140
Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr		
145	150	155
Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr		
	165	170
Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu		
	180	185
Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys		
	195	200
Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp		
	210	215
Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser		
	225	230
Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln		
	245	250
Gly Phe Asp Trp Tyr His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly		
	260	265
Lys Tyr Asp Gln Ile Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu		
	275	280
Asn Ala Gly Ala Val Thr Ile Arg Asp Glu Tyr Val Phe Ala Ser Lys		
	290	295
Ala Thr Arg Tyr Arg Tyr Glu Arg Arg Ala Glu Thr Ile Leu His Glu		
	305	310
Leu Ala His Met Trp Phe Gly Val Leu Val Thr Met Gln Trp Trp Asp		
	325	330
Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile Ser		
	340	345
Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn		
	355	360
Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His		
	370	375
Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe		
	385	390
Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln		
	405	410
Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His Phe		
	420	425
Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly Ala		
	435	440
		445

Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp
 450 455 460
 Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp
 465 470 475 480
 Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro
 485 490 495
 Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys
 500 505 510
 Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys
 515 520 525
 Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala
 530 535 540
 Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp
 545 550 555 560
 Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe
 565 570 575
 Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu Met
 580 585 590
 Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val Ala
 595 600 605
 Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile Leu
 610 615 620
 Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp Ala
 625 630 635 640
 Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly Ala
 645 650 655
 Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln Ala
 660 665 670
 Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg Asp
 675 680 685
 Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu Arg
 690 695 700
 Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala Val
 705 710 715 720
 Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala Ser
 725 730 735
 Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu Val
 740 745 750
 Lys Ala Ala Ala Tyr Lys His Val Thr Ala Val Asp Ser Gly Leu Ser
 755 760 765

Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly Ser
 770 775 780
 Ser Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu Asp
 785 790 795 800
 Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val Leu
 805 810 815
 Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg Thr
 820 825 830
 Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile Val
 835 840 845
 Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn Arg Ala Ala
 850 855 860
 Asp Ala Ala
 865

<210> 105
 <211> 1578
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1578)
 <223> FRXA01014

<400> 105
 gat gat ctg tgg ctc aac gag tcc ttc gcc act tgg tcc gcg gca att 48
 Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile
 1 5 10 15
 tct cag gct gag gaa act gaa tac aac act gca tgg gtg act ttc gcc 96
 Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala
 20 25 30
 aat gtg gag aag tcg tgg gcg tac cag cag gat cag ctg cct tcc acc 144
 Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr
 35 40 45
 cac ccg gtg ttc tct gac gga tac gac att gag act gtc gac cag aac 192
 His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn
 50 55 60
 ttc gac ggc atc acc tac gca aag ggc gcc tcg gtg ctc aag cag ctg 240
 Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65 70 75 80
 cag gca tac gtt ggc cgt gag gaa ttc ctg gca ggc gta cgc agg cac 288
 Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
 85 90 95
 ttt gcc aac cac gca tgg ggc aac gcc agc ttt gat gat ctg ctc ggc 336
 Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
 100 105 110

gcc ctc gag cag tcc tcc ggc cgc gac ctc tcc gac tgg gca aac cag	384
Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln	
115 120 125	
tgg ctc aag acc acc ggc atc aac acc ctc ggc gca aag ttc acc acc	432
Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr	
130 135 140	
gac aac ggc aaa tac acc tcc ttc tcc gtc acc cag acc ggc gcc gcg	480
Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala	
145 150 155 160	
ccg ggt gcc ggt gag ctg cgg act cac cgc atc gcg gtg ggt ctt tat	528
Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr	
165 170 175	
aag ctt gtc gac gga tcc ctc aac cgc tac gca cga gta gaa ctt gac	576
Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp	
180 185 190	
tgc agt ggc gcg tcg aca agc gtt gaa gag atc gtt gga ctt gag cag	624
Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln	
195 200 205	
gct gac ttc gtg ctg gtc aac gat gat gat ctg acg tat gcg ctg ctg	672
Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu	
210 215 220	
gat ctg gat gat gat tca cgc aat ttt gtc atc gac aat att gat aag	720
Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys	
225 230 235 240	
ttc agc gac cct atg cct cgc acg ctg gtg tgg tcc gct gcg tgg gag	768
Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu	
245 250 255	
atg act cgc gct ggt cag atg aag gct cgt gat ttc atc gcg ctg gtt	816
Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val	
260 265 270	
gct cgt ggc gct gct gcg gaa act gaa att gct gtg ctg gag cgc att	864
Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile	
275 280 285	
ctc gcg cag gct acc tct gcg ctg aag agc tac gcc gac cca gcg tgg	912
Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp	
290 295 300	
gca gaa gca act gga aat gac ctg ctg gcc gat gct ttc ctt gag ggt	960
Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly	
305 310 315 320	
gct cgc tcc gca gaa cca gac tcc gac act cag ttg gcg ttc att cag	1008
Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln	
325 330 335	
gct ctg gca aaa gca acg ctc aat gat gct gct gcc gat tac ttc cgc	1056
Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg	
340 345 350	
gac att ctt gcc ggc aac gtc gaa ggc ctg acc gtg gat cct gac ctg	1104

Asp Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu
 355 360 365
 cgt tgg tgg gca ctg act gcg ctt atc gcc cgt ggt gac atc gag gct 1152
 Arg Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala
 370 375 380
 gtc gaa gat gca atc gcc gct gaa ctt tcc cgc gac aac tcc agt gcc 1200
 Val Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala
 385 390 395 400
 tcc ttc ctc gca tca ctt cga gcc ggt gcc gct gtg aac act gaa gaa 1248
 Ser Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu
 405 410 415
 gtg aag gct gct gca tac aag cat gtc ccg gca gtt gat agt ggc cta 1296
 Val Lys Ala Ala Ala Tyr Lys His Val Pro Ala Val Asp Ser Gly Leu
 420 425 430
 tcc aac ctg gag ctg cgc cac aag att gaa ggc ctc aca ttc act ggc 1344
 Ser Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly
 435 440 445
 tct ttt gaa ctg ctg caa gcc tac aac gag cag tac ttc gaa atc ctt 1392
 Ser Phe Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu
 450 455 460
 gat gat gtg tgg gcg aac ttc tcc ggc gaa atg gca cag cag atc gtc 1440
 Asp Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val
 465 470 475 480
 ctc gga ctg ttc cct tca tgg aac gtt tcc gaa gag ggt ctc aag cgt 1488
 Leu Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg
 485 490 495
 acc gac gag ttt ctt gat ggc gaa cat gtc gca ggc atc aag cga att 1536
 Thr Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile
 500 505 510
 gtt tcc gaa tcc ctc gac cgc act gcc cgt gct ctg cgc aac 1578
 Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
 515 520 525

<210> 106

<211> 526

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 106

Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile
 1 5 10 15
 Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala
 20 25 30
 Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr
 35 40 45
 His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn
 50 55 60

Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65 70 75 80
 Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
 85 90 95
 Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
 100 105 110
 Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln
 115 120 125
 Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr
 130 135 140
 Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala
 145 150 155 160
 Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr
 165 170 175
 Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp
 180 185 190
 Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln
 195 200 205
 Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu
 210 215 220
 Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys
 225 230 235 240
 Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu
 245 250 255
 Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val
 260 265 270
 Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile
 275 280 285
 Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp
 290 295 300
 Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly
 305 310 315 320
 Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln
 325 330 335
 Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg
 340 345 350
 Asp Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu
 355 360 365
 Arg Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala
 370 375 380

Val Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala
 385 390 395 400

Ser Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu
 405 410 415

Val Lys Ala Ala Ala Tyr Lys His Val Pro Ala Val Asp Ser Gly Leu
 420 425 430

Ser Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly
 435 440 445

Ser Phe Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu
 450 455 460

Asp Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val
 465 470 475 480

Leu Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg
 485 490 495

Thr Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile
 500 505 510

Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
 515 520 525

<210> 107
 <211> 964
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(964)
 <223> FRXA01018

<400> 107
 tcttaaagtt ttctagcaat ccacactagg cgcgaactat cgtggtgtca ttgcgcacct 60

tctaagggta gcgccccctc aaatttcaag gagcattaaa ttg acg tcc act aat 115
 Leu Thr Ser Thr Asn
 1 5

ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt 211
 Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
 25 30 35

tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt 259
 Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
 40 45 50

att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg 307
 Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
 55 60 65

tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag	355
Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu	
70 75 80 85	
acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg	403
Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu	
90 95 100	
cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac	451
Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His	
105 110 115	
cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt	499
Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe	
120 125 130	
gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac	547
Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp	
135 140 145	
ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag	595
Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys	
150 155 160 165	
atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac	643
Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr	
170 175 180	
gat acc cac att tcc cga gtg gac tat ccc ctc tcc acc tac ctg att	691
Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu Ser Thr Tyr Leu Ile	
185 190 195	
gcg gtg tgc gcg ggt cgt tac cac gag gtg tgc gat gtc tgg aag ggt	739
Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys Asp Val Trp Lys Gly	
200 205 210	
acg ctc acc cac cat gca gaa aca cct gcc gat cag cca act gag ctg	787
Thr Leu Thr His His Ala Glu Thr Pro Ala Asp Gln Pro Thr Glu Leu	
215 220 225	
act gtt ccg ctt gct ctc tac tgc cgc agt tct ttg gct aaa gat ctt	835
Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser Leu Ala Lys Asp Leu	
230 235 240 245	
gat gcg gtg cgt ctg ttt acc gaa acg aag cag ggc ttt gat tgg tac	883
Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln Gly Phe Asp Trp Tyr	
250 255 260	
cac cgc aac ttc ggt gtg gcg tac cca ttc ggc aag tac gat cag atc	931
His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly Lys Tyr Asp Gln Ile	
265 270 275	
ttc gtc cct gaa ttt aat gct ggc gcg atg gag	964
Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu	
280 285	

<210> 108

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Leu Thr Ser Thr Asn Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg
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 Leu Leu Ser Val Glu Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly
 20 25 30
 Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys
 35 40 45
 Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val
 50 55 60
 Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys
 65 70 75 80
 Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro
 85 90 95
 Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr
 100 105 110
 Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr
 115 120 125
 Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys
 130 135 140
 Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr
 145 150 155 160
 Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr
 165 170 175
 Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu
 180 185 190
 Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys
 195 200 205
 Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp
 210 215 220
 Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser
 225 230 235 240
 Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln
 245 250 255
 Gly Phe Asp Trp Tyr His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly
 260 265 270
 Lys Tyr Asp Gln Ile Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
 275 280 285

<210> 109

<211> 1383
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1360)
 <223> RXA01147

<400> 109

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gggcccgcgc tgtttccaag aatttggtta cccttgttct atg cat gta act gac 115
                                     Met His Val Thr Asp
                                     1      5

gat ttc tta agt ttt att gcc cta agc cca agt tcc tat cac gcg gcc 163
Asp Phe Leu Ser Phe Ile Ala Leu Ser Pro Ser Ser Tyr His Ala Ala
      10      15      20

gcg gcg gtg gag cgc agg ttg ctc cat gag ggg ttc att cgt cag gaa 211
Ala Ala Val Glu Arg Arg Leu Leu His Glu Gly Phe Ile Arg Gln Glu
      25      30      35

gat acc gat gaa tgg gat gcc cgc cct ggt ggg cat gtg acg gtg cgt 259
Asp Thr Asp Glu Trp Asp Ala Arg Pro Gly Gly His Val Thr Val Arg
      40      45      50

ggg gga gca gta gtg gcg tgg tgg gtg cct gag gat gct tcg cca gat 307
Gly Gly Ala Val Val Ala Trp Trp Val Pro Glu Asp Ala Ser Pro Asp
      55      60      65

tcc ggg ttc cgc atc att ggg tca cat act gat tca ccg ggt ttc aag 355
Ser Gly Phe Arg Ile Ile Gly Ser His Thr Asp Ser Pro Gly Phe Lys
      70      75      80      85

tta aag ccc cgt ggg gat ctt tcc tca cac ggt tgg cag cag gcc ggc 403
Leu Lys Pro Arg Gly Asp Leu Ser Ser His Gly Trp Gln Gln Ala Gly
      90      95      100

gtc gag gtt tac ggc gga ccg atc ctg cca agc tgg ctg gat cgc gag 451
Val Glu Val Tyr Gly Gly Pro Ile Leu Pro Ser Trp Leu Asp Arg Glu
      105      110      115

ctg gcc tta gca ggc cgc att gtg ctt gcc gac ggg tcc gtc aag ctt 499
Leu Ala Leu Ala Gly Arg Ile Val Leu Ala Asp Gly Ser Val Lys Leu
      120      125      130

gtc aac acc ggc ccg att ctg cgc atc ccg cac gtg gct att cat ttg 547
Val Asn Thr Gly Pro Ile Leu Arg Ile Pro His Val Ala Ile His Leu
      135      140      145

gac cgt act gtt aat tcc caa ctc acc ctt aat cca cag cgt cac ctg 595
Asp Arg Thr Val Asn Ser Gln Leu Thr Leu Asn Pro Gln Arg His Leu
      150      155      160      165

cag cct gtg ttt gct gtt ggt gag ccc gac gta tca att ctg gat gtc 643
Gln Pro Val Phe Ala Val Gly Glu Pro Asp Val Ser Ile Leu Asp Val
      170      175      180

att gct ggt gct gcg gta gtg gat cct gca gat att gtc agc cat gat 691

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Ile Ala Gly	Ala Ala Val	Val Asp	Pro Ala Asp	Ile Val	Ser His Asp	
185			190		195	
ctg atc acg	gtg gct acc	caa gat	gct gaa gta	ttt ggc	gca cat ggg	739
Leu Ile Thr	Val Ala Thr	Gln Asp	Ala Glu Val	Phe Gly	Ala His Gly	
200		205		210		
gat ttc ttg	gcg tct ggt	cgc ctg	gat aac ctg	agc agc	gtg cat cca	787
Asp Phe Leu	Ala Ser Gly	Arg Leu	Asp Asn Leu	Ser Ser	Val His Pro	
215		220		225		
tcc atg act	gca ttg att	gcg gct	tcg caa tct	gac gat	act ggt tcg	835
Ser Met Thr	Ala Leu Ile	Ala Ala	Ser Gln Ser	Asp Asp	Thr Gly Ser	
230		235		240	245	
gat att ttg	gtt ctt gct	gca ttc	gat cat gaa	gaa gtg	gga agt aat	883
Asp Ile Leu	Val Leu Ala	Ala Phe	Asp His Glu	Glu Glu	Val Gly Ser	
	250		255		260	
tcc acc tcg	ggt gcc ggg	ggc ccc	ctg ttg gag	gat gtg	ctc aac cgt	931
Ser Thr Ser	Gly Ala Gly	Gly Pro	Leu Leu Glu	Asp Val	Leu Asn Arg	
	265		270		275	
act gct cgt	gcg ttg ggt	gca gat	gaa gat gag	cga cgc	cgg atg ttt	979
Thr Ala Arg	Ala Leu Gly	Ala Asp	Glu Asp Glu	Arg Arg	Arg Met Phe	
	280		285		290	
aac cgt tcc	acc atg gtc	tca gct	gac gcg gca	cac tcc	att cac ccc	1027
Asn Arg Ser	Thr Met Val	Ser Ala	Asp Ala Ala	His Ser	Ile His Pro	
	295		300		305	
aac ttc ccc	gag aag cat	gat caa	gct aat tac	ccc atc	att ggt aaa	1075
Asn Phe Pro	Glu Lys His	Asp Gln	Ala Asn Tyr	Pro Ile	Ile Gly Lys	
310		315		320	325	
ggt cct gta	ttg aag gtc	aac gcc	aac cag cgc	tac acc	tcc gat gca	1123
Gly Pro Val	Leu Lys Val	Asn Ala	Asn Gln Arg	Tyr Thr	Ser Asp Ala	
	330		335		340	
gtc act tca	ggc atg tgg	atc agg	gca tgt cag	att gcc	ggt gtg cca	1171
Val Thr Ser	Gly Met Trp	Ile Arg	Ala Cys Gln	Ile Ala	Gly Val Pro	
	345		350		355	
cac cag gtg	ttt gcc ggc	aac aac	gat gtg ccg	tgt ggt	tcc acc atc	1219
His Gln Val	Phe Ala Gly	Asn Asn	Asp Val Pro	Cys Gly	Ser Thr Ile	
	360		365		370	
ggc ccg atc	agt gcg act	cgc ctg	ggt atc gat	tct gtc	gat gtc ggt	1267
Gly Pro Ile	Ser Ala Thr	Arg Leu	Gly Ile Asp	Ser Val	Asp Val Gly	
	375		380		385	
att cca ttg	ctg tcc atg	cac tcc	gca cgc gaa	atg gcc	gga gtg aag	1315
Ile Pro Leu	Leu Ser Met	His Ser	Ala Arg Glu	Met Ala	Gly Val Lys	
390		395		400	405	
gat ctg atg	tgg ttt gaa	caa gcc	ctg gaa gcc	tat ctg	gta aat	1360
Asp Leu Met	Trp Phe Glu	Gln Ala	Leu Glu Ala	Tyr Leu	Val Asn	
	410		415		420	
taacgccgag	ttcaatcaag	aca				1383

<210> 110
 <211> 420
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 110

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Met His Val Thr Asp Asp Phe Leu Ser Phe Ile Ala Leu Ser Pro Ser
 1           5           10           15

Ser Tyr His Ala Ala Ala Val Glu Arg Arg Leu Leu His Glu Gly
          20           25           30

Phe Ile Arg Gln Glu Asp Thr Asp Glu Trp Asp Ala Arg Pro Gly Gly
          35           40           45

His Val Thr Val Arg Gly Gly Ala Val Val Ala Trp Trp Val Pro Glu
          50           55           60

Asp Ala Ser Pro Asp Ser Gly Phe Arg Ile Ile Gly Ser His Thr Asp
          65           70           75           80

Ser Pro Gly Phe Lys Leu Lys Pro Arg Gly Asp Leu Ser Ser His Gly
          85           90           95

Trp Gln Gln Ala Gly Val Glu Val Tyr Gly Gly Pro Ile Leu Pro Ser
          100          105          110

Trp Leu Asp Arg Glu Leu Ala Leu Ala Gly Arg Ile Val Leu Ala Asp
          115          120          125

Gly Ser Val Lys Leu Val Asn Thr Gly Pro Ile Leu Arg Ile Pro His
          130          135          140

Val Ala Ile His Leu Asp Arg Thr Val Asn Ser Gln Leu Thr Leu Asn
          145          150          155          160

Pro Gln Arg His Leu Gln Pro Val Phe Ala Val Gly Glu Pro Asp Val
          165          170          175

Ser Ile Leu Asp Val Ile Ala Gly Ala Ala Val Val Asp Pro Ala Asp
          180          185          190

Ile Val Ser His Asp Leu Ile Thr Val Ala Thr Gln Asp Ala Glu Val
          195          200          205

Phe Gly Ala His Gly Asp Phe Leu Ala Ser Gly Arg Leu Asp Asn Leu
          210          215          220

Ser Ser Val His Pro Ser Met Thr Ala Leu Ile Ala Ala Ser Gln Ser
          225          230          235          240

Asp Asp Thr Gly Ser Asp Ile Leu Val Leu Ala Ala Phe Asp His Glu
          245          250          255

Glu Val Gly Ser Asn Ser Thr Ser Gly Ala Gly Gly Pro Leu Leu Glu
          260          265          270

Asp Val Leu Asn Arg Thr Ala Arg Ala Leu Gly Ala Asp Glu Asp Glu
          275          280          285
  
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Arg Arg Arg Met Phe Asn Arg Ser Thr Met Val Ser Ala Asp Ala Ala
 290 295 300

His Ser Ile His Pro Asn Phe Pro Glu Lys His Asp Gln Ala Asn Tyr
 305 310 315 320

Pro Ile Ile Gly Lys Gly Pro Val Leu Lys Val Asn Ala Asn Gln Arg
 325 330 335

Tyr Thr Ser Asp Ala Val Thr Ser Gly Met Trp Ile Arg Ala Cys Gln
 340 345 350

Ile Ala Gly Val Pro His Gln Val Phe Ala Gly Asn Asn Asp Val Pro
 355 360 365

Cys Gly Ser Thr Ile Gly Pro Ile Ser Ala Thr Arg Leu Gly Ile Asp
 370 375 380

Ser Val Asp Val Gly Ile Pro Leu Leu Ser Met His Ser Ala Arg Glu
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Met Ala Gly Val Lys Asp Leu Met Trp Phe Glu Gln Ala Leu Glu Ala
 405 410 415

Tyr Leu Val Asn
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<210> 111
 <211> 1260
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1237)
 <223> RXA01161

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tttgatcgca cacctgccta ggctactagg gttggagact atg agt gat cct tca 115
 Met Ser Asp Pro Ser
 1 5

aca aac aat ttc ccc aca tcg gta tat gca cag cgt ctt gcg gat gca 163
 Thr Asn Asn Phe Pro Thr Ser Val Tyr Ala Gln Arg Leu Ala Asp Ala
 10 15 20

caa gaa ggc gca cgc aag gct ggc ttg aac ggt ttg atc atc ggt aca 211
 Gln Glu Gly Ala Arg Lys Ala Gly Leu Asn Gly Leu Ile Ile Gly Thr
 25 30 35

ggc gca gaa ctt gcg tat cta acc ggc agc tgg atc tcc acc cat gag 259
 Gly Ala Glu Leu Ala Tyr Leu Thr Gly Ser Trp Ile Ser Thr His Glu
 40 45 50

cgt cta acc gct ttg gtg atc ccc agc gaa gga acc gca acc att gtt 307
 Arg Leu Thr Ala Leu Val Ile Pro Ser Glu Gly Thr Ala Thr Ile Val
 55 60 65

ctt ccc gct gta gac cgc gga gac tta gca ctg tct gct att cca gga	355
Leu Pro Ala Val Asp Arg Gly Asp Leu Ala Leu Ser Ala Ile Pro Gly	
70 75 80 85	
cta gac atc aat gtg gcc gga tgg gtt gat ggc gat aat gcc cat gag	403
Leu Asp Ile Asn Val Ala Gly Trp Val Asp Gly Asp Asn Ala His Glu	
90 95 100	
ttg gcc gta gat gct ctc ggt gtt tca gag ttc gaa gca ttg ggt att	451
Leu Ala Val Asp Ala Leu Gly Val Ser Glu Phe Glu Ala Leu Gly Ile	
105 110 115	
ggt tcc tcc atc acg gca gat cac ctg att cct atc cag aac ctg gtg	499
Gly Ser Ser Ile Thr Ala Asp His Leu Ile Pro Ile Gln Asn Leu Val	
120 125 130	
ggc tcc acc tgc cgc atg gag ttg gca gtt caa gtg ctg aaa gaa ttg	547
Gly Ser Thr Cys Arg Met Glu Leu Ala Val Gln Val Leu Lys Glu Leu	
135 140 145	
ttt gtc tct aaa gac gaa gca gag atc gag cag ctt cgc ggc gca ggt	595
Phe Val Ser Lys Asp Glu Ala Glu Ile Glu Gln Leu Arg Gly Ala Gly	
150 155 160 165	
gca gcc att gac cgt gtc cac gcc aaa gtc ccg gag ctt ctt caa gac	643
Ala Ala Ile Asp Arg Val His Ala Lys Val Pro Glu Leu Leu Gln Asp	
170 175 180	
gga cgc acc gaa gca gag gtt gca gca cag ctc aac gat ctc atc ttg	691
Gly Arg Thr Glu Ala Glu Val Ala Ala Gln Leu Asn Asp Leu Ile Leu	
185 190 195	
gaa gag cac tct gag gtg gac ttc gtg att gtg gga tcc gct gaa aac	739
Glu Glu His Ser Glu Val Asp Phe Val Ile Val Gly Ser Ala Glu Asn	
200 205 210	
ggc gcg aac cct cac cac ggt ttc tct gac cga gtc ctc cgc aat ggc	787
Gly Ala Asn Pro His His Gly Phe Ser Asp Arg Val Leu Arg Asn Gly	
215 220 225	
gac atc gtg gtg gtt gat ata gga ggc acc ttc ggc cct ggt tac cac	835
Asp Ile Val Val Val Asp Ile Gly Gly Thr Phe Gly Pro Gly Tyr His	
230 235 240 245	
tct gac tgc aca cgc acc tac att gtg ggc gga aac cct gac gat gcg	883
Ser Asp Cys Thr Arg Thr Tyr Ile Val Gly Gly Asn Pro Asp Asp Ala	
250 255 260	
gat cca gag ttc gct aag ttc tac caa gtg ctc tac gaa gca cag ctc	931
Asp Pro Glu Phe Ala Lys Phe Tyr Gln Val Leu Tyr Glu Ala Gln Leu	
265 270 275	
gca gcc gtt gcg cat gtt cgc cct ggc gtt act gca gaa tca gtg gac	979
Ala Ala Val Ala His Val Arg Pro Gly Val Thr Ala Glu Ser Val Asp	
280 285 290	
gct gtt gct cgc gat cac att gct gcg gct gga tac ggc gaa tac ttc	1027
Ala Val Ala Arg Asp His Ile Ala Ala Ala Gly Tyr Gly Glu Tyr Phe	
295 300 305	
att cac cgc aca gga cac ggc att ggt cta tcc acc cat gag gag cca	1075

Ile His Arg Thr Gly His Gly Ile Gly Leu Ser Thr His Glu Glu Pro
 310 315 320 325
 ttc atc atg gcg ggt aac tca ctc gtg ttg gaa gcc gga atg gcc ttt 1123
 Phe Ile Met Ala Gly Asn Ser Leu Val Leu Glu Ala Gly Met Ala Phe
 330 335 340
 tcc att gag cct ggc atc tac att gaa gga atc cac gga gcg cgc atc 1171
 Ser Ile Glu Pro Gly Ile Tyr Ile Glu Gly Ile His Gly Ala Arg Ile
 345 350 355
 gaa gac atc gtt gtg gtg aat gaa gac ggt tgt gaa acc ctc aac aac 1219
 Glu Asp Ile Val Val Val Asn Glu Asp Gly Cys Glu Thr Leu Asn Asn
 360 365 370
 cag ccc aag gaa ctg cgt tgagcattct tctcctaggc gga 1260
 Gln Pro Lys Glu Leu Arg
 375

<210> 112
 <211> 379
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 112
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 Arg Leu Ala Asp Ala Gln Glu Gly Ala Arg Lys Ala Gly Leu Asn Gly
 20 25 30
 Leu Ile Ile Gly Thr Gly Ala Glu Leu Ala Tyr Leu Thr Gly Ser Trp
 35 40 45
 Ile Ser Thr His Glu Arg Leu Thr Ala Leu Val Ile Pro Ser Glu Gly
 50 55 60
 Thr Ala Thr Ile Val Leu Pro Ala Val Asp Arg Gly Asp Leu Ala Leu
 65 70 75 80
 Ser Ala Ile Pro Gly Leu Asp Ile Asn Val Ala Gly Trp Val Asp Gly
 85 90 95
 Asp Asn Ala His Glu Leu Ala Val Asp Ala Leu Gly Val Ser Glu Phe
 100 105 110
 Glu Ala Leu Gly Ile Gly Ser Ser Ile Thr Ala Asp His Leu Ile Pro
 115 120 125
 Ile Gln Asn Leu Val Gly Ser Thr Cys Arg Met Glu Leu Ala Val Gln
 130 135 140
 Val Leu Lys Glu Leu Phe Val Ser Lys Asp Glu Ala Glu Ile Glu Gln
 145 150 155 160
 Leu Arg Gly Ala Gly Ala Ala Ile Asp Arg Val His Ala Lys Val Pro
 165 170 175
 Glu Leu Leu Gln Asp Gly Arg Thr Glu Ala Glu Val Ala Ala Gln Leu
 180 185 190

Asn Asp Leu Ile Leu Glu Glu His Ser Glu Val Asp Phe Val Ile Val
 195 200 205
 Gly Ser Ala Glu Asn Gly Ala Asn Pro His His Gly Phe Ser Asp Arg
 210 215 220
 Val Leu Arg Asn Gly Asp Ile Val Val Val Asp Ile Gly Gly Thr Phe
 225 230 235 240
 Gly Pro Gly Tyr His Ser Asp Cys Thr Arg Thr Tyr Ile Val Gly Gly
 245 250 255
 Asn Pro Asp Asp Ala Asp Pro Glu Phe Ala Lys Phe Tyr Gln Val Leu
 260 265 270
 Tyr Glu Ala Gln Leu Ala Ala Val Ala His Val Arg Pro Gly Val Thr
 275 280 285
 Ala Glu Ser Val Asp Ala Val Ala Arg Asp His Ile Ala Ala Ala Gly
 290 295 300
 Tyr Gly Glu Tyr Phe Ile His Arg Thr Gly His Gly Ile Gly Leu Ser
 305 310 315 320
 Thr His Glu Glu Pro Phe Ile Met Ala Gly Asn Ser Leu Val Leu Glu
 325 330 335
 Ala Gly Met Ala Phe Ser Ile Glu Pro Gly Ile Tyr Ile Glu Gly Ile
 340 345 350
 His Gly Ala Arg Ile Glu Asp Ile Val Val Val Asn Glu Asp Gly Cys
 355 360 365
 Glu Thr Leu Asn Asn Gln Pro Lys Glu Leu Arg
 370 375

<210> 113
 <211> 980
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(957)
 <223> RXN01181

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 tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac 96
 Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30
 ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt 144
 Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45

ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt	192
Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg	
50 55 60	
ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct	240
Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala	
65 70 75 80	
ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag	288
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys	
85 90 95	
cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca	336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala	
100 105 110	
tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc	384
Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile	
115 120 125	
aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac	432
Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp	
130 135 140	
gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc	480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser	
145 150 155 160	
gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc	528
Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala	
165 170 175	
att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca	576
Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala	
180 185 190	
acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt	624
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly	
195 200 205	
gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc	672
Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg	
210 215 220	
gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat	720
Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp	
225 230 235 240	
gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc	768
Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser	
245 250 255	
cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt	816
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val	
260 265 270	
ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac	864
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr	
275 280 285	
aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa	912

Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300

cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc 957
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

taaacgctag ttaaagatca gga 980

<210> 114

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
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Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45

Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
 50 55 60

Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65 70 75 80

Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
 85 90 95

Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
 100 105 110

Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
 115 120 125

Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140

Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160

Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175

Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190

Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205

Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220

Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240

Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
 245 250 255

Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
 260 265 270

Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
 275 280 285

Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
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Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

<210> 115

<211> 980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA01181

<400> 115

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tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac	96
Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His	
20 25 30	
ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt	144
Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly	
35 40 45	
ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt	192
Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg	
50 55 60	
ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct	240
Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala	
65 70 75 80	
ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag	288
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys	
85 90 95	
cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca	336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala	
100 105 110	
tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc	384
Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile	
115 120 125	
aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac	432
Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp	

130	135	140	
gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc			480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser			
145	150	155	160
gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc			528
Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala			
165	170	175	
att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca			576
Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala			
180	185	190	
acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt			624
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly			
195	200	205	
gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc			672
Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg			
210	215	220	
gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat			720
Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp			
225	230	235	240
gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc			768
Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser			
245	250	255	
cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt			816
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val			
260	265	270	
ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac			864
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr			
275	280	285	
aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa			912
Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln			
290	295	300	
cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc			957
Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser			
305	310	315	
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<210> 116

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

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Tyr	Pro	Glu	Ser	Tyr	Ser	Val	Ile	Ala	Ser	Asn	Glu	Ala	Ser	Lys	His
			20					25					30		

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45
 Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
 50 55 60
 Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65 70 75 80
 Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
 85 90 95
 Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
 100 105 110
 Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
 115 120 125
 Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140
 Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160
 Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175
 Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190
 Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205
 Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220
 Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240
 Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
 245 250 255
 Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
 260 265 270
 Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
 275 280 285
 Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

<210> 117

<211> 2127

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2104)

<223> RXN01277

<400> 117

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                                         Met Thr Asp Tyr Thr
                                         1       5

ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa 163
Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
          10              15              20

tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
          25              30              35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
          40              45              50

tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
          55              60              65

cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa 355
Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
          70              75              80              85

agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg 403
Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
          90              95              100

gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg 451
Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
          105              110              115

ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat 499
Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
          120              125              130

gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat 547
Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
          135              140              145

gat tcg ccg ttt gaa ttg aag gag gcg aag tcc gat gtc acg tgg gtt 595
Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser Asp Val Thr Trp Val
          150              155              160              165

gat ctg gat acg ttg ctg gtg ggc acg gat acc ggc gag ggg tca ctg 643
Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr Gly Glu Gly Ser Leu
          170              175              180

acg gat tct ggg tac ccg gcg ccg gtg ctc acg tgg aag cgt ggg act 691
Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr Trp Lys Arg Gly Thr
          185              190              195

ccg ctt gag cag gcg gag ttg ttc ttt gag ggg tcg cgt cag gat gtg 739
Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly Ser Arg Gln Asp Val

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200	205	210	
gcg act cat gcg tgg cgg gat tca aca cct ggt ttt gag cgg acg ttt Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly Phe Glu Arg Thr Phe 215 220 225			787
gtg tca agg tcg ttg gat ttc tat aat tcg gag acg tcg ctg gaa acc Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu Thr Ser Leu Glu Thr 230 235 240 245			835
gag ggt ggc ctg gtc aag ctt gat gtg ccg acc gat tgc gat gtc att Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr Asp Cys Asp Val Ile 250 255 260			883
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att cca gca ggt ggc ttg gga gtg ctg ctg tta aag gag ttc ctt gag Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu Lys Glu Phe Leu Glu 280 285 290			979
ggc ggg cgc gat ttt cag cct gtg ttt acg cct act gag tcg acg tcg Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro Thr Glu Ser Thr Ser 295 300 305			1027
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aat aat gtc tcc aca gaa atc gtc aca gtg ccg ctc aat gat ccg aca Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro Leu Asn Asp Pro Thr 330 335 340			1123
acg gag cat gaa cac att gac ctc cca gag cat gtc acc gcg cat gtg Thr Glu His Glu His Ile Asp Leu Pro Glu His Val Thr Ala His Val 345 350 355			1171
gtt gct acc tcc ccg ttg gat ggc gat gaa att tgg gtg cag gca gcg Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile Trp Val Gln Ala Ala 360 365 370			1219
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ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln 390 395 400 405			1315
gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro 410 415 420			1363
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cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro 440 445 450			1459

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aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca 1555
 Asn Leu Arg Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala
 470 475 480 485

acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc 1603
 Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu
 490 495 500

gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att 1651
 Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile
 505 510 515

cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag 1699
 Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln
 520 525 530

tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat 1747
 Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp
 535 540 545

atg ttg cgc tat cac acc tgg tca gcg ggt gct tcg tgg atg gcg gag 1795
 Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala Ser Trp Met Ala Glu
 550 555 560 565

tac ggc aac cct gac gat ccg gag gaa ccg gcg gtg att gag cag tac 1843
 Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala Val Ile Glu Gln Tyr
 570 575 580

tcg ccg gtg cag gcg gtg gtg ggc gtc gag aag cga att tat cca ccc 1891
 Ser Pro Val Gln Ala Val Val Gly Val Glu Lys Arg Ile Tyr Pro Pro
 585 590 595

gca ttg gtg acg acc tca acc ccg gac gac cgc gtc cac ccc gcg cac 1939
 Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg Val His Pro Ala His
 600 605 610

gcg cgc ctt ttt gct caa gct ttg ctt gat gcg ggc cag gcc gtg gat 1987
 Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala Gly Gln Ala Val Asp
 615 620 625

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 Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly Ala Ala Asp Asn Lys
 630 635 640 645

cag acc gcg ttt gtg gaa tcg ctg atc tac acc tgg atc gag aag act 2083
 Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr Trp Ile Glu Lys Thr
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ttg gat cag cag ggt agc att taataacctat gattatgcga agg 2127
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 665

<210> 118
 <211> 668
 <212> PRT

<213> Corynebacterium glutamicum

<400> 118

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Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
          35           40           45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
 50           55           60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
 65           70           75           80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
          85           90           95

Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
          100          105          110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
          115          120          125

Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
          130          135          140

Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
          145          150          155          160

Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
          165          170          175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
          180          185          190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
          195          200          205

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
          210          215          220

Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
          225          230          235          240

Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
          245          250          255

Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
          260          265          270

Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
          275          280          285

Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
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Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu

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Val Leu Thr Leu	Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro					
	325			330		335
Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His						
	340			345		350
Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile						
	355			360		365
Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala						
	370			375		380
Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe						
	385			390		395
Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp						
	405			410		415
Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro						
	420			425		430
Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr						
	435			440		445
Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr						
	450			455		460
Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu						
	465			470		475
Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp						
	485			490		495
His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro						
	500			505		510
Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser						
	515			520		525
Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln						
	530			535		540
Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala						
	545			550		555
Ser Trp Met Ala Glu Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala						
	565			570		575
Val Ile Glu Gln Tyr Ser Pro Val Gln Ala Val Val Gly Val Glu Lys						
	580			585		590
Arg Ile Tyr Pro Pro Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg						
	595			600		605
Val His Pro Ala His Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala						
	610			615		620
Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly						
	625			630		635
						640

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Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile
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<210> 119

<211> 1812

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1789)

<223> FRXA01277

<400> 119

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 Met Thr Asp Tyr Thr
 1 5

ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa 163
 Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
 10 15 20

tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
 Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
 25 30 35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
 Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
 40 45 50

tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
 Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
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cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa 355
 Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
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agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg 403
 Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
 90 95 100

gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg 451
 Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
 105 110 115

ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat 499
 Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
 120 125 130

gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat 547
 Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
 135 140 145

gat tcg ccg ttt gaa ttg aag gag gcg aag tcc gat gtc acg tgg gtt	595
Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser Asp Val Thr Trp Val	
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Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr Gly Glu Gly Ser Leu	
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Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr Trp Lys Arg Gly Thr	
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Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly Ser Arg Gln Asp Val	
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Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly Phe Glu Arg Thr Phe	
215 220 225	
gtg tca agg tcg ttg gat ttc tat aat tcg gag acg tcg ctg gaa acc	835
Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu Thr Ser Leu Glu Thr	
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gag ggt ggc ctg gtc aag ctt gat gtg ccg acc gat tgc gat gtc att	883
Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr Asp Cys Asp Val Ile	
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Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg Thr Asp Phe Ala Gly	
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Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu Lys Glu Phe Leu Glu	
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Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro Thr Glu Ser Thr Ser	
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Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu Val Leu Thr Leu Leu	
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330 335 340	
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Thr Glu His Glu His Ile Asp Leu Pro Glu His Val Thr Ala His Val	
345 350 355	
gtt gct acc tcc ccg ttg gat ggc gat gaa att tgg gtg cag gca gcg	1219
Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile Trp Val Gln Ala Ala	
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agt ttc acc gaa gcg cca acg ttg ctg cgt gcg gag ctg cct ggt gcg	1267
Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala Glu Leu Pro Gly Ala	
375 380 385	
ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag	1315

Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln
 390 395 400 405
 gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg 1363
 Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro
 410 415 420
 tac ttt att aca gga gcc ttc gag gag gaa cca caa aac acc ctg gtc 1411
 Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val
 425 430 435
 cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg 1459
 His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro
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 Asn Leu Arg Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala
 470 475 480 485
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 Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu
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 Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile
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 Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln
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 Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp
 535 540 545
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<212> PRT

<213> Corynebacterium glutamicum

<400> 120

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Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
 35 40 45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
 50 55 60
 Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
 65 70 75 80
 Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
 85 90 95
 Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
 100 105 110
 Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
 115 120 125
 Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
 130 135 140
 Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
 145 150 155 160
 Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
 165 170 175
 Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
 180 185 190
 Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
 195 200 205
 Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
 210 215 220
 Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
 225 230 235 240
 Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
 245 250 255
 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
 260 265 270
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
 275 280 285
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
 290 295 300
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
 305 310 315 320
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
 325 330 335
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
 340 345 350
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala

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                                         Met Ala Lys Asn Ala
                                         1           5

tac agc aca aca gca cca acc aag gtg tcc aag gat gcc act ctt cca 163
Tyr Ser Thr Thr Ala Pro Thr Lys Val Ser Lys Asp Ala Thr Leu Pro
              10              15              20

gtt cgt gga acg gtc gct gaa ctc aag ctc gaa aaq aaq ttg cca aaq 211

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Val Arg Gly Thr Val Ala Glu Leu Lys Leu Glu Lys Lys Leu Pro Lys
 25 30 35

aag att gat gcc atc atc gtc gcg att ttt gaa ggc gaa gat tcc atc 259
 Lys Ile Asp Ala Ile Ile Val Ala Ile Phe Glu Gly Glu Asp Ser Ile
 40 45 50

gaa ctc gcc ggc ggc gaa atc ctc gat ttc atc ttc agt acc gag cag 307
 Glu Leu Ala Gly Gly Glu Ile Leu Asp Phe Ile Phe Ser Thr Glu Gln
 55 60 65

cag gcc gac atc ctc act cag ctc gaa gct gtc ggc gca aag gcc acc 355
 Gln Ala Asp Ile Leu Thr Gln Leu Glu Ala Val Gly Ala Lys Ala Thr
 70 75 80 85

gca aac agc atc acc cgc gtc cca ggc acc gac gtt gcg cct gtc att 403
 Ala Asn Ser Ile Thr Arg Val Pro Gly Thr Asp Val Ala Pro Val Ile
 90 95 100

gcg gtt ggt ttg ggc aag gct gat ttg ctt gac gac gag acc ctc cgc 451
 Ala Val Gly Leu Gly Lys Ala Asp Leu Leu Asp Asp Glu Thr Leu Arg
 105 110 115

cgc gct tcc ggc acg gcg gcc cgc tcc ctc ggt ggt ttt gaa aat gtc 499
 Arg Ala Ser Gly Thr Ala Ala Arg Ser Leu Gly Gly Phe Glu Asn Val
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<210> 122

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

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Lys Lys Leu Pro Lys Lys Ile Asp Ala Ile Ile Val Ala Ile Phe Glu
 35 40 45

Gly Glu Asp Ser Ile Glu Leu Ala Gly Gly Glu Ile Leu Asp Phe Ile
 50 55 60

Phe Ser Thr Glu Gln Gln Ala Asp Ile Leu Thr Gln Leu Glu Ala Val
 65 70 75 80

Gly Ala Lys Ala Thr Ala Asn Ser Ile Thr Arg Val Pro Gly Thr Asp
 85 90 95

Val Ala Pro Val Ile Ala Val Gly Leu Gly Lys Ala Asp Leu Leu Asp
 100 105 110

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 115 120 125

Gly Phe Glu Asn Val Ala Thr Thr Ile Gly Asp Leu Gly Leu
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 <223> RXA02048

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 Met Arg Arg Leu Arg
 1 5
 tcc acc ccg gtc cct ggt aca cgc gat tcc tac aca gga att gat ttc 163
 Ser Thr Pro Val Pro Gly Thr Arg Asp Ser Tyr Thr Gly Ile Asp Phe
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 aac tta ggc ttc cac atc cga cgc tac gag ctt gat ctc acc tac cgc 211
 Asn Leu Gly Phe His Ile Arg Arg Tyr Glu Leu Asp Leu Thr Tyr Arg
 25 30 35
 gta gca ccc aac ctg ctc atg ggc acc gca acg ctg cac atg gat aat 259
 Val Ala Pro Asn Leu Leu Met Gly Thr Ala Thr Leu His Met Asp Asn
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 Tyr Arg Ala Leu Asp Ala Leu Thr Leu Asp Leu Gly Gly Ser Leu Arg
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 Val Glu Lys Val Thr Ala Lys Gly Thr Ala Gly Thr His Ile Gln Val
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 Ala Arg Phe Arg His Ala Gly Arg Lys Leu Arg Ile Thr Phe Arg Asn
 90 95 100
 caa atc ccg gtt gac cag gaa ttt tca ctc acc atc cgc tac cgc ggc 451
 Gln Ile Pro Val Asp Gln Glu Phe Ser Leu Thr Ile Arg Tyr Arg Gly
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 aac ccg cgc ccc ctg cgc agc gaa tgg ggc atg atc ggc tgg gaa gag 499
 Asn Pro Arg Pro Leu Arg Ser Glu Trp Gly Met Ile Gly Trp Glu Glu
 120 125 130
 ctc gac aac ggc gcc ctc gtc gcc gcc cag cca aac ggc gcg ccg agc 547
 Leu Asp Asn Gly Ala Leu Val Ala Ala Gln Pro Asn Gly Ala Pro Ser
 135 140 145
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 Trp Phe Pro Cys Asp Asp Thr Pro Asp Glu Lys Ala Leu Phe Asp Val
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tat gtg cct gtg ggg gat gcg gcc ttg cgg gct cgg att ttg gag gac Tyr Val Pro Val Gly Asp Ala Ala Leu Arg Ala Arg Ile Leu Glu Asp 230 235 240 245	835
ttt gcc aaa caa gtc gac atg tta gac gcc tac gaa aaa ctc ttc ggc Phe Ala Lys Gln Val Asp Met Leu Asp Ala Tyr Glu Lys Leu Phe Gly 250 255 260	883
ccc tac cca ttc cgc agc tac cgc gta gtc atc acc gaa gac gaa ctc Pro Tyr Pro Phe Arg Ser Tyr Arg Val Val Ile Thr Glu Asp Glu Leu 265 270 275	931
gaa atc cca ctc gaa gcc caa ggc ctc tcc agc ttc gga gcc aac cac Glu Ile Pro Leu Glu Ala Gln Gly Leu Ser Ser Phe Gly Ala Asn His 280 285 290	979
gcc acc ggc gaa gga acc tgg gaa cga ctc atc gcc cac gaa ctc tcc Ala Thr Gly Glu Gly Thr Trp Glu Arg Leu Ile Ala His Glu Leu Ser 295 300 305	1027
cac cag tgg ttt ggc aac tca ctc ggc ctc gcc caa tgg aac gac atc His Gln Trp Phe Gly Asn Ser Leu Gly Leu Ala Gln Trp Asn Asp Ile 310 315 320 325	1075
tgg ctc aac gaa ggc ttc gcc tgt tac gcg gaa tgg ctc tgg ttt gag Trp Leu Asn Glu Gly Phe Ala Cys Tyr Ala Glu Trp Leu Trp Phe Glu 330 335 340	1123
gca gct gga gtt aag tcg gct gcg gaa agt gcg ttg gaa ttc tat cga Ala Ala Gly Val Lys Ser Ala Ala Glu Ser Ala Leu Glu Phe Tyr Arg 345 350 355	1171
ggc ctg gag gcg ctg ccg aag gat att ttg ctg gcc aac ccc ggc gcg Gly Leu Glu Ala Leu Pro Lys Asp Ile Leu Leu Ala Asn Pro Gly Ala 360 365 370	1219
aag gat atg ttc gac gac cgc gtc tac aag cgc ggc gct ctg act gtc Lys Asp Met Phe Asp Asp Arg Val Tyr Lys Arg Gly Ala Leu Thr Val 375 380 385	1267
cat gca ttg cgg gaa ttg ctt ggc gat gat gca ttc ttc aaa gct gtg His Ala Leu Arg Glu Leu Leu Gly Asp Asp Ala Phe Phe Lys Ala Val 390 395 400 405	1315

cgc tcc tac gtt gcc gaa ggc cga cac gga ctc gtt gaa ccc cgc gac 1363
 Arg Ser Tyr Val Ala Glu Gly Arg His Gly Leu Val Glu Pro Arg Asp
 410 415 420
 ctg aaa cga cac ctc tac gca gtc tcc aca gac cac gca gct tta gat 1411
 Leu Lys Arg His Leu Tyr Ala Val Ser Thr Asp His Ala Ala Leu Asp
 425 430 435
 gca gtg tgg cag tcc tgg ctt cgc gat ctg gag ttg ccg gag ttt cct 1459
 Ala Val Trp Gln Ser Trp Leu Arg Asp Leu Glu Leu Pro Glu Phe Pro
 440 445 450
 tct ggt ggt ttg gac tagtgcgcta tctgacgctg gcc 1497
 Ser Gly Gly Leu Asp
 455

<210> 124

<211> 458

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 124

Met Arg Arg Leu Arg Ser Thr Pro Val Pro Gly Thr Arg Asp Ser Tyr
 1 5 10 15
 Thr Gly Ile Asp Phe Asn Leu Gly Phe His Ile Arg Arg Tyr Glu Leu
 20 25 30
 Asp Leu Thr Tyr Arg Val Ala Pro Asn Leu Leu Met Gly Thr Ala Thr
 35 40 45
 Leu His Met Asp Asn Tyr Arg Ala Leu Asp Ala Leu Thr Leu Asp Leu
 50 55 60
 Gly Gly Ser Leu Arg Val Glu Lys Val Thr Ala Lys Gly Thr Ala Gly
 65 70 75 80
 Thr His Ile Gln Val Ala Arg Phe Arg His Ala Gly Arg Lys Leu Arg
 85 90 95
 Ile Thr Phe Arg Asn Gln Ile Pro Val Asp Gln Glu Phe Ser Leu Thr
 100 105 110
 Ile Arg Tyr Arg Gly Asn Pro Arg Pro Leu Arg Ser Glu Trp Gly Met
 115 120 125
 Ile Gly Trp Glu Glu Leu Asp Asn Gly Ala Leu Val Ala Ala Gln Pro
 130 135 140
 Asn Gly Ala Pro Ser Trp Phe Pro Cys Asp Asp Thr Pro Asp Glu Lys
 145 150 155 160
 Ala Leu Phe Asp Val His Phe His Thr Asp Asn Gly Tyr Ala Ala Ile
 165 170 175
 Ile Thr Gly Asp Leu Ile Ser Lys His Val Ser Gly Ser Met Thr Thr
 180 185 190
 Trp His Tyr Gln Ser Arg Glu Pro Met Ala Thr Tyr Leu Ala Ala Val
 195 200 205

His Val Gly Glu Tyr Asp Thr Val Ser Leu Gly Val Ser Glu Ser Gly
 210 215 220
 Val Val Val Glu Ala Tyr Val Pro Val Gly Asp Ala Ala Leu Arg Ala
 225 230 235 240
 Arg Ile Leu Glu Asp Phe Ala Lys Gln Val Asp Met Leu Asp Ala Tyr
 245 250 255
 Glu Lys Leu Phe Gly Pro Tyr Pro Phe Arg Ser Tyr Arg Val Val Ile
 260 265 270
 Thr Glu Asp Glu Leu Glu Ile Pro Leu Glu Ala Gln Gly Leu Ser Ser
 275 280 285
 Phe Gly Ala Asn His Ala Thr Gly Glu Gly Thr Trp Glu Arg Leu Ile
 290 295 300
 Ala His Glu Leu Ser His Gln Trp Phe Gly Asn Ser Leu Gly Leu Ala
 305 310 315 320
 Gln Trp Asn Asp Ile Trp Leu Asn Glu Gly Phe Ala Cys Tyr Ala Glu
 325 330 335
 Trp Leu Trp Phe Glu Ala Ala Gly Val Lys Ser Ala Ala Glu Ser Ala
 340 345 350
 Leu Glu Phe Tyr Arg Gly Leu Glu Ala Leu Pro Lys Asp Ile Leu Leu
 355 360 365
 Ala Asn Pro Gly Ala Lys Asp Met Phe Asp Asp Arg Val Tyr Lys Arg
 370 375 380
 Gly Ala Leu Thr Val His Ala Leu Arg Glu Leu Leu Gly Asp Asp Ala
 385 390 395 400
 Phe Phe Lys Ala Val Arg Ser Tyr Val Ala Glu Gly Arg His Gly Leu
 405 410 415
 Val Glu Pro Arg Asp Leu Lys Arg His Leu Tyr Ala Val Ser Thr Asp
 420 425 430
 His Ala Ala Leu Asp Ala Val Trp Gln Ser Trp Leu Arg Asp Leu Glu
 435 440 445
 Leu Pro Glu Phe Pro Ser Gly Gly Leu Asp
 450 455

<210> 125

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXN00621

<400> 125

188

gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245

cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
 250 255 260

tgaagtacgc gtgcttcctt tcg 906

<210> 126
 <211> 261
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 126
 Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
 1 5 10 15
 Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
 20 25 30
 Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
 35 40 45
 Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
 50 55 60
 Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65 70 75 80
 Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
 85 90 95
 Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
 100 105 110
 Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
 115 120 125
 Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
 130 135 140
 Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
 145 150 155 160
 Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
 165 170 175
 Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
 180 185 190
 Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
 195 200 205
 Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
 210 215 220
 Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr

190

gtc acc acc tct ggc cgc tac ctt gcg tat tcc acc gat gtc acg ggc 595
 Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser Thr Asp Val Thr Gly
 150 155 160 165

gaa gag cgc ttt acg ttg cgc atc aag gat cta gaa act ggc gag ctg 643
 Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu Glu Thr Gly Glu Leu
 170 175 180

ctt cct gat acc ctg act ggc att ttc tac ggt gct act tgg gtg ggg 691
 Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly Ala Thr Trp Val Gly
 185 190 195

gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat 739
 Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
 200 205 210

act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg 787
 Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
 215 220 225

gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245

cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
 250 255 260

tgaagtacgc gtgcttcctt tcg 906

<210> 128
 <211> 261
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 128
 Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
 1 5 10 15
 Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
 20 25 30
 Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
 35 40 45
 Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
 50 55 60
 Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65 70 75 80
 Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
 85 90 95
 Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
 100 105 110
 Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
 115 120 125

Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
 130 135 140

Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
 145 150 155 160

Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
 165 170 175

Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
 180 185 190

Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
 195 200 205

Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
 210 215 220

Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr
 225 230 235 240

Trp Val Gly Thr Thr Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg
 245 250 255

Leu Gln Asp His Leu
 260

<210> 129
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1516)
 <223> RXN00622

<400> 129
 ttttaccagc gcgttgatga tgcgtggcgt ccagatactg tgtggcgcca caaggtgggt 60

accccggttg aagaagacgt gttggtgtac cagcagcctg atg aac gtt att cca 115
 Met Asn Val Ile Pro
 1 5

cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
 Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
 10 15 20

gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca 211
 Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro
 25 30 35

gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac 259
 Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr
 40 45 50

gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca 307
 Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr
 55 60 65

cac aac gcc gag ggc ccg aac ttt tcg gtg ggg tgg gct ggc gtc gac	355
His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp	
70 75 80 85	
aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat	403
Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp	
90 95 100	
gac gtg cgc att gag ggt gtc gat acc tac cgc gat ttc atc atc ctg	451
Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg Asp Phe Ile Ile Leu	
105 110 115	
ggc tac agg tcc ggc gcg atc ggc cag gtc gcg atc atg aag ctt atc	499
Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala Ile Met Lys Leu Ile	
120 125 130	
gac gga acc ttc ggc gat ttc caa cag ctg gaa ttt gac gag gaa atc	547
Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu Phe Asp Glu Glu Ile	
135 140 145	
tac acc gtc gca tcg ggc gga aac cca gaa tgg gac gcc ccc gtc att	595
Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp Asp Ala Pro Val Ile	
150 155 160 165	
cgc ctt tct tac gga tca ttc acc acc ccg gcg cag ctg ttt aac tac	643
Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala Gln Leu Phe Asn Tyr	
170 175 180	
tgg att gaa tcc ggc gaa cgc acg ctg ctg aag cag cag gaa gtg ctc	691
Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys Gln Gln Glu Val Leu	
185 190 195	
ggc gga tac aag ccg tca gac tat gtg gcc tcc cga ttg tgg gtc act	739
Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser Arg Leu Trp Val Thr	
200 205 210	
gcg aaa gat ggc gcg cag att cca gtg tcc ttg gtg cac cgc acc gac	787
Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu Val His Arg Thr Asp	
215 220 225	
ctg gat gta tcc aag ccc aac ccc acg ttg ctc tac ggc tat ggt tcc	835
Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu Tyr Gly Tyr Gly Ser	
230 235 240 245	
tac gaa tca tcc att gat cca ggc ttc tct atc gcg cgt ttg tca ctg	883
Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile Ala Arg Leu Ser Leu	
250 255 260	
atg gat cgt ggc atg att ttt gcg att gcc cac gtt cgt ggc ggt ggc	931
Met Asp Arg Gly Met Ile Phe Ala Ile Ala His Val Arg Gly Gly Gly	
265 270 275	
gaa atg ggt cgt ggc tgg tac gac aac ggc aaa acc acc acg aag aaa	979
Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys Thr Thr Thr Lys Lys	
280 285 290	
aac acc ttc acc gac ttc att gat gtt gcc gac gcc ctc atc gag cag	1027
Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp Ala Leu Ile Glu Gln	
295 300 305	

aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt 1075
Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly
310 315 320 325

ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag 1123
Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys
330 335 340

gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc 1171
Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
345 350 355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat 1219
Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
360 365 370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca 1267
Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
375 380 385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca 1315
Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
390 395 400 405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta 1363
Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
410 415 420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act 1411
Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
425 430 435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg 1459
Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
440 445 450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt 1507
Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
455 460 465

gtg acc gaa taaaacttgt tcgactagcg aac 1539
Val Thr Glu
470

<210> 130

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
1 5 10 15

Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
20 25 30

Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
35 40 45

Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp

50					55					60					
Ile	Trp	Leu	Val	Thr	His	Asn	Ala	Glu	Gly	Pro	Asn	Phe	Ser	Val	Gly
65						70					75				80
Trp	Ala	Gly	Val	Asp	Lys	Leu	Asn	Ser	Leu	Asp	Ala	Leu	Ala	Pro	Leu
				85					90					95	
Val	Ala	His	Lys	Asp	Asp	Val	Arg	Ile	Glu	Gly	Val	Asp	Thr	Tyr	Arg
			100					105					110		
Asp	Phe	Ile	Ile	Leu	Gly	Tyr	Arg	Ser	Gly	Ala	Ile	Gly	Gln	Val	Ala
		115					120					125			
Ile	Met	Lys	Leu	Ile	Asp	Gly	Thr	Phe	Gly	Asp	Phe	Gln	Gln	Leu	Glu
	130					135					140				
Phe	Asp	Glu	Glu	Ile	Tyr	Thr	Val	Ala	Ser	Gly	Gly	Asn	Pro	Glu	Trp
145						150					155				160
Asp	Ala	Pro	Val	Ile	Arg	Leu	Ser	Tyr	Gly	Ser	Phe	Thr	Thr	Pro	Ala
				165					170					175	
Gln	Leu	Phe	Asn	Tyr	Trp	Ile	Glu	Ser	Gly	Glu	Arg	Thr	Leu	Leu	Lys
			180					185					190		
Gln	Gln	Glu	Val	Leu	Gly	Gly	Tyr	Lys	Pro	Ser	Asp	Tyr	Val	Ala	Ser
		195					200					205			
Arg	Leu	Trp	Val	Thr	Ala	Lys	Asp	Gly	Ala	Gln	Ile	Pro	Val	Ser	Leu
		210				215					220				
Val	His	Arg	Thr	Asp	Leu	Asp	Val	Ser	Lys	Pro	Asn	Pro	Thr	Leu	Leu
225						230					235				240
Tyr	Gly	Tyr	Gly	Ser	Tyr	Glu	Ser	Ser	Ile	Asp	Pro	Gly	Phe	Ser	Ile
				245					250					255	
Ala	Arg	Leu	Ser	Leu	Met	Asp	Arg	Gly	Met	Ile	Phe	Ala	Ile	Ala	His
			260					265					270		
Val	Arg	Gly	Gly	Gly	Glu	Met	Gly	Arg	Gly	Trp	Tyr	Asp	Asn	Gly	Lys
		275					280					285			
Thr	Thr	Thr	Lys	Lys	Asn	Thr	Phe	Thr	Asp	Phe	Ile	Asp	Val	Ala	Asp
		290				295					300				
Ala	Leu	Ile	Glu	Gln	Lys	Ile	Ser	Ala	Pro	Glu	Met	Leu	Val	Ala	Glu
305						310					315				320
Gly	Gly	Ser	Ala	Gly	Gly	Met	Leu	Met	Gly	Ala	Ile	Ala	Asn	Met	Ala
				325					330					335	
Gly	Asp	Arg	Phe	Lys	Ala	Ile	Glu	Ala	Asn	Val	Pro	Phe	Val	Asp	Pro
			340					345					350		
Leu	Thr	Ser	Met	Leu	Met	Pro	Glu	Leu	Pro	Leu	Thr	Val	Ile	Glu	Trp
		355					360					365			
Asp	Glu	Trp	Gly	Asp	Pro	Leu	His	Asp	Lys	Asp	Val	Tyr	Glu	Tyr	Met
	370					375					380				

Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn
 385 390 395 400

Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu
 405 410 415

Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu
 420 425 430

Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
 435 440 445

Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
 450 455 460

Asn Gln Ala Thr Gly Val Thr Glu
 465 470

<210> 131
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1516)
 <223> FRXA00622

<400> 131
 ttttaccagc gcgttgatga tgcgtggcgt ccagatactg tgtggcgcca caaggtgggt 60

accccggttg aagaagacgt gttggtgtac cacgagcctg atg aac gtt att cca 115
 Met Asn Val Ile Pro
 1 5

cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
 Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
 10 15 20

gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca 211
 Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro
 25 30 35

gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac 259
 Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr
 40 45 50

gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca 307
 Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr
 55 60 65

cac aac gcc gag ggc ccg aac ttt tgc gtg ggg tgg gct ggc gtc gac 355
 His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp
 70 75 80 85

aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat 403
 Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp
 90 95 100

gac gtg cgc att gag ggt gtc gat acc tac cgc gat ttc atc atc ctg	451
Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg Asp Phe Ile Ile Leu	
105 110 115	
ggc tac agg tcc ggc gcg atc ggc cag gtc gcg atc atg aag ctt atc	499
Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala Ile Met Lys Leu Ile	
120 125 130	
gac gga acc ttc ggc gat ttc caa cag ctg gaa ttt gac gag gaa atc	547
Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu Phe Asp Glu Glu Ile	
135 140 145	
tac acc gtc gca tgc ggc gga aac cca gaa tgg gac gcc ccc gtc att	595
Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp Asp Ala Pro Val Ile	
150 155 160 165	
cgc ctt tct tac gga tca ttc acc acc ccg gcg cag ctg ttt aac tac	643
Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala Gln Leu Phe Asn Tyr	
170 175 180	
tgg att gaa tcc ggc gaa cgc acg ctg ctg aag cag cag gaa gtg ctc	691
Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys Gln Gln Glu Val Leu	
185 190 195	
ggc gga tac aag ccg tca gac tat gtg gcc tcc cga ttg tgg gtc act	739
Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser Arg Leu Trp Val Thr	
200 205 210	
gcg aaa gat ggc gcg cag att cca gtg tcc ttg gtg cac cgc acc gac	787
Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu Val His Arg Thr Asp	
215 220 225	
ctg gat gta tcc aag ccc aac ccc acg ttg ctc tac ggc tat ggt tcc	835
Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu Tyr Gly Tyr Gly Ser	
230 235 240 245	
tac gaa tca tcc att gat cca ggc ttc tct atc gcg cgt ttg tca ctg	883
Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile Ala Arg Leu Ser Leu	
250 255 260	
atg gat cgt ggc atg att ttt gcg att gcc cac gtt cgt ggc ggt ggc	931
Met Asp Arg Gly Met Ile Phe Ala Ile Ala His Val Arg Gly Gly Gly	
265 270 275	
gaa atg ggt cgt ggc tgg tac gac aac ggc aaa acc acc acg aag aaa	979
Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys Thr Thr Thr Lys Lys	
280 285 290	
aac acc ttc acc gac ttc att gat gtt gcc gac gcc ctc atc gag cag	1027
Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp Ala Leu Ile Glu Gln	
295 300 305	
aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt	1075
Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly	
310 315 320 325	
ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag	1123
Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys	
330 335 340	
gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc	1171

Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
 345 350 355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat 1219
 Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
 360 365 370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca 1267
 Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
 375 380 385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca 1315
 Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
 390 395 400 405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta 1363
 Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
 410 415 420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act 1411
 Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
 425 430 435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg 1459
 Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
 440 445 450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt 1507
 Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
 455 460 465

gtg acc gaa taaaacttgt tcgactagcg aac 1539
 Val Thr Glu
 470

<210> 132

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
 1 5 10 15

Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
 20 25 30

Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
 35 40 45

Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
 50 55 60

Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly
 65 70 75 80

Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu
 85 90 95

Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg

100	105	110
Asp Phe Ile Ile Leu Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala 115 120 125		
Ile Met Lys Leu Ile Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu 130 135 140		
Phe Asp Glu Glu Ile Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp 145 150 155 160		
Asp Ala Pro Val Ile Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala 165 170 175		
Gln Leu Phe Asn Tyr Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys 180 185 190		
Gln Gln Glu Val Leu Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser 195 200 205		
Arg Leu Trp Val Thr Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu 210 215 220		
Val His Arg Thr Asp Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu 225 230 235 240		
Tyr Gly Tyr Gly Ser Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile 245 250 255		
Ala Arg Leu Ser Leu Met Asp Arg Gly Met Ile Phe Ala Ile Ala His 260 265 270		
Val Arg Gly Gly Gly Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys 275 280 285		
Thr Thr Thr Lys Lys Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp 290 295 300		
Ala Leu Ile Glu Gln Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu 305 310 315 320		
Gly Gly Ser Ala Gly Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala 325 330 335		
Gly Asp Arg Phe Lys Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro 340 345 350		
Leu Thr Ser Met Leu Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp 355 360 365		
Asp Glu Trp Gly Asp Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met 370 375 380		
Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn 385 390 395 400		
Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu 405 410 415		
Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu 420 425 430		

Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
 435 440 445

Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
 450 455 460

Asn Gln Ala Thr Gly Val Thr Glu
 465 470

<210> 133

<211> 1629

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1606)

<223> RXN00982

<400> 133

gaaaacaaac gtccttgaag ccgtaatgcc ccgttcgaca ataaaaagg tagtagcagt 60

tcttgccgcc tcgactgcgc ttagccccctt tttggtatca atg ccc act gca gca 115
 Met Pro Thr Ala Ala
 1 5

gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att 163
 Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile
 10 15 20

gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat 211
 Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp
 25 30 35

ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa 259
 Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln
 40 45 50

ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc 307
 Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly
 55 60 65

gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc 355
 Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala
 70 75 80 85

atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc 403
 Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val
 90 95 100

ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc 451
 Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe
 105 110 115

ctc tcg ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag 499
 Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu
 120 125 130

atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc 547

Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala	
135 140 145	
aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc	595
Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser	
150 155 160 165	
atc ttc gga ctg tcc tac gga acc tac ctc gga tcg gtc tac gcc acc	643
Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr	
170 175 180	
cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg	691
Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala	
185 190 195	
ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag ggc tac	739
Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr	
200 205 210	
aaa aac tcc ctc aac gac ttc ttc acc tgg gtt gca gaa aac aac gac	787
Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp	
215 220 225	
acg tat ggc ctc ggc act acc cca cta gcc gtg tac caa aac tgg tca	835
Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser	
230 235 240 245	
aac aag atc gtc gcc gaa acc gga acc aac cca acc gtt gct cca cca	883
Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro	
250 255 260	
cca gca caa gtt ggc gat gtc cca cca gca ttc gca tgg gcc ggc caa	931
Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln	
265 270 275	
gca ggc gca gac atg atg acc gcc acc aac cca acc tcc gtg caa ctc	979
Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu	
280 285 290	
cag ggc ctt gcc acc cag ctc cta aac cct gga tcc aac cag tca ctg	1027
Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu	
295 300 305	
agc cct ctg ctc aac gtc acc cgc gcc tac att cca cag cca tca acc	1075
Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr	
310 315 320 325	
tgg ccc atg ctc gca ggc gcc atc tca ggg caa aca ccc atc cct gac	1123
Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln Thr Pro Ile Pro Asp	
330 335 340	
gta act gac acc ggc gac gac cca tac gtc atc gaa agc atc aac gcc	1171
Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile Glu Ser Ile Asn Ala	
345 350 355	
agc gtc aac atg cag cgc atg gtc atg tgc aac gaa aac acc gtc gca	1219
Ser Val Asn Met Gln Arg Met Val Met Cys Asn Glu Asn Thr Val Ala	
360 365 370	
cca gac cca gta gca atg gca cgc atg gcc tgg aca agc atg gtc acc	1267
Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp Thr Ser Met Val Thr	

375 380 385

ggc gac gtc ttt gac att tac tcc gtt aaa ttc agc tcc gga caa gcc 1315
 Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe Ser Ser Gly Gln Ala
 390 395 400 405

tgc tcc ggc atc acc cca aca agc ggc cgc cag cca acc gac gga tct 1363
 Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln Pro Thr Asp Gly Ser
 410 415 420

caa cta gca gtc caa cca cta ctc ctc cag gga acc agc gac cca caa 1411
 Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly Thr Ser Asp Pro Gln
 425 430 435

acc cca tac tgg acc cac aac gag ctt gcc gac gcc atg aac gcc cac 1459
 Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp Ala Met Asn Ala His
 440 445 450

gtg gtc acc gtc aac gga cca gga cac ggc caa tcc atc ggc ggc acc 1507
 Val Val Thr Val Asn Gly Pro Gly His Gly Gln Ser Ile Gly Gly Thr
 455 460 465

aac caa gca atc aac gac att gtt gtg gac tac ctc cgc acc gga cac 1555
 Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly His
 470 475 480 485

acc gac gcc acc tgg gtc gaa ggc aac aca ccc acc cca att acg gct 1603
 Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr Ala
 490 495 500

ggc taattgcttt ccacttagta gat 1629
 Gly

<210> 134

<211> 502

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro
 1 5 10 15

Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro
 20 25 30

Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val
 35 40 45

Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser
 50 55 60

Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met
 65 70 75 80

Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln
 85 90 95

Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala
 100 105 110

Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
 115 120 125
 Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
 130 135 140
 Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
 145 150 155 160
 Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
 165 170 175
 Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
 180 185 190
 Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
 195 200 205
 Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
 210 215 220
 Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
 225 230 235 240
 Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
 245 250 255
 Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
 260 265 270
 Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
 275 280 285
 Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
 290 295 300
 Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
 305 310 315 320
 Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
 325 330 335
 Thr Pro Ile Pro Asp Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile
 340 345 350
 Glu Ser Ile Asn Ala Ser Val Asn Met Gln Arg Met Val Met Cys Asn
 355 360 365
 Glu Asn Thr Val Ala Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp
 370 375 380
 Thr Ser Met Val Thr Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe
 385 390 395 400
 Ser Ser Gly Gln Ala Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln
 405 410 415
 Pro Thr Asp Gly Ser Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly
 420 425 430

Thr Ser Asp Pro Gln Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp
 435 440 445

Ala Met Asn Ala His Val Val Thr Val Asn Gly Pro Gly His Gly Gln
 450 455 460

Ser Ile Gly Gly Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr
 465 470 475 480

Leu Arg Thr Gly His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro
 485 490 495

Thr Pro Ile Thr Ala Gly
 500

<210> 135

<211> 1114

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> FRXA00977

<400> 135

gaaaacaaac gtccttgaag ccgtaatgcc ccgttcgaca ataaaaaggg tagtagcagt 60

tcttgccgcc tcgactgcgc ttagccctt tttggtatca atg ccc act gca gca 115
 Met Pro Thr Ala Ala
 1 5

gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att 163
 Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile
 10 15 20

gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat 211
 Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp
 25 30 35

ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa 259
 Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln
 40 45 50

ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc 307
 Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly
 55 60 65

gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc 355
 Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala
 70 75 80 85

atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc 403
 Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val
 90 95 100

ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc 451
 Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe
 105 110 115

ctc tcg ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag 499
 Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu
 120 125 130

atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc 547
 Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala
 135 140 145

aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc 595
 Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser
 150 155 160 165

atc ttc gga ctg tcc tac gga acc tac ctc gga tcg gtc tac gcc acc 643
 Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr
 170 175 180

cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg 691
 Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala
 185 190 195

ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag gcc tac 739
 Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr
 200 205 210

aaa aac tcc ctc aac gac ttc ttc acc tgg gtt gca gaa aac aac gac 787
 Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp
 215 220 225

acg tat ggc ctc ggc act acc cca cta gcc gtg tac caa aac tgg tca 835
 Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser
 230 235 240 245

aac aag atc gtc gcc gaa acc gga acc aac cca acc gtt gct cca cca 883
 Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro
 250 255 260

cca gca caa gtt ggc gat gtc cca cca gca ttc gca tgg gcc gcc caa 931
 Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln
 265 270 275

gca ggc gca gac atg atg acc gcc acc aac cca acc tcc gtg caa ctc 979
 Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu
 280 285 290

cag ggc ctt gcc acc cag ctc cta aac cct gga tcc aac cag tca ctg 1027
 Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu
 295 300 305

agc cct ctg ctc aac gtc acc cgc gcc tac att cca cag cca tca acc 1075
 Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr
 310 315 320 325

tgg ccc atg ctc gca ggc gcc atc tca ggg caa aca ccc 1114
 Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln Thr Pro
 330 335

<210> 136

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro
 1 5 10 15
 Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro
 20 25 30
 Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val
 35 40 45
 Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser
 50 55 60
 Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met
 65 70 75 80
 Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln
 85 90 95
 Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala
 100 105 110
 Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
 115 120 125
 Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
 130 135 140
 Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
 145 150 155 160
 Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
 165 170 175
 Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
 180 185 190
 Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
 195 200 205
 Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
 210 215 220
 Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
 225 230 235 240
 Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
 245 250 255
 Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
 260 265 270
 Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
 275 280 285
 Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
 290 295 300
 Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
 305 310 315 320

Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
 325 330 335

Thr Pro

<210> 137

<211> 269

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(246)

<223> FRXA00982

<400> 137

tct	caa	cta	gca	gtc	caa	cca	cta	ctc	ctc	cag	gga	acc	agc	gac	cca	48
Ser	Gln	Leu	Ala	Val	Gln	Pro	Leu	Leu	Leu	Gln	Gly	Thr	Ser	Asp	Pro	
1				5					10					15		
caa	acc	cca	tac	tgg	acc	cac	aac	gag	ctt	gcc	gac	gcc	atg	aac	gcc	96
Gln	Thr	Pro	Tyr	Trp	Thr	His	Asn	Glu	Leu	Ala	Asp	Ala	Met	Asn	Ala	
			20					25					30			
cac	gtg	gtc	acc	gtc	aac	gga	cca	gga	cac	ggc	caa	tcc	atc	ggc	ggc	144
His	Val	Val	Thr	Val	Asn	Gly	Pro	Gly	His	Gly	Gln	Ser	Ile	Gly	Gly	
			35				40					45				
acc	aac	caa	gca	atc	aac	gac	att	gtt	gtg	gac	tac	ctc	cgc	acc	gga	192
Thr	Asn	Gln	Ala	Ile	Asn	Asp	Ile	Val	Val	Asp	Tyr	Leu	Arg	Thr	Gly	
	50					55				60						
cac	acc	gac	gcc	acc	tgg	gtc	gaa	ggc	aac	aca	ccc	acc	cca	att	acg	240
His	Thr	Asp	Ala	Thr	Trp	Val	Glu	Gly	Asn	Thr	Pro	Thr	Pro	Ile	Thr	
65					70				75						80	
gct	ggc	taattgcttt	ccacttagta	gat												269
Ala	Gly															

<210> 138

<211> 82

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Ser	Gln	Leu	Ala	Val	Gln	Pro	Leu	Leu	Leu	Gln	Gly	Thr	Ser	Asp	Pro
1				5					10					15	
Gln	Thr	Pro	Tyr	Trp	Thr	His	Asn	Glu	Leu	Ala	Asp	Ala	Met	Asn	Ala
			20					25					30		
His	Val	Val	Thr	Val	Asn	Gly	Pro	Gly	His	Gly	Gln	Ser	Ile	Gly	Gly
			35				40					45			
Thr	Asn	Gln	Ala	Ile	Asn	Asp	Ile	Val	Val	Asp	Tyr	Leu	Arg	Thr	Gly
	50					55				60					

His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr
 65 70 75 80

Ala Gly

<210> 139

<211> 1419

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1396)

<223> RXA00152

<400> 139

gtcattgata tccaaggcac gaccgcgatt gtatggaaag aagcctaaat ttttaacaat 60

caaatagtac tggccattcc caactaaaac tggagtaacg atg aca gga cta atc 115
 Met Thr Gly Leu Ile
 1 5

ctc gcc ata gtt ttc ctg gtc ttt gtc gcc gtc gtg gtg atc aag tcc 163
 Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser
 10 15 20

ata gcc ctg att ccc cag ggt gaa gcc gcc gtc att gaa cgc ctt ggt 211
 Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly
 25 30 35

agc tac acc cgc acc gtt tca ggt ggc ctg acc ctg ctg gtt cca ttc 259
 Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe
 40 45 50

gtg gac cga gta cgc gca agg atc gac acc cgt gag cgc gtg gtc tca 307
 Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser
 55 60 65

ttc cca ccg cag gct gtt att acc caa gac aac ctg acc gtg gcc atc 355
 Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile
 70 75 80 85

gat atc gtg gtg acc ttc caa atc aac gaa cca gag cgc gcc atc tac 403
 Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro Glu Arg Ala Ile Tyr
 90 95 100

ggc gtg gac aac tac atc gtc ggt gtg gag cag att tct gta gca aca 451
 Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln Ile Ser Val Ala Thr
 105 110 115

ctt cga gac gtt gtc ggt ggc atg acc ctg gaa gaa acc ctc act tca 499
 Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu Glu Thr Leu Thr Ser
 120 125 130

cgt gac gtg atc aac cgc cgc ctc cgt ggc gag ctc gat gca gca acc 547
 Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr
 135 140 145

acc aaa tgg ggc ctg cgc atc agc cgt gtg gaa cta aag gca att gat	595
Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu Leu Lys Ala Ile Asp	
150 155 160 165	
ccg cca cca tcc atc cag caa tcg atg gaa aag cag atg aag gca gac	643
Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys Gln Met Lys Ala Asp	
170 175 180	
cgt gaa aag cgc gcc acc att ttg acc gca gaa ggt cag cgc gaa gcc	691
Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu Gly Gln Arg Glu Ala	
185 190 195	
gac atc aaa act gcc gaa ggt gaa aag caa gcc aag atc ctc caa gct	739
Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala Lys Ile Leu Gln Ala	
200 205 210	
gag ggt gaa aag cac gca tcc atc ctg aac gca gaa gca gaa cgc caa	787
Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala Glu Ala Glu Arg Gln	
215 220 225	
gcg atg atc ctg cgc gcc gaa ggt gaa cgc gca gca cgc tac ctc cag	835
Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala Ala Arg Tyr Leu Gln	
230 235 240 245	
gcg cag ggt gaa gcc cga gca atc caa aag gtc aac gca gca atc aag	883
Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val Asn Ala Ala Ile Lys	
250 255 260	
tct gcc aag ttg acc cca gag gtt ctt gct tat caa tac ctc gaa aag	931
Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr Gln Tyr Leu Glu Lys	
265 270 275	
ctt cct aag atc gca gag ggc aac gcc tcc aag atg tgg gtc atc cca	979
Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys Met Trp Val Ile Pro	
280 285 290	
agc cag ttc tcc gat tct ctg gaa ggt ttt gcg aag cag ttc ggc gca	1027
Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala Lys Gln Phe Gly Ala	
295 300 305	
aag gat gca gaa ggt gtc ttc cgc tac gaa cca aac acc gtg gat gaa	1075
Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro Asn Thr Val Asp Glu	
310 315 320 325	
gaa acc cgc gac atc gca aac gcc gac aac gtg gaa gac tgg ttc tcc	1123
Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val Glu Asp Trp Phe Ser	
330 335 340	
acc gaa tca gac cct gaa atc gca gca gca gtc gcc gca gca aac gcc	1171
Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val Ala Ala Asn Ala	
345 350 355	
gtg gcc aac aag cca gtc gat cca gaa ccc ggt gag atc ctt tcc aag	1219
Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly Glu Ile Leu Ser Lys	
360 365 370	
aag acc gca cga cgc gtt gaa cct gaa gca gta ttg gag gct ttg caa	1267
Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val Leu Glu Ala Leu Gln	
375 380 385	
aac gga acc act aca caa cct gag gtt gag gca gca cct cct acc gca	1315

Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala Ala Pro Pro Thr Ala
 390 395 400 405

aac ttc gcc caa gaa ttc cct gca cca cag gca aac cct gaa gat tac 1363
 Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala Asn Pro Glu Asp Tyr
 410 415 420

tcc gac caa cac cga gag aat cct tac gga aac taatcaggca taagaaaagg 1416
 Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 425 430

cgg 1419

<210> 140
 <211> 432
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 140
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Val Val Ile Lys Ser Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val
 20 25 30

Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr
 35 40 45

Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg
 50 55 60

Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn
 65 70 75 80

Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro
 85 90 95

Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln
 100 105 110

Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu
 115 120 125

Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu
 130 135 140

Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu
 145 150 155 160

Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys
 165 170 175

Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu
 180 185 190

Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala
 195 200 205

Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala
 210 215 220

Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala
 225 230 235 240
 Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val
 245 250 255
 Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr
 260 265 270
 Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys
 275 280 285
 Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala
 290 295 300
 Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro
 305 310 315 320
 Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val
 325 330 335
 Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val
 340 345 350
 Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly
 355 360 365
 Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val
 370 375 380
 Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala
 385 390 395 400
 Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala
 405 410 415
 Asn Pro Glu Asp Tyr Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 420 425 430

<210> 141
 <211> 1098
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1075)
 <223> RXA02558

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 cattcttttt cagcacccca gacttaaaaag gagcaccacc atg agc acc ata gaa 115
 Met Ser Thr Ile Glu
 1 5

gag cgc act cct gga gct gtc gcc aca gaa cca gtg gga cac gaa ggc	163
Glu Arg Thr Pro Gly Ala Val Ala Thr Glu Pro Val Gly His Glu Gly	
10 15 20	
gca cgc gtc agc att aat gag aag aac gtg tgg tct ttg ggc gca ggt	211
Ala Arg Val Ser Ile Asn Glu Lys Asn Val Trp Ser Leu Gly Ala Gly	
25 30 35	
cca gca gct ttc gca ctg ctc gca atg att gtg ctc atg att gcc agt	259
Pro Ala Ala Phe Ala Leu Leu Ala Met Ile Val Leu Met Ile Ala Ser	
40 45 50	
gga gtt ttc ttc gct caa tcc atc aac act tta gaa aac gat ggc ggt	307
Gly Val Phe Phe Ala Gln Ser Ile Asn Thr Leu Glu Asn Asp Gly Gly	
55 60 65	
gga aca ctt gcg gtt acg gga ctg att gcc agc atc gtc gtt ttc act	355
Gly Thr Leu Ala Val Thr Gly Leu Ile Ala Ser Ile Val Val Phe Thr	
70 75 80 85	
gtt gca ttg gtg gtc acc ata act tcg gtg aag gtg gtc agc cct gga	403
Val Ala Leu Val Thr Ile Thr Ser Val Lys Val Val Ser Pro Gly	
90 95 100	
cat act ctg act gtg cag ttc ttt gga cga tac atc gga acc ctg cgt	451
His Thr Leu Thr Val Gln Phe Phe Gly Arg Tyr Ile Gly Thr Leu Arg	
105 110 115	
cga act ggg ttg tct ttc gtt ccc cca ctg tct gtg acg aag aaa gtg	499
Arg Thr Gly Leu Ser Phe Val Pro Pro Leu Ser Val Thr Lys Lys Val	
120 125 130	
tcc gtg agg gtc cga aac ttt gaa acc aac gaa gcc aaa gtt aat gac	547
Ser Val Arg Val Arg Asn Phe Glu Thr Asn Glu Ala Lys Val Asn Asp	
135 140 145	
tac aac ggc aac ccc atc aac att gca gcg atc atc gtg tgg cag gta	595
Tyr Asn Gly Asn Pro Ile Asn Ile Ala Ala Ile Ile Val Trp Gln Val	
150 155 160 165	
gcc gat act gca cag gct agc ttc tct gtg gag gat ttc gaa gag ttc	643
Ala Asp Thr Ala Gln Ala Ser Phe Ser Val Glu Asp Phe Glu Glu Phe	
170 175 180	
ctg cac cag cag gcc gag tcc gca ctg cgt cac gtg gca acc cag cac	691
Leu His Gln Gln Ala Glu Ser Ala Leu Arg His Val Ala Thr Gln His	
185 190 195	
ccc tat gat tcc cca gtt gat ggt cgt gtt tcc ttg cgt ggc gct acc	739
Pro Tyr Asp Ser Pro Val Asp Gly Arg Val Ser Leu Arg Gly Ala Thr	
200 205 210	
gat gag gtc agt gaa gaa ctc gca gat gag gtg gca caa cga gca gct	787
Asp Glu Val Ser Glu Glu Leu Ala Asp Glu Val Ala Gln Arg Ala Ala	
215 220 225	
gtt gca ggt ctt gaa atc gtc gaa gcc cgc atc tct tcc ttg agc tac	835
Val Ala Gly Leu Glu Ile Val Glu Ala Arg Ile Ser Ser Leu Ser Tyr	
230 235 240 245	
gca ccg gaa att gcc cag gcg atg ctg cag cgc cag cag gct tcc gcg	883

Ala Pro Glu Ile Ala Gln Ala Met Leu Gln Arg Gln Gln Ala Ser Ala
 250 255 260

att gtt gat gcc cgc gaa aag atc gtc gag ggc gct gtc acc atg gtg 931
 Ile Val Asp Ala Arg Glu Lys Ile Val Glu Gly Ala Val Thr Met Val
 265 270 275

gaa acc gca ctt gac cag ctt gag caa cgt gaa att gtg gat ttg gat 979
 Glu Thr Ala Leu Asp Gln Leu Glu Gln Arg Glu Ile Val Asp Leu Asp
 280 285 290

cca gag cga cgc gcc gcg atg gtt tcc aac ctg ttg gtt gtg ttg tgt 1027
 Pro Glu Arg Arg Ala Ala Met Val Ser Asn Leu Leu Val Val Leu Cys
 295 300 305

tcc gac acc aat gct cag cca atc gtc aac gcc ggt agc ctc tac caa 1075
 Ser Asp Thr Asn Ala Gln Pro Ile Val Asn Ala Gly Ser Leu Tyr Gln
 310 315 320 325

taagacaatg gcccgcaaac agg 1098

<210> 142
 <211> 325
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 142
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Val Gly His Glu Gly Ala Arg Val Ser Ile Asn Glu Lys Asn Val Trp
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Ser Leu Gly Ala Gly Pro Ala Ala Phe Ala Leu Leu Ala Met Ile Val
 35 40 45

Leu Met Ile Ala Ser Gly Val Phe Phe Ala Gln Ser Ile Asn Thr Leu
 50 55 60

Glu Asn Asp Gly Gly Gly Thr Leu Ala Val Thr Gly Leu Ile Ala Ser
 65 70 75 80

Ile Val Val Phe Thr Val Ala Leu Val Val Thr Ile Thr Ser Val Lys
 85 90 95

Val Val Ser Pro Gly His Thr Leu Thr Val Gln Phe Phe Gly Arg Tyr
 100 105 110

Ile Gly Thr Leu Arg Arg Thr Gly Leu Ser Phe Val Pro Pro Leu Ser
 115 120 125

Val Thr Lys Lys Val Ser Val Arg Val Arg Asn Phe Glu Thr Asn Glu
 130 135 140

Ala Lys Val Asn Asp Tyr Asn Gly Asn Pro Ile Asn Ile Ala Ala Ile
 145 150 155 160

Ile Val Trp Gln Val Ala Asp Thr Ala Gln Ala Ser Phe Ser Val Glu
 165 170 175

Asp Phe Glu Glu Phe Leu His Gln Gln Ala Glu Ser Ala Leu Arg His
 180 185 190

Val Ala Thr Gln His Pro Tyr Asp Ser Pro Val Asp Gly Arg Val Ser
 195 200 205

Leu Arg Gly Ala Thr Asp Glu Val Ser Glu Glu Leu Ala Asp Glu Val
 210 215 220

Ala Gln Arg Ala Ala Val Ala Gly Leu Glu Ile Val Glu Ala Arg Ile
 225 230 235 240

Ser Ser Leu Ser Tyr Ala Pro Glu Ile Ala Gln Ala Met Leu Gln Arg
 245 250 255

Gln Gln Ala Ser Ala Ile Val Asp Ala Arg Glu Lys Ile Val Glu Gly
 260 265 270

Ala Val Thr Met Val Glu Thr Ala Leu Asp Gln Leu Glu Gln Arg Glu
 275 280 285

Ile Val Asp Leu Asp Pro Glu Arg Arg Ala Ala Met Val Ser Asn Leu
 290 295 300

Leu Val Val Leu Cys Ser Asp Thr Asn Ala Gln Pro Ile Val Asn Ala
 305 310 315 320

Gly Ser Leu Tyr Gln
 325

<210> 143

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXA00500

<400> 143

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tttcgatctg gccacggcc gagaggtacg ctgattctc gtg tta gta cta gcc 115
 Val Leu Val Leu Ala
 1 5

cta gac acc tca acc cct gac ctg atc gtc ggc gtc gtc gac tcc gac 163
 Leu Asp Thr Ser Thr Pro Asp Leu Ile Val Gly Val Val Asp Ser Asp
 10 15 20

acc gga aac acc cgc gcc gaa acc atc atc gag gac acc cgc gca cac 211
 Thr Gly Asn Thr Arg Ala Glu Thr Ile Ile Glu Asp Thr Arg Ala His
 25 30 35

aac gag cag ctg acg ccc acc gtc cag aag acg ctt ctg gac gcc aac 259
 Asn Glu Gln Leu Thr Pro Thr Val Gln Lys Thr Leu Leu Asp Ala Asn
 40 45 50

ttg agc ttt tca gat atc gac gcg atc gtc gtg ggt tgc ggc ccg gga 307

Leu Ser Phe Ser Asp Ile Asp Ala Ile Val Val Gly Cys Gly Pro Gly
 55 60 65
 ccg ttc act gga ctt cga gta ggc atg gtg tcc ggc gca gcg ttc ggt 355
 Pro Phe Thr Gly Leu Arg Val Gly Met Val Ser Gly Ala Ala Phe Gly
 70 75 80 85
 gat gcc ctg gga atc cct gtc tat gga gtc tgc tca ctc gac gcg atc 403
 Asp Ala Leu Gly Ile Pro Val Tyr Gly Val Cys Ser Leu Asp Ala Ile
 90 95 100
 gct cac aat att ggt gca cgc aac atc ccg cac gca tta gtt gcc act 451
 Ala His Asn Ile Gly Ala Arg Asn Ile Pro His Ala Leu Val Ala Thr
 105 110 115
 gat gcg cgc cgc cgt gaa atc tac tgg gca acc tac cgc tcc ggc gaa 499
 Asp Ala Arg Arg Arg Glu Ile Tyr Trp Ala Thr Tyr Arg Ser Gly Glu
 120 125 130
 cgt gat cag gga cca gat gtc atc gca cca gca aac atc cag atc agc 547
 Arg Asp Gln Gly Pro Asp Val Ile Ala Pro Ala Asn Ile Gln Ile Ser
 135 140 145
 ggc gct gta gac acc att tcg att cct gag cac ctg gtg gaa aaa ctc 595
 Gly Ala Val Asp Thr Ile Ser Ile Pro Glu His Leu Val Glu Lys Leu
 150 155 160 165
 cca gaa gaa ctc cag aat gtc acc atg cat agc ggc aaa cct gcc ccc 643
 Pro Glu Glu Leu Gln Asn Val Thr Met His Ser Gly Lys Pro Ala Pro
 170 175 180
 gca agc ttg gtg gca gtg gct gat ttc agt gtg gaa cca caa cca ttg 691
 Ala Ser Leu Val Ala Val Ala Asp Phe Ser Val Glu Pro Gln Pro Leu
 185 190 195
 gtt cct ctt tac ctg cgc cgc cca gat gcc aaa gaa cca aaa cca aaa 739
 Val Pro Leu Tyr Leu Arg Arg Pro Asp Ala Lys Glu Pro Lys Pro Lys
 200 205 210
 cct aaa tct gca gcc atc ccc gag gtg gat ctt tca tgagtgaaca 785
 Pro Lys Ser Ala Ala Ile Pro Glu Val Asp Leu Ser
 215 220 225
 attcgagcta cgg 798

 <210> 144
 <211> 225
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 144
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 Val Val Asp Ser Asp Thr Gly Asn Thr Arg Ala Glu Thr Ile Ile Glu
 20 25 30
 Asp Thr Arg Ala His Asn Glu Gln Leu Thr Pro Thr Val Gln Lys Thr
 35 40 45

Leu Leu Asp Ala Asn Leu Ser Phe Ser Asp Ile Asp Ala Ile Val Val
 50 55 60
 Gly Cys Gly Pro Gly Pro Phe Thr Gly Leu Arg Val Gly Met Val Ser
 65 70 75 80
 Gly Ala Ala Phe Gly Asp Ala Leu Gly Ile Pro Val Tyr Gly Val Cys
 85 90 95
 Ser Leu Asp Ala Ile Ala His Asn Ile Gly Ala Arg Asn Ile Pro His
 100 105 110
 Ala Leu Val Ala Thr Asp Ala Arg Arg Arg Glu Ile Tyr Trp Ala Thr
 115 120 125
 Tyr Arg Ser Gly Glu Arg Asp Gln Gly Pro Asp Val Ile Ala Pro Ala
 130 135 140
 Asn Ile Gln Ile Ser Gly Ala Val Asp Thr Ile Ser Ile Pro Glu His
 145 150 155 160
 Leu Val Glu Lys Leu Pro Glu Glu Leu Gln Asn Val Thr Met His Ser
 165 170 175
 Gly Lys Pro Ala Pro Ala Ser Leu Val Ala Val Ala Asp Phe Ser Val
 180 185 190
 Glu Pro Gln Pro Leu Val Pro Leu Tyr Leu Arg Arg Pro Asp Ala Lys
 195 200 205
 Glu Pro Lys Pro Lys Pro Lys Ser Ala Ala Ile Pro Glu Val Asp Leu
 210 215 220

Ser
 225

<210> 145
 <211> 630
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(607)
 <223> RXA00501

<400> 145
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 caaacctaa atctgcagcc atccccgagg tggatctttc atg agt gaa caa ttc 115
 Met Ser Glu Gln Phe
 1 5
 gag cta cgg gaa ctc cgc agg gaa gac gcg ggg cgc tgc gcc gac ctg 163
 Glu Leu Arg Glu Leu Arg Arg Glu Asp Ala Gly Arg Cys Ala Asp Leu
 10 15 20
 gag caa atc ctg ttc cca ggt gat aac ccc tgg cca cgt gat gtc ttt 211
 Glu Gln Ile Leu Phe Pro Gly Asp Asn Pro Trp Pro Arg Asp Val Phe
 25 30 35

gcc gtg gag ttt tcc cac ccc acc aat ttc tac atc ggc gct ttc gac 259
 Ala Val Glu Phe Ser His Pro Thr Asn Phe Tyr Ile Gly Ala Phe Asp
 40 45 50

gaa gga tac ttg gtg gcg tac gca ggt ctt gcc atg atg gga cct gcg 307
 Glu Gly Tyr Leu Val Ala Tyr Ala Gly Leu Ala Met Met Gly Pro Ala
 55 60 65

gat gat cca gag ttt gaa atc cac acc att ggt gtc gat ccg gaa ttc 355
 Asp Asp Pro Glu Phe Glu Ile His Thr Ile Gly Val Asp Pro Glu Phe
 70 75 80 85

caa aga aaa ggc ttg gga cgc gta ctc atg gat caa atg atg cat gca 403
 Gln Arg Lys Gly Leu Gly Arg Val Leu Met Asp Gln Met Met His Ala
 90 95 100

gcg gac agc cac gac ggt cca gtt ttc ttg gaa gtc cgc acc gac aac 451
 Ala Asp Ser His Asp Gly Pro Val Phe Leu Glu Val Arg Thr Asp Asn
 105 110 115

gta ccc gcg att tcc atg tac gag gct ttc ggc ttt aaa acc ttg gcc 499
 Val Pro Ala Ile Ser Met Tyr Glu Ala Phe Gly Phe Lys Thr Leu Ala
 120 125 130

gtg cgc aaa aac tac tac cgg cca tcc gga gct gac gcc tac acc atg 547
 Val Arg Lys Asn Tyr Tyr Arg Pro Ser Gly Ala Asp Ala Tyr Thr Met
 135 140 145

caa cgc cca cgc ttg agc gat cgc aaa gat caa cag aca gac aca gag 595
 Gln Arg Pro Arg Leu Ser Asp Arg Lys Asp Gln Gln Thr Asp Thr Glu
 150 155 160 165

ggg aca ccc agc taaaccatga tcgttttggg aat 630
 Gly Thr Pro Ser

<210> 146

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

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Arg Cys Ala Asp Leu Glu Gln Ile Leu Phe Pro Gly Asp Asn Pro Trp
 20 25 30

Pro Arg Asp Val Phe Ala Val Glu Phe Ser His Pro Thr Asn Phe Tyr
 35 40 45

Ile Gly Ala Phe Asp Glu Gly Tyr Leu Val Ala Tyr Ala Gly Leu Ala
 50 55 60

Met Met Gly Pro Ala Asp Asp Pro Glu Phe Glu Ile His Thr Ile Gly
 65 70 75 80

Val Asp Pro Glu Phe Gln Arg Lys Gly Leu Gly Arg Val Leu Met Asp
 85 90 95

Gln Met Met His Ala Ala Asp Ser His Asp Gly Pro Val Phe Leu Glu
 100 105 110

Val Arg Thr Asp Asn Val Pro Ala Ile Ser Met Tyr Glu Ala Phe Gly
 115 120 125

Phe Lys Thr Leu Ala Val Arg Lys Asn Tyr Tyr Arg Pro Ser Gly Ala
 130 135 140

Asp Ala Tyr Thr Met Gln Arg Pro Arg Leu Ser Asp Arg Lys Asp Gln
 145 150 155 160

Gln Thr Asp Thr Glu Gly Thr Pro Ser
 165

<210> 147

<211> 1155

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA00502

<400> 147

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agatcaacag acagacacag aggggacacc cagctaaacc atg atc gtt ttg gga 115
 Met Ile Val Leu Gly
 1 5

att gaa agc tcc tgc gat gaa aca ggc gta ggc gta gtc aaa ctt gac 163
 Ile Glu Ser Ser Cys Asp Glu Thr Gly Val Gly Val Val Lys Leu Asp
 10 15 20

ggc gaa gga aac cta gag atc ctc gcc gac tca gtg gcc tcc tcc atg 211
 Gly Glu Gly Asn Leu Glu Ile Leu Ala Asp Ser Val Ala Ser Ser Met
 25 30 35

caa gaa cat gcc cgc ttt ggt ggc gtc gtg cca gaa atc gcc tcc cgg 259
 Gln Glu His Ala Arg Phe Gly Gly Val Val Pro Glu Ile Ala Ser Arg
 40 45 50

gcg cac ctg gaa tct atg gtc ccc gtg atg cgt gaa gcg ttg agg cag 307
 Ala His Leu Glu Ser Met Val Pro Val Met Arg Glu Ala Leu Arg Gln
 55 60 65

gcg ggc gtc gac agg cca gat gct gtg gct gca acc gtg ggc cct ggt 355
 Ala Gly Val Asp Arg Pro Asp Ala Val Ala Ala Thr Val Gly Pro Gly
 70 75 80 85

ttg gcg ggc gcg ctg ctc gtt gga gcc agc gct gcg aag gcg tat gcc 403
 Leu Ala Gly Ala Leu Leu Val Gly Ala Ser Ala Ala Lys Ala Tyr Ala
 90 95 100

gct gcg tgg gga gtt ccg ttt tac gcg gtc aac cac ctg ggc gga cac 451
 Ala Ala Trp Gly Val Pro Phe Tyr Ala Val Asn His Leu Gly Gly His
 105 110 115

gtc gcc gtg gcc aat ctg gaa ggt gaa act ctt cca cac gcg gtg gct Val Ala Val Ala Asn Leu Glu Gly Glu Thr Leu Pro His Ala Val Ala 120 125 130	499
ttg ctg gtt tcc ggc gga cac act caa ttg ttg gaa gtc gac gcg gtg Leu Leu Val Ser Gly Gly His Thr Gln Leu Leu Glu Val Asp Ala Val 135 140 145	547
gga tta ccc atg aag gaa ttg gga tcc acc ctc gac gat gcc gct ggc Gly Leu Pro Met Lys Glu Leu Gly Ser Thr Leu Asp Asp Ala Ala Gly 150 155 160 165	595
gaa gcc tat gac aaa gtc tca agg ctg ttg gga ttg ggc tac cca ggc Glu Ala Tyr Asp Lys Val Ser Arg Leu Leu Gly Leu Gly Tyr Pro Gly 170 175 180	643
ggc ccc atc att gat aaa ttg gcg cgc cgg ggt aat cca gag gcc att Gly Pro Ile Ile Asp Lys Leu Ala Arg Arg Gly Asn Pro Glu Ala Ile 185 190 195	691
gct ttc ccc cgc gga ttg atg aaa aag tgc gat tct cgg cat gat ttc Ala Phe Pro Arg Gly Leu Met Lys Lys Ser Asp Ser Arg His Asp Phe 200 205 210	739
agc ttt tcc ggt ttg aaa acc tcc gtt gcc cgc tac gtg gaa gct gcg Ser Phe Ser Gly Leu Lys Thr Ser Val Ala Arg Tyr Val Glu Ala Ala 215 220 225	787
gaa aga aac ggt gaa gtt att tcc gtg gag gac gtc tgc gca tca ttc Glu Arg Asn Gly Glu Val Ile Ser Val Glu Asp Val Cys Ala Ser Phe 230 235 240 245	835
caa gaa gcg gtg tgt gat gtg ttg acg ttt aag gcc gtg cgt gcg tgc Gln Glu Ala Val Cys Asp Val Leu Thr Phe Lys Ala Val Arg Ala Cys 250 255 260	883
cgc gat gtc ggt gcg aag gtg ctg ctg ttg ggt gga gga gtg gct gcc Arg Asp Val Gly Ala Lys Val Leu Leu Leu Gly Gly Gly Val Ala Ala 265 270 275	931
aac tct cgt ctg cgg gag ctt gct caa gaa cgt tgc gat aaa gcc gac Asn Ser Arg Leu Arg Glu Leu Ala Gln Glu Arg Cys Asp Lys Ala Asp 280 285 290	979
atc gaa ctc cgg gtt cct cgt ttc aat ttg tgc acc gat aat ggt gtc Ile Glu Leu Arg Val Pro Arg Phe Asn Leu Cys Thr Asp Asn Gly Val 295 300 305	1027
atg att gca gcg ttg gcg gct caa aga atc cac gaa ggt gcc caa gaa Met Ile Ala Ala Leu Ala Ala Gln Arg Ile His Glu Gly Ala Gln Glu 310 315 320 325	1075
tca cca att tcg gtc gga act gat cct tct ttg tcc gtt gag acc cca Ser Pro Ile Ser Val Gly Thr Asp Pro Ser Leu Ser Val Glu Thr Pro 330 335 340	1123
cag gtg ttt taaacattta gtattagttc cat Gln Val Phe	1155

<210> 148

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

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Met Ile Val Leu Gly Ile Glu Ser Ser Cys Asp Glu Thr Gly Val Gly
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Val Ala Ser Ser Met Gln Glu His Ala Arg Phe Gly Gly Val Val Pro
      35           40           45

Glu Ile Ala Ser Arg Ala His Leu Glu Ser Met Val Pro Val Met Arg
      50           55           60

Glu Ala Leu Arg Gln Ala Gly Val Asp Arg Pro Asp Ala Val Ala Ala
      65           70           75           80

Thr Val Gly Pro Gly Leu Ala Gly Ala Leu Leu Val Gly Ala Ser Ala
      85           90           95

Ala Lys Ala Tyr Ala Ala Ala Trp Gly Val Pro Phe Tyr Ala Val Asn
      100           105           110

His Leu Gly Gly His Val Ala Val Ala Asn Leu Glu Gly Glu Thr Leu
      115           120           125

Pro His Ala Val Ala Leu Leu Val Ser Gly Gly His Thr Gln Leu Leu
      130           135           140

Glu Val Asp Ala Val Gly Leu Pro Met Lys Glu Leu Gly Ser Thr Leu
      145           150           155           160

Asp Asp Ala Ala Gly Glu Ala Tyr Asp Lys Val Ser Arg Leu Leu Gly
      165           170           175

Leu Gly Tyr Pro Gly Gly Pro Ile Ile Asp Lys Leu Ala Arg Arg Gly
      180           185           190

Asn Pro Glu Ala Ile Ala Phe Pro Arg Gly Leu Met Lys Lys Ser Asp
      195           200           205

Ser Arg His Asp Phe Ser Phe Ser Gly Leu Lys Thr Ser Val Ala Arg
      210           215           220

Tyr Val Glu Ala Ala Glu Arg Asn Gly Glu Val Ile Ser Val Glu Asp
      225           230           235           240

Val Cys Ala Ser Phe Gln Glu Ala Val Cys Asp Val Leu Thr Phe Lys
      245           250           255

Ala Val Arg Ala Cys Arg Asp Val Gly Ala Lys Val Leu Leu Leu Gly
      260           265           270

Gly Gly Val Ala Ala Asn Ser Arg Leu Arg Glu Leu Ala Gln Glu Arg
      275           280           285

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Cys Asp Lys Ala Asp Ile Glu Leu Arg Val Pro Arg Phe Asn Leu Cys
 290 295 300

Thr Asp Asn Gly Val Met Ile Ala Ala Leu Ala Ala Gln Arg Ile His
 305 310 315 320

Glu Gly Ala Gln Glu Ser Pro Ile Ser Val Gly Thr Asp Pro Ser Leu
 325 330 335

Ser Val Glu Thr Pro Gln Val Phe
 340

<210> 149

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> RXN02589

<400> 149

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atattgaagt tttaaagttg aacaggaaaa ataacaaata atg tct att tct gat 115
 Met Ser Ile Ser Asp
 1 5

aat tcc cgc gat caa tta gga gaa ctg cca gct ggt cgg cct ctc caa 163
 Asn Ser Arg Asp Gln Leu Gly Glu Leu Pro Ala Gly Arg Pro Leu Gln
 10 15 20

tcc gat ttt gat aat gac ctc gac tac cca cgt cta ggc agt gtc acg 211
 Ser Asp Phe Asp Asn Asp Leu Asp Tyr Pro Arg Leu Gly Ser Val Thr
 25 30 35

ttt agg cgt ggc acc ctc act gaa aac cag caa acc atg tgg gat gaa 259
 Phe Arg Arg Gly Thr Leu Thr Glu Asn Gln Gln Thr Met Trp Asp Glu
 40 45 50

aag tgg cct gaa ctg ggt cgc gtc ctc gaa gat gag ctg att gat gtt 307
 Lys Trp Pro Glu Leu Gly Arg Val Leu Glu Asp Glu Leu Ile Asp Val
 55 60 65

gat gcg tgg ttc ggg cgc gaa ggc gca aaa acc atc gta gag atc ggc 355
 Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr Ile Val Glu Ile Gly
 70 75 80 85

tct ggc act gga act tcg act gct gcc atg gct cca ctt gag gct gat 403
 Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala Pro Leu Glu Ala Asp
 90 95 100

acc aac att gtc gcc gtc gaa cta tac aag ccg ggc ttg gcc aag ttg 451
 Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro Gly Leu Ala Lys Leu
 105 110 115

atg ggc tct gtt gtc cgt gga gag atc gac aac gtg cgc atg gtc cgc 499
 Met Gly Ser Val Val Arg Gly Glu Ile Asp Asn Val Arg Met Val Arg
 120 125 130

gga gac ggc atc gag gtg ctc aac cgc atg ttt gcc gat ggg tcc ctg 547
 Gly Asp Gly Ile Glu Val Leu Asn Arg Met Phe Ala Asp Gly Ser Leu
 135 140 145

 gac ggc atc cgc gta tac ttc ccg gac cct tgg cca aag gcg cgc cac 595
 Asp Gly Ile Arg Val Tyr Phe Pro Asp Pro Trp Pro Lys Ala Arg His
 150 155 160 165

 aac aag cgc cgc atc atc cag tct ggt ccg ctg aac ctg ttt gca aag 643
 Asn Lys Arg Arg Ile Ile Gln Ser Gly Pro Leu Asn Leu Phe Ala Lys
 170 175 180

 aag ctc aag cca ggt gga gtt ctg cac gtt gct acc gac cac gct gat 691
 Lys Leu Lys Pro Gly Gly Val Leu His Val Ala Thr Asp His Ala Asp
 185 190 195

 tac gca gag tgg atc aat gag cta gtt gag gtc gaa cca ctg ctt gag 739
 Tyr Ala Glu Trp Ile Asn Glu Leu Val Glu Val Glu Pro Leu Leu Glu
 200 205 210

 tac aaa ggc tgg cca tgg gag gaa tgc cct cag ctg act gac cgt cag 787
 Tyr Lys Gly Trp Pro Trp Glu Glu Cys Pro Gln Leu Thr Asp Arg Gln
 215 220 225

 gtc atc acc aag ttt gaa ggc aaa ggc ttg gaa aaa gat cac gtg atc 835
 Val Ile Thr Lys Phe Glu Gly Lys Gly Leu Glu Lys Asp His Val Ile
 230 235 240 245

 aat gag tac ttg tgg cag aag gtg caa aac taatgtctga tgtgcatgag 885
 Asn Glu Tyr Leu Trp Gln Lys Val Gln Asn
 250 255

 gtc 888

<210> 150
 <211> 255
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 150
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 Gly Arg Pro Leu Gln Ser Asp Phe Asp Asn Asp Leu Asp Tyr Pro Arg
 20 25 30

 Leu Gly Ser Val Thr Phe Arg Arg Gly Thr Leu Thr Glu Asn Gln Gln
 35 40 45

 Thr Met Trp Asp Glu Lys Trp Pro Glu Leu Gly Arg Val Leu Glu Asp
 50 55 60

 Glu Leu Ile Asp Val Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr
 65 70 75 80

 Ile Val Glu Ile Gly Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala
 85 90 95

 Pro Leu Glu Ala Asp Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro

100 105 110
 Gly Leu Ala Lys Leu Met Gly Ser Val Val Arg Gly Glu Ile Asp Asn
 115 120 125
 Val Arg Met Val Arg Gly Asp Gly Ile Glu Val Leu Asn Arg Met Phe
 130 135 140
 Ala Asp Gly Ser Leu Asp Gly Ile Arg Val Tyr Phe Pro Asp Pro Trp
 145 150 155 160
 Pro Lys Ala Arg His Asn Lys Arg Arg Ile Ile Gln Ser Gly Pro Leu
 165 170 175
 Asn Leu Phe Ala Lys Lys Leu Lys Pro Gly Gly Val Leu His Val Ala
 180 185 190
 Thr Asp His Ala Asp Tyr Ala Glu Trp Ile Asn Glu Leu Val Glu Val
 195 200 205
 Glu Pro Leu Leu Glu Tyr Lys Gly Trp Pro Trp Glu Glu Cys Pro Gln
 210 215 220
 Leu Thr Asp Arg Gln Val Ile Thr Lys Phe Glu Gly Lys Gly Leu Glu
 225 230 235 240
 Lys Asp His Val Ile Asn Glu Tyr Leu Trp Gln Lys Val Gln Asn
 245 250 255

 <210> 151
 <211> 888
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(865)
 <223> FRXA02589

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 atattgaagt tttaaagttg aacaggaaaa ataacaaata atg tct att tct gat 115
 Met Ser Ile Ser Asp
 1 5

 aat tcc cgc gat caa tta gga gaa ctg cca gct ggt cgg cct ctc caa 163
 Asn Ser Arg Asp Gln Leu Gly Glu Leu Pro Ala Gly Arg Pro Leu Gln
 10 15 20

 tcc gat ttt gat aat gac ctc gac tac cca cgt cta ggc agt gtc acg 211
 Ser Asp Phe Asp Asn Asp Leu Asp Tyr Pro Arg Leu Gly Ser Val Thr
 25 30 35

 ttt agg cgt ggc acc ctc act gaa aac cag caa acc atg tgg gat gaa 259
 Phe Arg Arg Gly Thr Leu Thr Glu Asn Gln Gln Thr Met Trp Asp Glu
 40 45 50

 aag tgg cct gaa ctg ggt cgc gtc ctc gaa gat gag ctg att gat gtt 307
 Lys Trp Pro Glu Leu Gly Arg Val Leu Glu Asp Glu Leu Ile Asp Val

55	60	65	
gat gcg tgg ttc ggg cgc gaa ggc gca aaa acc atc gta gag atc ggc			355
Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr Ile Val Glu Ile Gly			
70	75	80	85
tct ggc act gga act tcg act gct gcc atg gct cca ctt gag gct gat			403
Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala Pro Leu Glu Ala Asp			
	90	95	100
acc aac att gtc gcc gtc gaa cta tac aag ccg ggc ttg gcc aag ttg			451
Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro Gly Leu Ala Lys Leu			
	105	110	115
atg ggc tct gtt gtc cgt gga gag atc gac aac gtg cgc atg gtc cgc			499
Met Gly Ser Val Val Arg Gly Glu Ile Asp Asn Val Arg Met Val Arg			
	120	125	130
gga gac ggc atc gag gtg ctc aac cgc atg ttt gcc gat ggg tcc ctg			547
Gly Asp Gly Ile Glu Val Leu Asn Arg Met Phe Ala Asp Gly Ser Leu			
	135	140	145
gac ggc atc cgc gta tac ttc ccg gac cct tgg cca aag gcg cgc cac			595
Asp Gly Ile Arg Val Tyr Phe Pro Asp Pro Trp Pro Lys Ala Arg His			
	150	155	160
aac aag cgc cgc atc atc cag tct ggt ccg ctg aac ctg ttt gca aag			643
Asn Lys Arg Arg Ile Ile Gln Ser Gly Pro Leu Asn Leu Phe Ala Lys			
	170	175	180
aag ctc aag cca ggt gga gtt ctg cac gtt gct acc gac cac gct gat			691
Lys Leu Lys Pro Gly Gly Val Leu His Val Ala Thr Asp His Ala Asp			
	185	190	195
tac gca gag tgg atc aat gag cta gtt gag gtc gaa cca ctg ctt gag			739
Tyr Ala Glu Trp Ile Asn Glu Leu Val Glu Val Glu Pro Leu Leu Glu			
	200	205	210
tac aaa ggc tgg cca tgg gag gaa tgc cct cag ctg act gac cgt cag			787
Tyr Lys Gly Trp Pro Trp Glu Glu Cys Pro Gln Leu Thr Asp Arg Gln			
	215	220	225
gtc atc acc aag ttt gaa ggc aaa ggc ttg gaa aaa gat cac gtg atc			835
Val Ile Thr Lys Phe Glu Gly Lys Gly Leu Glu Lys Asp His Val Ile			
	230	235	240
aat gag tac ttg tgg cag aag gtg caa aac taatgtctga tgtgcatgag			885
Asn Glu Tyr Leu Trp Gln Lys Val Gln Asn			
	250	255	
gtc			888

<210> 152

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Met	Ser	Ile	Ser	Asp	Asn	Ser	Arg	Asp	Gln	Leu	Gly	Glu	Leu	Pro	Ala
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Gly Arg Pro Leu Gln Ser Asp Phe Asp Asn Asp Leu Asp Tyr Pro Arg
 20 25 30
 Leu Gly Ser Val Thr Phe Arg Arg Gly Thr Leu Thr Glu Asn Gln Gln
 35 40 45
 Thr Met Trp Asp Glu Lys Trp Pro Glu Leu Gly Arg Val Leu Glu Asp
 50 55 60
 Glu Leu Ile Asp Val Asp Ala Trp Phe Gly Arg Glu Gly Ala Lys Thr
 65 70 75 80
 Ile Val Glu Ile Gly Ser Gly Thr Gly Thr Ser Thr Ala Ala Met Ala
 85 90 95
 Pro Leu Glu Ala Asp Thr Asn Ile Val Ala Val Glu Leu Tyr Lys Pro
 100 105 110
 Gly Leu Ala Lys Leu Met Gly Ser Val Val Arg Gly Glu Ile Asp Asn
 115 120 125
 Val Arg Met Val Arg Gly Asp Gly Ile Glu Val Leu Asn Arg Met Phe
 130 135 140
 Ala Asp Gly Ser Leu Asp Gly Ile Arg Val Tyr Phe Pro Asp Pro Trp
 145 150 155 160
 Pro Lys Ala Arg His Asn Lys Arg Arg Ile Ile Gln Ser Gly Pro Leu
 165 170 175
 Asn Leu Phe Ala Lys Lys Leu Lys Pro Gly Gly Val Leu His Val Ala
 180 185 190
 Thr Asp His Ala Asp Tyr Ala Glu Trp Ile Asn Glu Leu Val Glu Val
 195 200 205
 Glu Pro Leu Leu Glu Tyr Lys Gly Trp Pro Trp Glu Glu Cys Pro Gln
 210 215 220
 Leu Thr Asp Arg Gln Val Ile Thr Lys Phe Glu Gly Lys Gly Leu Glu
 225 230 235 240
 Lys Asp His Val Ile Asn Glu Tyr Leu Trp Gln Lys Val Gln Asn
 245 250 255

<210> 153

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> RXA00226

<400> 153

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attgttcattg atgtcacctg ttccatcggt acggaggggc atg aac tta tcg atg 115

															Met 1	Asn	Leu	Ser	Met 5	
ccg gcc ttc gct acc tgg gtt ctg atc cta gat ttc tca cgc acc ctc	Pro	Ala	Phe	Ala	Thr	Trp	Val	Leu	Ile	Leu	Asp	Phe	Ser	Arg	Thr	Leu				163
				10					15					20						
atg gca gcc cac aat ctc cag ggc aaa aac gcc ctg att ttc cgc gcc	Met	Ala	Ala	His	Asn	Leu	Gln	Gly	Lys	Asn	Ala	Leu	Ile	Phe	Arg	Ala				211
				25					30					35						
gac gcg ctc cag ccc gca agc agg gga gcc gac gtc atc atc gcg gac	Asp	Ala	Leu	Gln	Pro	Ala	Ser	Arg	Gly	Ala	Asp	Val	Ile	Ile	Ala	Asp				259
				40					45					50						
cct gcc aga cgc gcc ggg ggc aag cgc att aca aat ccg gca cag ctc	Pro	Ala	Arg	Arg	Ala	Gly	Gly	Lys	Arg	Ile	Thr	Asn	Pro	Ala	Gln	Leu				307
				55					60					65						
ctg cca cct ctg cct tcg ctt ctc gac gcc tgg atc aac caa cca ctc	Leu	Pro	Pro	Leu	Pro	Ser	Leu	Leu	Asp	Ala	Trp	Ile	Asn	Gln	Pro	Leu				355
				70					75					80					85	
gcc gtt aaa tgt gcc ccc ggc ctt gat ttt tcg gaa tgg cca ggt ctc	Ala	Val	Lys	Cys	Ala	Pro	Gly	Leu	Asp	Phe	Ser	Glu	Trp	Pro	Gly	Leu				403
				90					95					100						
gtc agt att gcc agc gtt gat gga ggc gtg aaa gaa gca tgc ctc tac	Val	Ser	Ile	Ala	Ser	Val	Asp	Gly	Gly	Val	Lys	Glu	Ala	Cys	Leu	Tyr				451
				105					110					115						
act acg gat ctg gca gat ggg gaa act cgc gaa gct atc gtg atc aaa	Thr	Thr	Asp	Leu	Ala	Asp	Gly	Glu	Thr	Arg	Glu	Ala	Ile	Val	Ile	Lys				499
				120					125					130						
gat ggg ctc att gac cgc atc acc aac ttt gaa gac gat gcc acg gga	Asp	Gly	Leu	Ile	Asp	Arg	Ile	Thr	Asn	Phe	Glu	Asp	Asp	Ala	Thr	Gly				547
				135					140					145						
caa gac ctt gcg gct gca cct ggt gag ttc atc atc gac cca gac ggt	Gln	Asp	Leu	Ala	Ala	Ala	Pro	Gly	Glu	Phe	Ile	Ile	Asp	Pro	Asp	Gly				595
				150					155					160					165	
gcc atc gtg cgc gcc ggg ttg gtt cgc cac tat gca gtg cgt gag cag	Ala	Ile	Val	Arg	Ala	Gly	Leu	Val	Arg	His	Tyr	Ala	Val	Arg	Glu	Gln				643
				170					175					180						
ctg tgg atg ttg gat gag cgg atc gca tac ctt acg ggc aat cgg att	Leu	Trp	Met	Leu	Asp	Glu	Arg	Ile	Ala	Tyr	Leu	Thr	Gly	Asn	Arg	Ile				691
				185					190					195						
cca gag ggt acc agc ggt ttt agg ttt att gaa gag gtt ccg ctg aag	Pro	Glu	Gly	Thr	Ser	Gly	Phe	Arg	Phe	Ile	Glu	Glu	Val	Pro	Leu	Lys				739
				200					205					210						
aag ctg aaa tcg gcg atg gca gca cat gat gcg ggg gcg gtt gaa att	Lys	Leu	Lys	Ser	Ala	Met	Ala	Ala	His	Asp	Ala	Gly	Ala	Val	Glu	Ile				787
				215					220					225						
tta gtg cgt ggt gtt gat gtt gat cct gat cag ttg cgg aaa aga ttg	Leu	Val	Arg	Gly	Val	Asp	Val	Asp	Pro	Asp	Gln	Leu	Arg	Lys	Arg	Leu				835

230	235	240	245	
cag ctg aag ggt acc aag gcg atg tct gtg gtg atc act cga att ggc				883
Gln Leu Lys Gly Thr Lys Ala Met Ser Val Val Ile Thr Arg Ile Gly				
	250	255	260	
agc cga ggg gtt gca ttg att tgt ggt cct cgc gag cgc gcc				925
Ser Arg Gly Val Ala Leu Ile Cys Gly Pro Arg Glu Arg Ala				
	265	270	275	
taaagccgat gcaaataaaa ttg				948

<210> 154
 <211> 275
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 154
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 Phe Ser Arg Thr Leu Met Ala Ala His Asn Leu Gln Gly Lys Asn Ala
 20 25 30
 Leu Ile Phe Arg Ala Asp Ala Leu Gln Pro Ala Ser Arg Gly Ala Asp
 35 40 45
 Val Ile Ile Ala Asp Pro Ala Arg Arg Ala Gly Gly Lys Arg Ile Thr
 50 55 60
 Asn Pro Ala Gln Leu Leu Pro Pro Leu Pro Ser Leu Leu Asp Ala Trp
 65 70 75 80
 Ile Asn Gln Pro Leu Ala Val Lys Cys Ala Pro Gly Leu Asp Phe Ser
 85 90 95
 Glu Trp Pro Gly Leu Val Ser Ile Ala Ser Val Asp Gly Gly Val Lys
 100 105 110
 Glu Ala Cys Leu Tyr Thr Thr Asp Leu Ala Asp Gly Glu Thr Arg Glu
 115 120 125
 Ala Ile Val Ile Lys Asp Gly Leu Ile Asp Arg Ile Thr Asn Phe Glu
 130 135 140
 Asp Asp Ala Thr Gly Gln Asp Leu Ala Ala Ala Pro Gly Glu Phe Ile
 145 150 155 160
 Ile Asp Pro Asp Gly Ala Ile Val Arg Ala Gly Leu Val Arg His Tyr
 165 170 175
 Ala Val Arg Glu Gln Leu Trp Met Leu Asp Glu Arg Ile Ala Tyr Leu
 180 185 190
 Thr Gly Asn Arg Ile Pro Glu Gly Thr Ser Gly Phe Arg Phe Ile Glu
 195 200 205
 Glu Val Pro Leu Lys Lys Leu Lys Ser Ala Met Ala Ala His Asp Ala
 210 215 220

Gly Ala Val Glu Ile Leu Val Arg Gly Val Asp Val Asp Pro Asp Gln
225 230 235 240

Leu Arg Lys Arg Leu Gln Leu Lys Gly Thr Lys Ala Met Ser Val Val
245 250 255

Ile Thr Arg Ile Gly Ser Arg Gly Val Ala Leu Ile Cys Gly Pro Arg
260 265 270

Glu Arg Ala
275

<210> 155

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXN01885

<400> 155

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acacggattt ttctaagggtt aatcaagtaa ggtttacctt atg act acg aaa cct 115
Met Thr Thr Lys Pro
1 5

atc atc cca gaa tca acc cac tcc gca gaa cgt gct ggt gga cat tgg 163
Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg Ala Gly Gly His Trp
10 15 20

atc ctt gcc agg ctt gga aag aaa gtg ctg cgc cct gga ggt cgt gaa 211
Ile Leu Ala Arg Leu Gly Lys Lys Val Leu Arg Pro Gly Gly Arg Glu
25 30 35

aca acg cag ttc ctg ctg gag aac ctt tct ttg acc ggt gct acc gtg 259
Thr Thr Gln Phe Leu Leu Glu Asn Leu Ser Leu Thr Gly Ala Thr Val
40 45 50

gtg gaa ttt gct cca gga ctt ggc gtg act gca cgt gac atc ctt ggc 307
Val Glu Phe Ala Pro Gly Leu Gly Val Thr Ala Arg Asp Ile Leu Gly
55 60 65

aag ggt ccg gct cgc tac atc gga gtg gat agc gac gcg gat gca tgc 355
Lys Gly Pro Ala Arg Tyr Ile Gly Val Asp Ser Asp Ala Asp Ala Cys
70 75 80 85

gcg aat gta cgt gcg atc tta cct gct ggt cct cac gag gtg cgc aat 403
Ala Asn Val Arg Ala Ile Leu Pro Ala Gly Pro His Glu Val Arg Asn
90 95 100

aca aat gcc acc gat act ggc ctt gaa agc gac tcg ttt gat gtt gtc 451
Thr Asn Ala Thr Asp Thr Gly Leu Glu Ser Asp Ser Phe Asp Val Val
105 110 115

atc ggc gaa gcg atg ttg acc atg cag acc gat aag cac aag ttg gag 499
Ile Gly Glu Ala Met Leu Thr Met Gln Thr Asp Lys His Lys Leu Glu
120 125 130

ctg atg cgc gag gca gct cga att ctg aaa cca ggc ggg ctg tac ggc 547
 Leu Met Arg Glu Ala Ala Arg Ile Leu Lys Pro Gly Gly Leu Tyr Gly
 135 140 145
 att cac gag ctg tcg ctg gtg cct gac aat gtc tcc act gcg gtg aaa 595
 Ile His Glu Leu Ser Leu Val Pro Asp Asn Val Ser Thr Ala Val Lys
 150 155 160 165
 gag gat att gct aag gcg ctg gct cgt tcc atc aaa gtc aat gcc cgc 643
 Glu Asp Ile Ala Lys Ala Leu Ala Arg Ser Ile Lys Val Asn Ala Arg
 170 175 180
 ccc atc acg gtg ccg gaa tgg gct gcg ttg gcg cgt gag gca ggg ttc 691
 Pro Ile Thr Val Pro Glu Trp Ala Ala Leu Ala Arg Glu Ala Gly Phe
 185 190 195
 gat gtg att aat att cgc caa gcc gac atg gcc ctt cta tcc ctc aag 739
 Asp Val Ile Asn Ile Arg Gln Ala Asp Met Ala Leu Leu Ser Leu Lys
 200 205 210
 cgg aac ctg aag gat gaa ggg cta aaa ggt gtc ttc acg att gtg agg 787
 Arg Asn Leu Lys Asp Glu Gly Leu Lys Gly Val Phe Thr Ile Val Arg
 215 220 225
 aac gtg att agc caa ccg gat ctg cgc aag cga gtg ctc gga atg cga 835
 Asn Val Ile Ser Gln Pro Asp Leu Arg Lys Arg Val Leu Gly Met Arg
 230 235 240 245
 aag act ttc acc gag cat aaa gat cac tta ggt gcg gtt ggc atc att 883
 Lys Thr Phe Thr Glu His Lys Asp His Leu Gly Ala Val Gly Ile Ile
 250 255 260
 ttg cag aag aga gcc caa tagggatctg aaatggaggg gtg 924
 Leu Gln Lys Arg Ala Gln
 265

<210> 156
 <211> 267
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 156
 Met Thr Thr Lys Pro Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg
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 Pro Gly Gly Arg Glu Thr Thr Gln Phe Leu Leu Glu Asn Leu Ser Leu
 35 40 45
 Thr Gly Ala Thr Val Val Glu Phe Ala Pro Gly Leu Gly Val Thr Ala
 50 55 60
 Arg Asp Ile Leu Gly Lys Gly Pro Ala Arg Tyr Ile Gly Val Asp Ser
 65 70 75 80
 Asp Ala Asp Ala Cys Ala Asn Val Arg Ala Ile Leu Pro Ala Gly Pro
 85 90 95

His Glu Val Arg Asn Thr Asn Ala Thr Asp Thr Gly Leu Glu Ser Asp
 100 105 110
 Ser Phe Asp Val Val Ile Gly Glu Ala Met Leu Thr Met Gln Thr Asp
 115 120 125
 Lys His Lys Leu Glu Leu Met Arg Glu Ala Ala Arg Ile Leu Lys Pro
 130 135 140
 Gly Gly Leu Tyr Gly Ile His Glu Leu Ser Leu Val Pro Asp Asn Val
 145 150 155 160
 Ser Thr Ala Val Lys Glu Asp Ile Ala Lys Ala Leu Ala Arg Ser Ile
 165 170 175
 Lys Val Asn Ala Arg Pro Ile Thr Val Pro Glu Trp Ala Ala Leu Ala
 180 185 190
 Arg Glu Ala Gly Phe Asp Val Ile Asn Ile Arg Gln Ala Asp Met Ala
 195 200 205
 Leu Leu Ser Leu Lys Arg Asn Leu Lys Asp Glu Gly Leu Lys Gly Val
 210 215 220
 Phe Thr Ile Val Arg Asn Val Ile Ser Gln Pro Asp Leu Arg Lys Arg
 225 230 235 240
 Val Leu Gly Met Arg Lys Thr Phe Thr Glu His Lys Asp His Leu Gly
 245 250 255
 Ala Val Gly Ile Ile Leu Gln Lys Arg Ala Gln
 260 265

<210> 157

<211> 924

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(901)

<223> FRXA01885

<400> 157

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acacggattt ttctaagggtt aatcaagtaa ggtttacctt atg act acg aaa cct 115
 Met Thr Thr Lys Pro
 1 5

atc atc cca gaa tca acc cac tcc gca gaa cgt gct ggt gga cat tgg 163
 Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg Ala Gly Gly His Trp
 10 15 20

atc ctt gcc agg ctt gga aag aaa gtg ctg cgc cct gga ggt cgt gaa 211
 Ile Leu Ala Arg Leu Gly Lys Lys Val Leu Arg Pro Gly Gly Arg Glu
 25 30 35

aca acg cag ttc ctg ctg gag aac ctt tct ttg acc ggt gct acc gtg 259

Thr	Thr	Gln	Phe	Leu	Leu	Glu	Asn	Leu	Ser	Leu	Thr	Gly	Ala	Thr	Val	
		40					45					50				
gtg	gaa	ttt	gct	cca	gga	ctt	ggc	gtg	act	gca	cgt	gac	atc	ctt	ggc	307
Val	Glu	Phe	Ala	Pro	Gly	Leu	Gly	Val	Thr	Ala	Arg	Asp	Ile	Leu	Gly	
	55					60					65					
aag	ggt	ccg	gct	cgc	tac	atc	gga	gtg	gat	agc	gac	gcg	gat	gca	tgc	355
Lys	Gly	Pro	Ala	Arg	Tyr	Ile	Gly	Val	Asp	Ser	Asp	Ala	Asp	Ala	Cys	
	70				75				80						85	
gcg	aat	gta	cgt	gcg	atc	tta	cct	gct	ggg	cct	cac	gag	gtg	cgc	aat	403
Ala	Asn	Val	Arg	Ala	Ile	Leu	Pro	Ala	Gly	Pro	His	Glu	Val	Arg	Asn	
				90					95					100		
aca	aat	gcc	acc	gat	act	ggc	ctt	gaa	agc	gac	tcg	ttt	gat	gtt	gtc	451
Thr	Asn	Ala	Thr	Asp	Thr	Gly	Leu	Glu	Ser	Asp	Ser	Phe	Asp	Val	Val	
		105						110					115			
atc	ggc	gaa	gcg	atg	ttg	acc	atg	cag	acc	gat	aag	cac	aag	ttg	gag	499
Ile	Gly	Glu	Ala	Met	Leu	Thr	Met	Gln	Thr	Asp	Lys	His	Lys	Leu	Glu	
	120						125					130				
ctg	atg	cgc	gag	gca	gct	cga	att	ctg	aaa	cca	ggc	ggg	ctg	tac	ggc	547
Leu	Met	Arg	Glu	Ala	Ala	Arg	Ile	Leu	Lys	Pro	Gly	Gly	Leu	Tyr	Gly	
	135					140					145					
att	cac	gag	ctg	tcg	ctg	gtg	cct	gac	aat	gtc	tcc	act	gcg	gtg	aaa	595
Ile	His	Glu	Leu	Ser	Leu	Val	Pro	Asp	Asn	Val	Ser	Thr	Ala	Val	Lys	
	150				155				160						165	
gag	gat	att	gct	aag	gcg	ctg	gct	cgt	tcc	atc	aaa	gtc	aat	gcc	cgc	643
Glu	Asp	Ile	Ala	Lys	Ala	Leu	Ala	Arg	Ser	Ile	Lys	Val	Asn	Ala	Arg	
				170				175						180		
ccc	atc	acg	gtg	ccg	gaa	tgg	gct	gcg	ttg	gcg	cgt	gag	gca	ggg	ttc	691
Pro	Ile	Thr	Val	Pro	Glu	Trp	Ala	Ala	Leu	Ala	Arg	Glu	Ala	Gly	Phe	
			185					190					195			
gat	gtg	att	aat	att	cgc	caa	gcc	gac	atg	gcc	ctt	cta	tcc	ctc	aag	739
Asp	Val	Ile	Asn	Ile	Arg	Gln	Ala	Asp	Met	Ala	Leu	Leu	Ser	Leu	Lys	
	200						205					210				
cgg	aac	ctg	aag	gat	gaa	ggg	cta	aaa	ggg	gtc	ttc	acg	att	gtg	agg	787
Arg	Asn	Leu	Lys	Asp	Glu	Gly	Leu	Lys	Gly	Val	Phe	Thr	Ile	Val	Arg	
	215					220				225						
aac	gtg	att	agc	caa	ccg	gat	ctg	cgc	aag	cga	gtg	ctc	gga	atg	cga	835
Asn	Val	Ile	Ser	Gln	Pro	Asp	Leu	Arg	Lys	Arg	Val	Leu	Gly	Met	Arg	
	230				235				240					245		
aag	act	ttc	acc	gag	cat	aaa	gat	cac	tta	ggg	gcg	gtt	ggc	atc	att	883
Lys	Thr	Phe	Thr	Glu	His	Lys	Asp	His	Leu	Gly	Ala	Val	Gly	Ile	Ile	
				250				255						260		
ttg	cag	aag	aga	gcc	caa	tagggatctg	aaatggaggg	gtg								924
Leu	Gln	Lys	Arg	Ala	Gln											
				265												

<210> 158

<211> 267

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 158

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Met Thr Thr Lys Pro Ile Ile Pro Glu Ser Thr His Ser Ala Glu Arg
 1             5             10             15

Ala Gly Gly His Trp Ile Leu Ala Arg Leu Gly Lys Lys Val Leu Arg
      20             25             30

Pro Gly Gly Arg Glu Thr Thr Gln Phe Leu Leu Glu Asn Leu Ser Leu
      35             40             45

Thr Gly Ala Thr Val Val Glu Phe Ala Pro Gly Leu Gly Val Thr Ala
 50             55             60

Arg Asp Ile Leu Gly Lys Gly Pro Ala Arg Tyr Ile Gly Val Asp Ser
 65             70             75             80

Asp Ala Asp Ala Cys Ala Asn Val Arg Ala Ile Leu Pro Ala Gly Pro
      85             90             95

His Glu Val Arg Asn Thr Asn Ala Thr Asp Thr Gly Leu Glu Ser Asp
      100            105            110

Ser Phe Asp Val Val Ile Gly Glu Ala Met Leu Thr Met Gln Thr Asp
      115            120            125

Lys His Lys Leu Glu Leu Met Arg Glu Ala Ala Arg Ile Leu Lys Pro
      130            135            140

Gly Gly Leu Tyr Gly Ile His Glu Leu Ser Leu Val Pro Asp Asn Val
      145            150            155            160

Ser Thr Ala Val Lys Glu Asp Ile Ala Lys Ala Leu Ala Arg Ser Ile
      165            170            175

Lys Val Asn Ala Arg Pro Ile Thr Val Pro Glu Trp Ala Ala Leu Ala
      180            185            190

Arg Glu Ala Gly Phe Asp Val Ile Asn Ile Arg Gln Ala Asp Met Ala
      195            200            205

Leu Leu Ser Leu Lys Arg Asn Leu Lys Asp Glu Gly Leu Lys Gly Val
      210            215            220

Phe Thr Ile Val Arg Asn Val Ile Ser Gln Pro Asp Leu Arg Lys Arg
      225            230            235            240

Val Leu Gly Met Arg Lys Thr Phe Thr Glu His Lys Asp His Leu Gly
      245            250            255

Ala Val Gly Ile Ile Leu Gln Lys Arg Ala Gln
      260            265

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<210> 159

<211> 894

<212> DNA

<213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(871)
 <223> RXA02592

<400> 159

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aaacaccacc attgtttcct ccatcgacga tgccatcacc accattttgc gatggatgaa 60

cggcgaagac atccgcgacc tcaactggac ccgcgcataa atg gcc tca ttt ccg    115
                                   Met Ala Ser Phe Pro
                                   1          5

gag ctt ccg gct ctt cgt cgc ttg gct acc ttg ggc agg tcg tgg ggt    163
Glu Leu Pro Ala Leu Arg Arg Leu Ala Thr Leu Gly Arg Ser Trp Gly
              10              15              20

tta ctg tct gat ttc aaa tac gaa caa acc cga cct gac atc ttt tac    211
Leu Leu Ser Asp Phe Lys Tyr Glu Gln Thr Arg Pro Asp Ile Phe Tyr
              25              30              35

gga aac ctg gcc ctc gat acc tcg agt ctg gtg gcg gct ttg tct gaa    259
Gly Asn Leu Ala Leu Asp Thr Ser Ser Leu Val Ala Ala Leu Ser Glu
              40              45              50

gat att tct ggc gcc gga tta aat gac ctg aaa gtt ctc gac gtc ggc    307
Asp Ile Ser Gly Ala Gly Leu Asn Asp Leu Lys Val Leu Asp Val Gly
              55              60              65

ggc gga ccc gga tac ttc gcc gaa gcc ttt gag aca ctg ggc gcc acc    355
Gly Gly Pro Gly Tyr Phe Ala Glu Ala Phe Glu Thr Leu Gly Ala Thr
              70              75              80              85

tac ttc tcc gtc gaa ccc gac gtt ggc gaa atg tcc gca gct ggc atc    403
Tyr Phe Ser Val Glu Pro Asp Val Gly Glu Met Ser Ala Ala Gly Ile
              90              95              100

gac gtc cac gga tca gtc cgc gga tcc ggc ctc gac ctg ccg ttt ctt    451
Asp Val His Gly Ser Val Arg Gly Ser Gly Leu Asp Leu Pro Phe Leu
              105              110              115

ccc gat tcc ttt gac gtg gtg tac tcc tcc aac gtt gca gaa cat gtc    499
Pro Asp Ser Phe Asp Val Val Tyr Ser Ser Asn Val Ala Glu His Val
              120              125              130

tcc gca ccg tgg gaa ttg gga gaa gaa atg ctc cgc gtc acc cgc agc    547
Ser Ala Pro Trp Glu Leu Gly Glu Glu Met Leu Arg Val Thr Arg Ser
              135              140              145

ggc ggc ctg gca atc ctg agc tac acc att tgg tta ggg ccc ttc ggc    595
Gly Gly Leu Ala Ile Leu Ser Tyr Thr Ile Trp Leu Gly Pro Phe Gly
              150              155              160              165

ggc cat gaa acc gga ctg tgg gaa cac tac gtt ggc gga gaa ttt gcc    643
Gly His Glu Thr Gly Leu Trp Glu His Tyr Val Gly Gly Glu Phe Ala
              170              175              180

cgc gat cgc tac acg aag aaa cac ggg cac ccg cct aag aac gtt ttc    691
Arg Asp Arg Tyr Thr Lys Lys His Gly His Pro Pro Lys Asn Val Phe
              185              190              195

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ggg gag tca ctg ttt aat gtg tcc tgc cgg gag ggg ctg gaa tgg gga 739
 Gly Glu Ser Leu Phe Asn Val Ser Cys Arg Glu Gly Leu Glu Trp Gly
 200 205 210

gcc tcc gtg ggc aat gcg gaa ttg gtt gcc gct ttt ccc cgc tac cac 787
 Ala Ser Val Gly Asn Ala Glu Leu Val Ala Ala Phe Pro Arg Tyr His
 215 220 225

ccg tat tgg gtc tgg tgg atg gtt aaa gtc cca gtg ctc cga gaa ttc 835
 Pro Tyr Trp Val Trp Trp Met Val Lys Val Pro Val Leu Arg Glu Phe
 230 235 240 245

gcg gta agt aac ttg gtg ttg gtg ttt aaa aag cac tgaggttttg 881
 Ala Val Ser Asn Leu Val Leu Val Phe Lys Lys His
 250 255

aggaattcat cgc 894

<210> 160

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Ala Ser Phe Pro Glu Leu Pro Ala Leu Arg Arg Leu Ala Thr Leu
 1 5 10 15

Gly Arg Ser Trp Gly Leu Leu Ser Asp Phe Lys Tyr Glu Gln Thr Arg
 20 25 30

Pro Asp Ile Phe Tyr Gly Asn Leu Ala Leu Asp Thr Ser Ser Leu Val
 35 40 45

Ala Ala Leu Ser Glu Asp Ile Ser Gly Ala Gly Leu Asn Asp Leu Lys
 50 55 60

Val Leu Asp Val Gly Gly Gly Pro Gly Tyr Phe Ala Glu Ala Phe Glu
 65 70 75 80

Thr Leu Gly Ala Thr Tyr Phe Ser Val Glu Pro Asp Val Gly Glu Met
 85 90 95

Ser Ala Ala Gly Ile Asp Val His Gly Ser Val Arg Gly Ser Gly Leu
 100 105 110

Asp Leu Pro Phe Leu Pro Asp Ser Phe Asp Val Val Tyr Ser Ser Asn
 115 120 125

Val Ala Glu His Val Ser Ala Pro Trp Glu Leu Gly Glu Glu Met Leu
 130 135 140

Arg Val Thr Arg Ser Gly Gly Leu Ala Ile Leu Ser Tyr Thr Ile Trp
 145 150 155 160

Leu Gly Pro Phe Gly Gly His Glu Thr Gly Leu Trp Glu His Tyr Val
 165 170 175

Gly Gly Glu Phe Ala Arg Asp Arg Tyr Thr Lys Lys His Gly His Pro
 180 185 190

Pro Lys Asn Val Phe Gly Glu Ser Leu Phe Asn Val Ser Cys Arg Glu
 195 200 205

Gly Leu Glu Trp Gly Ala Ser Val Gly Asn Ala Glu Leu Val Ala Ala
 210 215 220

Phe Pro Arg Tyr His Pro Tyr Trp Val Trp Trp Met Val Lys Val Pro
 225 230 235 240

Val Leu Arg Glu Phe Ala Val Ser Asn Leu Val Leu Val Phe Lys Lys
 245 250 255

His

<210> 161

<211> 720

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(697)

<223> RXN01795

<400> 161

agaccatatt gaagacctcg aagctgttga gcctggctac atcgtcaagc ctcgcctgta 60

caacttcgct gaatacgggtg tcccacaatt ccgcgaacgt gtg ctc att gtt ggc 115
 Val Leu Ile Val Gly
 1 5

att cgc cgt gac acc ggc ttt gat ttc aag cac cca gct cct acc cat 163
 Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His Pro Ala Pro Thr His
 10 15 20

ggc cct cgc ggt gac atg ccg tat aag act gcc ggc gaa gcg ctc aaa 211
 Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala Gly Glu Ala Leu Lys
 25 30 35

ggc gtg aag gat gtc ccc aca aac aac aac cac atg aag atc atg cct 259
 Gly Val Lys Asp Val Pro Thr Asn Asn Asn His Met Lys Ile Met Pro
 40 45 50

cgc acc gtt gaa gtg ctt aag cgc atc cct gag ggc gaa aac ttc acc 307
 Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu Gly Glu Asn Phe Thr
 55 60 65

gcg atc ccc aaa gat gac ccc tac tac gtc aag ggc atg att agt cac 355
 Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys Gly Met Ile Ser His
 70 75 80 85

gtt tac cgt cgc ttg cac cgt gat gag cca tcc aaa acc ctt atc gcc 403
 Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser Lys Thr Leu Ile Ala
 90 95 100

ggt ggc ggc ggg ggt aca tgg gga tac cat tat gaa aaa aat cga gca 451
 Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr Glu Lys Asn Arg Ala
 105 110 115

ttg acc aac cgc gag cgg gct aga att caa tcg ttc ccc gat gac ttt 499
 Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser Phe Pro Asp Asp Phe
 120 125 130
 gag ttt ttg gga tca aac acc gaa gtc cgc cgc caa atc ggt aat gct 547
 Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg Gln Ile Gly Asn Ala
 135 140 145
 gtt cct cct gta ggt atg cac gct gtg ggt gag cga ctg atg aac ctg 595
 Val Pro Pro Val Gly Met His Ala Val Gly Glu Arg Leu Met Asn Leu
 150 155 160 165
 tac acc ggg aat tac act ccc gtc gat cta gag gaa cag cac gcg tac 643
 Tyr Thr Gly Asn Tyr Thr Pro Val Asp Leu Glu Glu Gln His Ala Tyr
 170 175 180
 ctg cag acg ctc tcc att aag gaa cgt ctc gcg ctg gct gat cag gaa 691
 Leu Gln Thr Leu Ser Ile Lys Glu Arg Leu Ala Leu Ala Asp Gln Glu
 185 190 195
 gct gat taagtagata tatgaagccc acc 720
 Ala Asp

<210> 162

<211> 199

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

Val Leu Ile Val Gly Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His
 1 5 10 15
 Pro Ala Pro Thr His Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala
 20 25 30
 Gly Glu Ala Leu Lys Gly Val Lys Asp Val Pro Thr Asn Asn Asn His
 35 40 45
 Met Lys Ile Met Pro Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu
 50 55 60
 Gly Glu Asn Phe Thr Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys
 65 70 75 80
 Gly Met Ile Ser His Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser
 85 90 95
 Lys Thr Leu Ile Ala Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr
 100 105 110
 Glu Lys Asn Arg Ala Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser
 115 120 125
 Phe Pro Asp Asp Phe Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg
 130 135 140
 Gln Ile Gly Asn Ala Val Pro Pro Val Gly Met His Ala Val Gly Glu
 145 150 155 160

Arg Leu Met Asn Leu Tyr Thr Gly Asn Tyr Thr Pro Val Asp Leu Glu
 165 170 175

Glu Gln His Ala Tyr Leu Gln Thr Leu Ser Ile Lys Glu Arg Leu Ala
 180 185 190

Leu Ala Asp Gln Glu Ala Asp
 195

<210> 163

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA01795

<400> 163

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caacttcgct gaatacgggtg tcccacaatt ccgcgaacgt gtg ctc att gtt ggc 115
 Val Leu Ile Val Gly
 1 5

att cgc cgt gac acc ggc ttt gat ttc aag cac cca gct cct acc cat 163
 Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His Pro Ala Pro Thr His
 10 15 20

ggc cct cgc ggt gac atg ccg tat aag act gcc ggc gaa gcg ctc aaa 211
 Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala Gly Glu Ala Leu Lys
 25 30 35

ggc gtg aag gat gtc ccc aca aac aac aac cac atg aag atc atg cct 259
 Gly Val Lys Asp Val Pro Thr Asn Asn Asn His Met Lys Ile Met Pro
 40 45 50

cgc acc gtt gaa gtg ctt aag cgc atc cct gag ggc gaa aac ttc acc 307
 Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu Gly Glu Asn Phe Thr
 55 60 65

gcg atc ccc aaa gat gac ccc tac tac gtc aag ggc atg att agt cac 355
 Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys Gly Met Ile Ser His
 70 75 80 85

gtt tac cgt cgc ttg cac cgt gat gag cca tcc aaa acc ctt atc gcc 403
 Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser Lys Thr Leu Ile Ala
 90 95 100

ggt ggc ggc ggg ggt aca tgg gga tac cat tat gaa aaa aat cga gca 451
 Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr Glu Lys Asn Arg Ala
 105 110 115

ttg acc aac cgc gag cgg gct aga att caa tcg ttc ccc gat gac ttt 499
 Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser Phe Pro Asp Asp Phe
 120 125 130

gag ttt ttg gga tca aac acc caa gtc cgc cgc caa 535
 Glu Phe Leu Gly Ser Asn Thr Gln Val Arg Arg Gln

135

140

145

<210> 164

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Val Leu Ile Val Gly Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His
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Pro Ala Pro Thr His Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala
 20 25 30

Gly Glu Ala Leu Lys Gly Val Lys Asp Val Pro Thr Asn Asn Asn His
 35 40 45

Met Lys Ile Met Pro Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu
 50 55 60

Gly Glu Asn Phe Thr Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys
 65 70 75 80

Gly Met Ile Ser His Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser
 85 90 95

Lys Thr Leu Ile Ala Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr
 100 105 110

Glu Lys Asn Arg Ala Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser
 115 120 125

Phe Pro Asp Asp Phe Glu Phe Leu Gly Ser Asn Thr Gln Val Arg Arg
 130 135 140

Gln
 145

<210> 165

<211> 1614

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1591)

<223> RXA01214

<400> 165

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gccagagttg aatcgctcga cttttttcaa aggggccggg gtg ctg gca gca acg 115
 Val Leu Ala Ala Thr
 1 5

gtg gtg ggt gcg cag gtg ctg gtg gcg tgt tcc tca gat gat gtg cgt 163
 Val Val Gly Ala Gln Val Leu Val Ala Cys Ser Ser Asp Asp Val Arg
 10 15 20

ggt tat ggg gga gag ccg cgg acg ttg cct att cca cca gca gat tta	211
Gly Tyr Gly Gly Glu Pro Arg Thr Leu Pro Ile Pro Pro Ala Asp Leu	
25 30 35	
ggt acg cgt gag gga tct agc gtg cac ttt gcc ctg gag gct cag act	259
Gly Thr Arg Glu Gly Ser Ser Val His Phe Ala Leu Glu Ala Gln Thr	
40 45 50	
ggg gag agt cag att ttg ccg gat gtc aca acg aag acg tgg ggt ttc	307
Gly Glu Ser Gln Ile Leu Pro Asp Val Thr Thr Lys Thr Trp Gly Phe	
55 60 65	
aat ggc act cat ttg ggg ccg acg ttg gtg gtg aag aaa ggt gat gac	355
Asn Gly Thr His Leu Gly Pro Thr Leu Val Val Lys Lys Gly Asp Asp	
70 75 80 85	
gtc cac gtt gat gtg ata aac aat ttg gat gaa atg acc act gtg cac	403
Val His Val Asp Val Ile Asn Asn Leu Asp Glu Met Thr Thr Val His	
90 95 100	
tgg cat ggc atg aag ttg ccg gcg att gct gat ggt ggt ccg cac tca	451
Trp His Gly Met Lys Leu Pro Ala Ile Ala Asp Gly Gly Pro His Ser	
105 110 115	
ccg atc ggg cct ggg cag acg tgg tca cca acg tgg act gtg gcc aat	499
Pro Ile Gly Pro Gly Gln Thr Trp Ser Pro Thr Trp Thr Val Ala Asn	
120 125 130	
gat gca gcc act ttg tgg tac cac ccg cac act cat ggc ctg aca ggt	547
Asp Ala Ala Thr Leu Trp Tyr His Pro His Thr His Gly Leu Thr Gly	
135 140 145	
ttg cat gcg tac cgt ggt ttg gcg ggg atg atc att gtg gaa gat gaa	595
Leu His Ala Tyr Arg Gly Leu Ala Gly Met Ile Ile Val Glu Asp Glu	
150 155 160 165	
gca aca gac aag ctg gat ctg cca cgc gag tac ggt gtg gac gat att	643
Ala Thr Asp Lys Leu Asp Leu Pro Arg Glu Tyr Gly Val Asp Asp Ile	
170 175 180	
ccg ctg gtt tta atg gat cac cgc ttc tta gaa gac ggt tcc ctt gat	691
Pro Leu Val Leu Met Asp His Arg Phe Leu Glu Asp Gly Ser Leu Asp	
185 190 195	
gag gaa gac ctc ccc gat ctt ggg ctg ttg ggc gat acc ccc act gcc	739
Glu Glu Asp Leu Pro Asp Leu Gly Leu Leu Gly Asp Thr Pro Thr Ala	
200 205 210	
aat ggc att acc aat gcg cac ttt gat gcc acc acg cgc cgg gtt cgg	787
Asn Gly Ile Thr Asn Ala His Phe Asp Ala Thr Thr Arg Arg Val Arg	
215 220 225	
ttc cgc gtg ctc aac ggc tcc aat atg cgg ttc tat aac ttg gcg ttt	835
Phe Arg Val Leu Asn Gly Ser Asn Met Arg Phe Tyr Asn Leu Ala Phe	
230 235 240 245	
tca gac acg cgc acc ttc caa gtc att gcc agc gat tcc ggt ttg ctg	883
Ser Asp Thr Arg Thr Phe Gln Val Ile Ala Ser Asp Ser Gly Leu Leu	
250 255 260	
gat gaa cct caa gac cgc acc acc ttg gct att ggc cca ggc gag cgg	931

Asp Glu Pro Gln Asp Arg Thr Thr Leu Ala Ile Gly Pro Gly Glu Arg	
265 270 275	
tgg gaa atc gtc gtg gag cta gag ccc ggc gag gac gtc acc ttg gaa	979
Trp Glu Ile Val Val Glu Leu Glu Pro Gly Glu Asp Val Thr Leu Glu	
280 285 290	
tct gta ggt ttt gag gac aac tac ggc gtc cct gat gat gag ttc gtg	1027
Ser Val Gly Phe Glu Asp Asn Tyr Gly Val Pro Asp Asp Glu Phe Val	
295 300 305	
ccc gat ttc ggc atg tca gat tcc ttc cag ctg ctc acc atc acc ggc	1075
Pro Asp Phe Gly Met Ser Asp Ser Phe Gln Leu Leu Thr Ile Thr Gly	
310 315 320 325	
cct tcc gat gat gct gcg caa gca cct gct ttg ccg ggc gtg ctg gtg	1123
Pro Ser Asp Asp Ala Ala Gln Ala Pro Ala Leu Pro Gly Val Leu Val	
330 335 340	
aaa tcc acc gaa cct gac gtc atc gat gcc act gaa cgc acc ttc atc	1171
Lys Ser Thr Glu Pro Asp Val Ile Asp Ala Thr Glu Arg Thr Phe Ile	
345 350 355	
atg aac acc ttc tcc atc aac gat cta cag atg gac atg cag cgc gtt	1219
Met Asn Thr Phe Ser Ile Asn Asp Leu Gln Met Asp Met Gln Arg Val	
360 365 370	
gac gtg gtg att gac cat gac cag cca gaa gtg tgg att gtc acc aac	1267
Asp Val Val Ile Asp His Asp Gln Pro Glu Val Trp Ile Val Thr Asn	
375 380 385	
gac aac tcc gac tgg ccc cac aac ttc cat gtc cac gac gcc cgg ttt	1315
Asp Asn Ser Asp Trp Pro His Asn Phe His Val His Asp Ala Arg Phe	
390 395 400 405	
aag gtg ctg aaa ttt gaa ggc acc gac gta gag ctc ttc aac gac ggc	1363
Lys Val Leu Lys Phe Glu Gly Thr Asp Val Glu Leu Phe Asn Asp Gly	
410 415 420	
tgg aaa gac acc gtc ggc ctg cca ccg gga gca acc gca act tta gcc	1411
Trp Lys Asp Thr Val Gly Leu Pro Pro Gly Ala Thr Ala Thr Leu Ala	
425 430 435	
gtg gaa ttt ggc cac tac cca gac ccg caa tgg ccc tac atg tat cac	1459
Val Glu Phe Gly His Tyr Pro Asp Pro Gln Trp Pro Tyr Met Tyr His	
440 445 450	
tgc cac atg ctc tac cac gag gat caa ggc atg atg ggg cag ttc gtc	1507
Cys His Met Leu Tyr His Glu Asp Gln Gly Met Met Gly Gln Phe Val	
455 460 465	
atc gtg gag cca ggc gac gag ccg gcg gcg gtg ctg ggg tcg ggc acg	1555
Ile Val Glu Pro Gly Asp Glu Pro Ala Ala Val Leu Gly Ser Gly Thr	
470 475 480 485	
ggc tcc agc att gac tcc gcc ggc gga cat gcg cac taggggcgtg	1601
Gly Ser Ser Ile Asp Ser Ala Gly Gly His Ala His	
490 495	
gggcggcgtc gat	1614

<210> 166
 <211> 497
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 166
 Val Leu Ala Ala Thr Val Val Gly Ala Gln Val Leu Val Ala Cys Ser
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 Ser Asp Asp Val Arg Gly Tyr Gly Gly Glu Pro Arg Thr Leu Pro Ile
 20 25 30
 Pro Pro Ala Asp Leu Gly Thr Arg Glu Gly Ser Ser Val His Phe Ala
 35 40 45
 Leu Glu Ala Gln Thr Gly Glu Ser Gln Ile Leu Pro Asp Val Thr Thr
 50 55 60
 Lys Thr Trp Gly Phe Asn Gly Thr His Leu Gly Pro Thr Leu Val Val
 65 70 75 80
 Lys Lys Gly Asp Asp Val His Val Asp Val Ile Asn Asn Leu Asp Glu
 85 90 95
 Met Thr Thr Val His Trp His Gly Met Lys Leu Pro Ala Ile Ala Asp
 100 105 110
 Gly Gly Pro His Ser Pro Ile Gly Pro Gly Gln Thr Trp Ser Pro Thr
 115 120 125
 Trp Thr Val Ala Asn Asp Ala Ala Thr Leu Trp Tyr His Pro His Thr
 130 135 140
 His Gly Leu Thr Gly Leu His Ala Tyr Arg Gly Leu Ala Gly Met Ile
 145 150 155 160
 Ile Val Glu Asp Glu Ala Thr Asp Lys Leu Asp Leu Pro Arg Glu Tyr
 165 170 175
 Gly Val Asp Asp Ile Pro Leu Val Leu Met Asp His Arg Phe Leu Glu
 180 185 190
 Asp Gly Ser Leu Asp Glu Glu Asp Leu Pro Asp Leu Gly Leu Leu Gly
 195 200 205
 Asp Thr Pro Thr Ala Asn Gly Ile Thr Asn Ala His Phe Asp Ala Thr
 210 215 220
 Thr Arg Arg Val Arg Phe Arg Val Leu Asn Gly Ser Asn Met Arg Phe
 225 230 235 240
 Tyr Asn Leu Ala Phe Ser Asp Thr Arg Thr Phe Gln Val Ile Ala Ser
 245 250 255
 Asp Ser Gly Leu Leu Asp Glu Pro Gln Asp Arg Thr Thr Leu Ala Ile
 260 265 270
 Gly Pro Gly Glu Arg Trp Glu Ile Val Val Glu Leu Glu Pro Gly Glu
 275 280 285

Asp Val Thr Leu Glu Ser Val Gly Phe Glu Asp Asn Tyr Gly Val Pro
 290 295 300
 Asp Asp Glu Phe Val Pro Asp Phe Gly Met Ser Asp Ser Phe Gln Leu
 305 310 315 320
 Leu Thr Ile Thr Gly Pro Ser Asp Asp Ala Ala Gln Ala Pro Ala Leu
 325 330 335
 Pro Gly Val Leu Val Lys Ser Thr Glu Pro Asp Val Ile Asp Ala Thr
 340 345 350
 Glu Arg Thr Phe Ile Met Asn Thr Phe Ser Ile Asn Asp Leu Gln Met
 355 360 365
 Asp Met Gln Arg Val Asp Val Val Ile Asp His Asp Gln Pro Glu Val
 370 375 380
 Trp Ile Val Thr Asn Asp Asn Ser Asp Trp Pro His Asn Phe His Val
 385 390 395 400
 His Asp Ala Arg Phe Lys Val Leu Lys Phe Glu Gly Thr Asp Val Glu
 405 410 415
 Leu Phe Asn Asp Gly Trp Lys Asp Thr Val Gly Leu Pro Pro Gly Ala
 420 425 430
 Thr Ala Thr Leu Ala Val Glu Phe Gly His Tyr Pro Asp Pro Gln Trp
 435 440 445
 Pro Tyr Met Tyr His Cys His Met Leu Tyr His Glu Asp Gln Gly Met
 450 455 460
 Met Gly Gln Phe Val Ile Val Glu Pro Gly Asp Glu Pro Ala Ala Val
 465 470 475 480
 Leu Gly Ser Gly Thr Gly Ser Ser Ile Asp Ser Ala Gly Gly His Ala
 485 490 495

His

<210> 167
 <211> 588
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(588)
 <223> RXA01250

<400> 167
 ctg gat atc ggc ggc atc gaa gcc aag acg tgg gga tac gtc tct gac 48
 Leu Asp Ile Gly Gly Ile Glu Ala Lys Thr Trp Gly Tyr Val Ser Asp
 1 5 10 15
 acc ggg gat gcg gcc att gag gcc acc gcc ggc gac gtc ctc cag gtc 96
 Thr Gly Asp Ala Ala Ile Glu Ala Thr Ala Gly Asp Val Leu Gln Val
 20 25 30

gat atc acc aat gac ctg cct gag agc acc tcc atc cac tgg cat ggc 144
Asp Ile Thr Asn Asp Leu Pro Glu Ser Thr Ser Ile His Trp His Gly
35 40 45

atc gca ctc cac aac gca gcc gag ggt gtg ccc ggc atg acc cag gac 192
Ile Ala Leu His Asn Ala Ala Asp Gly Val Pro Gly Met Thr Gln Asp
50 55 60

ccc att gaa cct ggc gag tct ttc tcc tat gtt ttt gaa gtc ccc cac 240
Pro Ile Glu Pro Gly Glu Ser Phe Ser Tyr Val Phe Glu Val Pro His
65 70 75 80

ggt ggc acc tac ttc tac cat tcc cac acc ggc ctg cag ctt gat cgc 288
Gly Gly Thr Tyr Phe Tyr His Ser His Thr Gly Leu Gln Leu Asp Arg
85 90 95

ggc ctc cac gcc cca ctg atc atc cgt gac ccg caa gac gct gag gac 336
Gly Leu His Ala Pro Leu Ile Ile Arg Asp Pro Gln Asp Ala Glu Asp
100 105 110

cag gac gtc gag tgg acc atc gtg ctc gac gac tgg gtc gat ggc att 384
Gln Asp Val Glu Trp Thr Ile Val Leu Asp Asp Trp Val Asp Gly Ile
115 120 125

cag ggc act ccc gac gat gag ctc gac aag ctc acc gga atg ggt tcg 432
Gln Gly Thr Pro Asp Asp Glu Leu Asp Lys Leu Thr Gly Met Gly Ser
130 135 140

ggc gac cat aac ggg agg atg gga atg gga ggt cac ggc cag atg atg 480
Gly Asp His Asn Gly Arg Met Gly Met Gly Gly His Gly Gln Met Met
145 150 155 160

cac ggc acc ccg gac cgg gta ctg ggc ggg gat gtc ggc gat gtg atg 528
His Gly Thr Pro Asp Arg Val Leu Gly Gly Asp Val Gly Asp Val Met
165 170 175

tat ccg cac tac ctc atc aac gga cgt atc ccc cgt gct cac cgg acc 576
Tyr Pro His Tyr Leu Ile Asn Gly Arg Ile Pro Arg Ala His Arg Thr
180 185 190

ttc gag gct cgc 588
Phe Glu Ala Arg
195

<210> 168
<211> 196
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 168
Leu Asp Ile Gly Gly Ile Glu Ala Lys Thr Trp Gly Tyr Val Ser Asp
1 5 10 15
Thr Gly Asp Ala Ala Ile Glu Ala Thr Ala Gly Asp Val Leu Gln Val
20 25 30
Asp Ile Thr Asn Asp Leu Pro Glu Ser Thr Ser Ile His Trp His Gly
35 40 45

Ile Ala Leu His Asn Ala Ala Asp Gly Val Pro Gly Met Thr Gln Asp
 50 55 60

Pro Ile Glu Pro Gly Glu Ser Phe Ser Tyr Val Phe Glu Val Pro His
 65 70 75 80

Gly Gly Thr Tyr Phe Tyr His Ser His Thr Gly Leu Gln Leu Asp Arg
 85 90 95

Gly Leu His Ala Pro Leu Ile Ile Arg Asp Pro Gln Asp Ala Glu Asp
 100 105 110

Gln Asp Val Glu Trp Thr Ile Val Leu Asp Asp Trp Val Asp Gly Ile
 115 120 125

Gln Gly Thr Pro Asp Asp Glu Leu Asp Lys Leu Thr Gly Met Gly Ser
 130 135 140

Gly Asp His Asn Gly Arg Met Gly Met Gly Gly His Gly Gln Met Met
 145 150 155 160

His Gly Thr Pro Asp Arg Val Leu Gly Gly Asp Val Gly Asp Val Met
 165 170 175

Tyr Pro His Tyr Leu Ile Asn Gly Arg Ile Pro Arg Ala His Arg Thr
 180 185 190

Phe Glu Ala Arg
 195

<210> 169

<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(721)

<223> RXA02477

<400> 169

cgagcagggc tgtttgaaaa gctgtaaatg acatgaccta aatgattgta ctgactggca 60

ctttaggtca tatgtcacac cgagtggaat aataaagctt atg cct ttg cgt aat 115
 Met Pro Leu Arg Asn
 1 5

gtt gat aga act ccg ccc gca gta tgg gaa gca ttg ctt gcc gga aac 163
 Val Asp Arg Thr Pro Pro Ala Val Trp Glu Ala Leu Leu Ala Gly Asn
 10 15 20

gaa aga ttc atc agt ttc aac gaa gat cga cca aac cag gac gcc ccg 211
 Glu Arg Phe Ile Ser Phe Asn Glu Asp Arg Pro Asn Gln Asp Ala Pro
 25 30 35

cgc aga aga gaa ctt cgc aat gga caa acg cct gca gct gtt gtt att 259
 Arg Arg Arg Glu Leu Arg Asn Gly Gln Thr Pro Ala Ala Val Val Ile
 40 45 50

tcc tgt tca gat tct cga gtg cca gtt gag att att ttt gac gtc ggt 307

Ser Cys Ser Asp Ser Arg Val Pro Val Glu Ile Ile Phe Asp Val Gly
55 60 65

ctc ggt gac ctc ttt gtt gtc cgt act gcc gga gaa atc ctc gac caa 355
Leu Gly Asp Leu Phe Val Val Arg Thr Ala Gly Glu Ile Leu Asp Gln
70 75 80 85

gca gtg ctt gcg tcc atc gaa tac gcc act gaa tcc atc ggc gtt cca 403
Ala Val Leu Ala Ser Ile Glu Tyr Ala Thr Glu Ser Ile Gly Val Pro
90 95 100

ttg gtt atc gtc atg ggc cac gaa tcc tgt ggt gca gtt gca gca act 451
Leu Val Ile Val Met Gly His Glu Ser Cys Gly Ala Val Ala Ala Thr
105 110 115

gca gca gca ctt gaa ggc ggt gca ctt ccc gga ggc tac caa cga gtt 499
Ala Ala Ala Leu Glu Gly Gly Ala Leu Pro Gly Gly Tyr Gln Arg Val
120 125 130

ttg gtt gaa aag gtt gca cca tcc att cta gaa gcc aag gca gag ggc 547
Leu Val Glu Lys Val Ala Pro Ser Ile Leu Glu Ala Lys Ala Glu Gly
135 140 145

ctg agc tcc atc aag gaa ttc gag gaa cac cac gtt gtg gca acg gta 595
Leu Ser Ser Ile Lys Glu Phe Glu Glu His His Val Val Ala Thr Val
150 155 160 165

aac caa ctg ttg tcc cgt tct cca gag att cat cag aag gtc gaa acc 643
Asn Gln Leu Leu Ser Arg Ser Pro Glu Ile His Gln Lys Val Glu Thr
170 175 180

ggt gag ttg gga atc att ggt ttg cgc tac cga ctc tct gac ggt cgt 691
Gly Glu Leu Gly Ile Ile Gly Leu Arg Tyr Arg Leu Ser Asp Gly Arg
185 190 195

act gaa cct gta att agc aag aac gtg ggt tagttttcgg tctgagattg 741
Thr Glu Pro Val Ile Ser Lys Asn Val Gly
200 205

cct 744

<210> 170

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Pro Leu Arg Asn Val Asp Arg Thr Pro Pro Ala Val Trp Glu Ala
1 5 10 15

Leu Leu Ala Gly Asn Glu Arg Phe Ile Ser Phe Asn Glu Asp Arg Pro
20 25 30

Asn Gln Asp Ala Pro Arg Arg Arg Glu Leu Arg Asn Gly Gln Thr Pro
35 40 45

Ala Ala Val Val Ile Ser Cys Ser Asp Ser Arg Val Pro Val Glu Ile
50 55 60

Ile Phe Asp Val Gly Leu Gly Asp Leu Phe Val Val Arg Thr Ala Gly

65	70	75	80
Glu Ile Leu Asp	Gln Ala Val Leu Ala Ser Ile Glu Tyr Ala Thr Glu		
	85	90	95
Ser Ile Gly Val Pro Leu Val Ile Val Met Gly His Glu Ser Cys Gly			
	100	105	110
Ala Val Ala Ala Thr Ala Ala Ala Leu Glu Gly Gly Ala Leu Pro Gly			
	115	120	125
Gly Tyr Gln Arg Val Leu Val Glu Lys Val Ala Pro Ser Ile Leu Glu			
	130	135	140
Ala Lys Ala Glu Gly Leu Ser Ser Ile Lys Glu Phe Glu Glu His His			
145	150	155	160
Val Val Ala Thr Val Asn Gln Leu Leu Ser Arg Ser Pro Glu Ile His			
	165	170	175
Gln Lys Val Glu Thr Gly Glu Leu Gly Ile Ile Gly Leu Arg Tyr Arg			
	180	185	190
Leu Ser Asp Gly Arg Thr Glu Pro Val Ile Ser Lys Asn Val Gly			
	195	200	205

<210> 171
 <211> 618
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> RXN00833

<400> 171
 agctttttgc atgtgtcata tcgtaccggt tgcataggcc tgttcgcgct tggatgaacct 60

tttctagcac caaaacaaaa ctctccctag tatgggggtcc atg gct aaa aca cat 115
 Met Ala Lys Thr His
 1 5

ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163
 Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
 10 15 20

gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
 Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
 25 30 35

tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
 Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
 40 45 50

tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
 Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
 55 60 65

gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355

Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
 70 75 80 85

ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
 Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
 90 95 100

gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
 Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
 105 110 115

atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499
 Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val
 120 125 130

atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547
 Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp
 135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
 Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu Asn
 150 155 160 165

taatttactt cgctcagggg aat 618

<210> 172
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 172
 Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
 1 5 10 15

Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
 20 25 30

Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45

Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60

Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80

Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95

Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110

Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
 115 120 125

Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
 130 135 140

Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
 145 150 155 160

Leu Ala Gly Leu Asn
165

<210> 173
<211> 469
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(469)
<223> FRXA00833

<400> 173
agctttttgc atgtgtcata tcgtaccgtt tgcataggcc tggtcgcgct tgggtgaacct 60
tttctagcac caaaacaaaa ctctccctag tatgggggtcc atg gct aaa aca cat 115
Met Ala Lys Thr His
1 5
ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163
Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
10 15 20
gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
25 30 35
tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
40 45 50
tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
55 60 65
gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355
Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
70 75 80 85
ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
90 95 100
gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
105 110 115
atc gtg ctc gaa ggc tca 469
Ile Val Leu Glu Gly Ser
120

<210> 174
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 174

Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
 1 5 10 15
 Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
 20 25 30
 Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45
 Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60
 Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80
 Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95
 Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110
 Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser
 115 120

<210> 175
 <211> 1146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1123)
 <223> RXA01224

<400> 175
 ttggcggcgg gaagttcagg cttgggggca aacagtgctt ggattttaga caaaaaactc 60
 acggaagtca tcctatggca ggcgcgccta ggatggtgcc atg agc atc ctt gac 115
 Met Ser Ile Leu Asp
 1 5
 acg ttg aaa act ccc gtg att gtc gcc ccg atg gct ggc ggc ccg tcc 163
 Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met Ala Gly Gly Pro Ser
 10 15 20
 act ccc gcg ttg gtc aat gca gca gca gag gca ggt tcc ctc ggg ttc 211
 Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala Gly Ser Leu Gly Phe
 25 30 35
 ttg gct ggt ggc gtc atg cct ctt gag cag ctg aaa cag gaa ttg tca 259
 Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu Lys Gln Glu Leu Ser
 40 45 50
 gag gta aaa ggc gtc ttt ggc gtc aac ctg ttt cgc ccg cag acg gat 307
 Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe Arg Pro Gln Thr Asp
 55 60 65
 gcg cct aag cct tca gac att gat gag ctg gcg gga ttg ttg tcc tcg 355
 Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala Gly Leu Leu Ser Ser
 70 75 80 85

gcg ttt cgg caa ttt ggc ctc gat gag ccg acg gtg cct acg ccg gat	403
Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr Val Pro Thr Pro Asp	
90 95 100	
ttg agc aat ggg tgg gag gct aaa ttt gag gcc gtt ctt gcc gct aag	451
Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala Val Leu Ala Ala Lys	
105 110 115	
ccc gcc gtt ttt tcc tgc acc ttt ggt att ttt agc gct gaa gaa ttc	499
Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe Ser Ala Glu Glu Phe	
120 125 130	
gcc cgg atc aaa gcc acc gga att gag gcg tgg gtg acg gtg acc aat	547
Ala Arg Ile Lys Ala Thr Ile Glu Ala Trp Val Thr Val Thr Asn	
135 140 145	
ccg gag gac gcg ctg gct gcg cag aaa gct ggc gcc aac gcg ctt gtc	595
Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly Ala Asn Ala Leu Val	
150 155 160 165	
gtg caa ggc ccc gag gcg ggt ggg cac cgc tct acc tgg tcc att gaa	643
Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser Thr Trp Ser Ile Glu	
170 175 180	
gtg gag ccg gac gag cgc gac ctg aaa acc ctc ctc gca gct gtc aaa	691
Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu Leu Ala Ala Val Lys	
185 190 195	
caa gcg ggc gtt tac ctc ccg ctc atc gca gcc ggc ggc ctt tca acc	739
Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala Gly Gly Leu Ser Thr	
200 205 210	
tcc gca gac gtg gca gca att tta gaa gcc ggc gcc agc gct gcc tcc	787
Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly Ala Ser Ala Ala Ser	
215 220 225	
tgt ggt tcc gcc ttt ttg ctt agc gac gaa gcc ggc acc agc tca ctt	835
Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala Gly Thr Ser Ser Leu	
230 235 240 245	
aac cgc gag atc ttg gac gcc gcc cca gca ctt ggt ttg gaa tcg gtg	883
Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu Gly Leu Glu Ser Val	
250 255 260	
tca tct cgc gca ttt tcg ggc cgt tat gcc agg gga gtg gaa acc agg	931
Ser Ser Arg Ala Phe Ser Gly Arg Tyr Ala Arg Gly Val Glu Thr Arg	
265 270 275	
ttc acc cgt tcg aac gag ggg tta ccc ccg ttg tac cca tac ctc aac	979
Phe Thr Arg Ser Asn Glu Gly Leu Pro Pro Leu Tyr Pro Tyr Leu Asn	
280 285 290	
cca atg atc aca tct tta cgt aag gtg gcg gga agt gca ggg aac tgg	1027
Pro Met Ile Thr Ser Leu Arg Lys Val Ala Gly Ser Ala Gly Asn Trp	
295 300 305	
gat tac gcc tac tgc ctg gta gga gtc ggc ctg gaa tcg att gcg aag	1075
Asp Tyr Ala Tyr Cys Leu Val Gly Val Gly Leu Glu Ser Ile Ala Lys	
310 315 320 325	

ggt agt gca aag cag ata ctg gaa tca tta aca cct tcc gct ttg ggc 1123
 Gly Ser Ala Lys Gln Ile Leu Glu Ser Leu Thr Pro Ser Ala Leu Gly
 330 335 340

taatgttggg gggagtgcctt tca 1146

<210> 176

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Ser Ile Leu Asp Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met
 1 5 10 15

Ala Gly Gly Pro Ser Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala
 20 25 30

Gly Ser Leu Gly Phe Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu
 35 40 45

Lys Gln Glu Leu Ser Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe
 50 55 60

Arg Pro Gln Thr Asp Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala
 65 70 75 80

Gly Leu Leu Ser Ser Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr
 85 90 95

Val Pro Thr Pro Asp Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala
 100 105 110

Val Leu Ala Ala Lys Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe
 115 120 125

Ser Ala Glu Glu Phe Ala Arg Ile Lys Ala Thr Gly Ile Glu Ala Trp
 130 135 140

Val Thr Val Thr Asn Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly
 145 150 155 160

Ala Asn Ala Leu Val Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser
 165 170 175

Thr Trp Ser Ile Glu Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu
 180 185 190

Leu Ala Ala Val Lys Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala
 195 200 205

Gly Gly Leu Ser Thr Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly
 210 215 220

Ala Ser Ala Ala Ser Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala
 225 230 235 240

Gly Thr Ser Ser Leu Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu
 245 250 255

Gly Leu Glu Ser Val Ser Ser Arg Ala Phe Ser Gly Arg Tyr Ala Arg
260 265 270

Gly Val Glu Thr Arg Phe Thr Arg Ser Asn Glu Gly Leu Pro Pro Leu
275 280 285

Tyr Pro Tyr Leu Asn Pro Met Ile Thr Ser Leu Arg Lys Val Ala Gly
290 295 300

Ser Ala Gly Asn Trp Asp Tyr Ala Tyr Cys Leu Val Gly Val Gly Leu
305 310 315 320

Glu Ser Ile Ala Lys Gly Ser Ala Lys Gln Ile Leu Glu Ser Leu Thr
325 330 335

Pro Ser Ala Leu Gly
340

<210> 177

<211> 516

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(493)

<223> RXA01182

<400> 177

gttaaaacgg aaactaatac cccaaaggat accgattcaa tttgtgatgt gtggtgttcg 60

ggcatatca agctaaacag atgcccccta caataggctt gtg ttc aat tta ttt 115
Val Phe Asn Leu Phe
1 5

ggt cgt aaa act cct cgc tct aac ctc cgc cca cca cgc ggt ccg ggc 163
Gly Arg Lys Thr Pro Arg Ser Asn Leu Arg Pro Pro Arg Gly Pro Gly
10 15 20

gat act gtg cgc ccg gaa gat tta aaa ttc ttg atg caa tgg gtg cag 211
Asp Thr Val Arg Pro Glu Asp Leu Lys Phe Leu Met Gln Trp Val Gln
25 30 35

gat aag cca ttt gtt gag gca ttc gtt gaa ccg gaa acg ctg gtc aat 259
Asp Lys Pro Phe Val Glu Ala Phe Val Glu Pro Glu Thr Leu Val Asn
40 45 50

gag atg tct gtc gtt ttg gtt gat gct cat ggg gtt ttt gtc cgc cga 307
Glu Met Ser Val Val Leu Val Asp Ala His Gly Val Phe Val Arg Arg
55 60 65

agg atc ggc ggt ccc aaa ggg att gat gtt atc gcg aaa aag ctc ggc 355
Arg Ile Gly Gly Pro Lys Gly Ile Asp Val Ile Ala Lys Lys Leu Gly
70 75 80 85

gtt ccg gtt tat gat gtt gag gag acc ggt tac ccc caa agg atg cgc 403
Val Pro Val Tyr Asp Val Glu Glu Thr Gly Tyr Pro Gln Arg Met Arg
90 95 100

gaa cgc att gaa tat gag cgc atc tta aga aag cgt gag gaa caa aaa 451

Glu Arg Ile Glu Tyr Glu Arg Ile Leu Arg Lys Arg Glu Glu Gln Lys
 105 110 115

gct cgc cgc gct aaa ttt gag cgc ggc gag aat cct gat ctt 493
 Ala Arg Arg Ala Lys Phe Glu Arg Gly Glu Asn Pro Asp Leu
 120 125 130

taactagcgt ttagctttcc gac 516

<210> 178

<211> 131

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 178

Val Phe Asn Leu Phe Gly Arg Lys Thr Pro Arg Ser Asn Leu Arg Pro
 1 5 10 15

Pro Arg Gly Pro Gly Asp Thr Val Arg Pro Glu Asp Leu Lys Phe Leu
 20 25 30

Met Gln Trp Val Gln Asp Lys Pro Phe Val Glu Ala Phe Val Glu Pro
 35 40 45

Glu Thr Leu Val Asn Glu Met Ser Val Val Leu Val Asp Ala His Gly
 50 55 60

Val Phe Val Arg Arg Arg Ile Gly Gly Pro Lys Gly Ile Asp Val Ile
 65 70 75 80

Ala Lys Lys Leu Gly Val Pro Val Tyr Asp Val Glu Glu Thr Gly Tyr
 85 90 95

Pro Gln Arg Met Arg Glu Arg Ile Glu Tyr Glu Arg Ile Leu Arg Lys
 100 105 110

Arg Glu Glu Gln Lys Ala Arg Arg Ala Lys Phe Glu Arg Gly Glu Asn
 115 120 125

Pro Asp Leu
 130

<210> 179

<211> 834

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(811)

<223> RXA02531

<400> 179

cacttcgctc cccaaggtac atccccgatg ccacttcttg gagccatcat cggtgccacc 60

aaacacattg aagtgggcac tggagtagtg gatatgcgtt atg aaa atc cct ttg 115
 Met Lys Ile Pro Leu
 1 5

tat atg gcc gag gaa gca gct gct ctc aat ctg ctt gcc gac ggc cga	163
Tyr Met Ala Glu Glu Ala Ala Ala Leu Asn Leu Leu Ala Asp Gly Arg	
10 15 20	
cta gcc ctc gga gtt tcc agg gga tca ccc gaa cca gcc gag aag ggt	211
Leu Ala Leu Gly Val Ser Arg Gly Ser Pro Glu Pro Ala Glu Lys Gly	
25 30 35	
tgg gaa gct ttc ggc tac gac ggc ggt gat gat cct aaa gct gca ggc	259
Trp Glu Ala Phe Gly Tyr Asp Gly Gly Asp Asp Pro Lys Ala Ala Gly	
40 45 50	
atg gca cgg gag aaa ttc ctt cgc ttc ctc gat gcc atc gat ggt cgc	307
Met Ala Arg Glu Lys Phe Leu Arg Phe Leu Asp Ala Ile Asp Gly Arg	
55 60 65	
ccc atg tcc atc gct tcc gag aat caa tac cca cgc ctc tac cat ccg	355
Pro Met Ser Ile Ala Ser Glu Asn Gln Tyr Pro Arg Leu Tyr His Pro	
70 75 80 85	
ggc act ccc ctg ccg atc ttc ccg cat gat ctt gac ttg ggt aaa tcc	403
Gly Thr Pro Leu Pro Ile Phe Pro His Asp Leu Asp Leu Gly Lys Ser	
90 95 100	
att tgg tgg ggc gcc ggt tcc cac aac acc gcc gaa caa gca gca cgc	451
Ile Trp Trp Gly Ala Gly Ser His Asn Thr Ala Glu Gln Ala Ala Arg	
105 110 115	
gat ggc gtt aac ttg atg agc tcc acc ctc gtc gcc gaa gcc acc ggc	499
Asp Gly Val Asn Leu Met Ser Ser Thr Leu Val Ala Glu Ala Thr Gly	
120 125 130	
caa tcc ttc ggg gat ctg caa gcc gat caa atc gcg ttc tac cgc caa	547
Gln Ser Phe Gly Asp Leu Gln Ala Asp Gln Ile Ala Phe Tyr Arg Gln	
135 140 145	
gct tgg aaa gaa gcc gga cac gat tgg acc cca cgt gtg tct gtc tcc	595
Ala Trp Lys Glu Ala Gly His Asp Trp Thr Pro Arg Val Ser Val Ser	
150 155 160 165	
agg tcc atc ttt ccg atc gtc acc gac cgc gac cgt gag ctt ttc gga	643
Arg Ser Ile Phe Pro Ile Val Thr Asp Arg Asp Arg Glu Leu Phe Gly	
170 175 180	
ctt cag gga caa ggc ggt gac caa gta gga atc ctg gat gat acc cga	691
Leu Gln Gly Gln Gly Gly Asp Gln Val Gly Ile Leu Asp Asp Thr Arg	
185 190 195	
tcc acg ttc ggt cgc agc tac gcc gga agt ccc gat gaa ctc atc gac	739
Ser Thr Phe Gly Arg Ser Tyr Ala Gly Ser Pro Asp Glu Leu Ile Asp	
200 205 210	
cag ctc caa gga aga caa agc tgt gat gga agc cga cac ctt gat gct	787
Gln Leu Gln Gly Arg Gln Ser Cys Asp Gly Ser Arg His Leu Asp Ala	
215 220 225	
cac cgc ccc caa cca aat ggg tgt tgagatcaac gcgtcgatcc tga	834
His Arg Pro Gln Pro Asn Gly Cys	
230 235	

<210> 180
 <211> 237
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 180

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Met Lys Ile Pro Leu Tyr Met Ala Glu Glu Ala Ala Ala Leu Asn Leu
 1             5             10             15

Leu Ala Asp Gly Arg Leu Ala Leu Gly Val Ser Arg Gly Ser Pro Glu
          20          25          30

Pro Ala Glu Lys Gly Trp Glu Ala Phe Gly Tyr Asp Gly Gly Asp Asp
      35          40          45

Pro Lys Ala Ala Gly Met Ala Arg Glu Lys Phe Leu Arg Phe Leu Asp
      50          55          60

Ala Ile Asp Gly Arg Pro Met Ser Ile Ala Ser Glu Asn Gln Tyr Pro
 65          70          75          80

Arg Leu Tyr His Pro Gly Thr Pro Leu Pro Ile Phe Pro His Asp Leu
          85          90          95

Asp Leu Gly Lys Ser Ile Trp Trp Gly Ala Gly Ser His Asn Thr Ala
          100          105          110

Glu Gln Ala Ala Arg Asp Gly Val Asn Leu Met Ser Ser Thr Leu Val
      115          120          125

Ala Glu Ala Thr Gly Gln Ser Phe Gly Asp Leu Gln Ala Asp Gln Ile
      130          135          140

Ala Phe Tyr Arg Gln Ala Trp Lys Glu Ala Gly His Asp Trp Thr Pro
 145          150          155          160

Arg Val Ser Val Ser Arg Ser Ile Phe Pro Ile Val Thr Asp Arg Asp
          165          170          175

Arg Glu Leu Phe Gly Leu Gln Gly Gln Gly Gly Asp Gln Val Gly Ile
          180          185          190

Leu Asp Asp Thr Arg Ser Thr Phe Gly Arg Ser Tyr Ala Gly Ser Pro
      195          200          205

Asp Glu Leu Ile Asp Gln Leu Gln Gly Arg Gln Ser Cys Asp Gly Ser
      210          215          220

Arg His Leu Asp Ala His Arg Pro Gln Pro Asn Gly Cys
 225          230          235

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<210> 181
 <211> 1614
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1591)
 <223> RXN00689

<400> 181
acagggaaat cctcccagaa ttaatcaccg aagctgcaca ccagatggct actgcagacc 60

tcaatcgtgc aaaggccctg ttaagaacgg atgcgatccg atg aat gct gca acc 115
Met Asn Ala Ala Thr
1 5

agg cgt gct tct ctg caa ctc ccc tat acc cat gtc gat gat ttc tac 163
Arg Arg Ala Ser Leu Gln Leu Pro Tyr Thr His Val Asp Asp Phe Tyr
10 15 20

atc aac ggt tcc tgg gtt aaa gca gaa gga aca caa cgc aac ccc gta 211
Ile Asn Gly Ser Trp Val Lys Ala Glu Gly Thr Gln Arg Asn Pro Val
25 30 35

gtt gat cct gcg gtc ggt caa gaa tgg gga tct gtt cca gaa gca acc 259
Val Asp Pro Ala Val Gly Gln Glu Trp Gly Ser Val Pro Glu Ala Thr
40 45 50

gca tct gaa ttg gac tct gcg gtg gga gct gca cgt aca gcg cta aag 307
Ala Ser Glu Leu Asp Ser Ala Val Gly Ala Ala Arg Thr Ala Leu Lys
55 60 65

tcg tgg agt gca ctt aca ggt gcg gaa cga aca ggc tac ctc ctg aaa 355
Ser Trp Ser Ala Leu Thr Gly Ala Glu Arg Thr Gly Tyr Leu Leu Lys
70 75 80 85

atc gcg acg gaa att gaa tcc cgt tct gaa gct cta gca ctt act aat 403
Ile Ala Thr Glu Ile Glu Ser Arg Ser Glu Ala Leu Ala Leu Thr Asn
90 95 100

acc cgc gaa aat ggt tcc ccc att tcc gag acc cgt gga gct gcg tcc 451
Thr Arg Glu Asn Gly Ser Pro Ile Ser Glu Thr Arg Gly Ala Ala Ser
105 110 115

aat gca gca gga att ttc cgt tac ttt gcc act ctc gcg cct tgg tta 499
Asn Ala Ala Gly Ile Phe Arg Tyr Phe Ala Thr Leu Ala Pro Trp Leu
120 125 130

gac ggc gaa gac atc cgc cca ttt cct gcc ggt agc gcc gaa tcc atc 547
Asp Gly Glu Asp Ile Arg Pro Phe Pro Ala Gly Ser Ala Glu Ser Ile
135 140 145

gtg gat aaa gat ccc atc ggt gtc tgc gca ctc atc gcc cca tgg aat 595
Val Asp Lys Asp Pro Ile Gly Val Cys Ala Leu Ile Ala Pro Trp Asn
150 155 160 165

ttc ccg atc aac ctt gta gtc atc aaa ctg gca cca gca ctt ctt gcc 643
Phe Pro Ile Asn Leu Val Val Ile Lys Leu Ala Pro Ala Leu Leu Ala
170 175 180

ggc tgt acc gtc atc atc aaa cca gcc tcc ccc acc cca ctg tcg atc 691
Gly Cys Thr Val Ile Ile Lys Pro Ala Ser Pro Thr Pro Leu Ser Ile
185 190 195

cgt ttc atc atc gaa gcc atc gaa gcc gcc gga gtg cca gca ggc gta 739
Arg Phe Ile Ile Glu Ala Ile Glu Ala Ala Gly Val Pro Ala Gly Val
200 205 210

gtc aac cta ctc acc ggt tca ggg cgt ttc ggt gat gcc ctt gtc cgc 787

Val Asn Leu Leu Thr Gly Ser Gly Arg Phe Gly Asp Ala Leu Val Arg	
215 220 225	
cac ccc gga gta gac aag gta gcg ttt acc gga tca acg cct gtt gga	835
His Pro Gly Val Asp Lys Val Ala Phe Thr Gly Ser Thr Pro Val Gly	
230 235 240 245	
aag aag atc gct gcc gcc tgc gga gaa cta ctc cga cca gtg act tta	883
Lys Lys Ile Ala Ala Ala Cys Gly Glu Leu Leu Arg Pro Val Thr Leu	
250 255 260	
gag cta ggc gga aaa tct tcc gcg att atc ctt cct gat gca gac atg	931
Glu Leu Gly Gly Lys Ser Ser Ala Ile Ile Leu Pro Asp Ala Asp Met	
265 270 275	
tca gta ctc tcg acg cgg ttg att cga tcc tgt atg cgc aac act gga	979
Ser Val Leu Ser Thr Arg Leu Ile Arg Ser Cys Met Arg Asn Thr Gly	
280 285 290	
caa acc tgc tac atc agt acc cgg att att gcc cct agc tca cgc tat	1027
Gln Thr Cys Tyr Ile Ser Thr Arg Ile Ile Ala Pro Ser Ser Arg Tyr	
295 300 305	
gcg gaa gtc gta caa aca gtg gca agc act atc gct gca ggt aga caa	1075
Ala Glu Val Val Gln Thr Val Ala Ser Thr Ile Ala Ala Gly Arg Gln	
310 315 320 325	
ggt gac ccc tat gat gaa gaa acg gtt ttt ggg cca gtt gcc agc gcc	1123
Gly Asp Pro Tyr Asp Glu Glu Thr Val Phe Gly Pro Val Ala Ser Ala	
330 335 340	
tct cag tac tca acc gtc atg tct tac att gac tcc gca cga gag gaa	1171
Ser Gln Tyr Ser Thr Val Met Ser Tyr Ile Asp Ser Ala Arg Glu Glu	
345 350 355	
ggt gca cga gtg gtt gca ggt gga acc cgg tca atc agc ctt tct gaa	1219
Gly Ala Arg Val Val Ala Gly Gly Thr Arg Ser Ile Ser Leu Ser Glu	
360 365 370	
ggt tta gaa tca ggc gag ttt atc caa cca acc gtg ttt gcc gat gtc	1267
Gly Leu Glu Ser Gly Glu Phe Ile Gln Pro Thr Val Phe Ala Asp Val	
375 380 385	
acc ccc gac atg cgg ata tca cgc gaa gaa atc ttc ggc cct gtt att	1315
Thr Pro Asp Met Arg Ile Ser Arg Glu Glu Ile Phe Gly Pro Val Ile	
390 395 400 405	
tcc atc cta aag tac gac gat aca aac ggt gtt tcc gaa gca atc gca	1363
Ser Ile Leu Lys Tyr Asp Asp Thr Asn Gly Val Ser Glu Ala Ile Ala	
410 415 420	
cta gcc aac aac acg aaa ttc ggt ctc ggt ggc ttg gta ttt ggt gcg	1411
Leu Ala Asn Asn Thr Lys Phe Gly Leu Gly Gly Leu Val Phe Gly Ala	
425 430 435	
gat gag gaa caa gca cta gaa gtc gcc cgt caa gtg gat tct ggt tcc	1459
Asp Glu Glu Gln Ala Leu Glu Val Ala Arg Gln Val Asp Ser Gly Ser	
440 445 450	
gta ggc atc aac ttc ttc ggt tcc aac cat tcc gcc cca ttt gga gga	1507
Val Gly Ile Asn Phe Phe Gly Ser Asn His Ser Ala Pro Phe Gly Gly	

455 460 465
 cgc cac gaa tcc ggt atg gga gtg gaa tac ggc atc gaa ggc ctc agt 1555
 Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly Ile Glu Gly Leu Ser
 470 475 480 485
 gct tac ctg aca tac aag agt att cac cga acc att tagttactga 1601
 Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr Ile
 490 495
 aagttctcag cta 1614

 <210> 182
 <211> 497
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 182
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 1 5 10 15
 Val Asp Asp Phe Tyr Ile Asn Gly Ser Trp Val Lys Ala Glu Gly Thr
 20 25 30
 Gln Arg Asn Pro Val Val Asp Pro Ala Val Gly Gln Glu Trp Gly Ser
 35 40 45
 Val Pro Glu Ala Thr Ala Ser Glu Leu Asp Ser Ala Val Gly Ala Ala
 50 55 60
 Arg Thr Ala Leu Lys Ser Trp Ser Ala Leu Thr Gly Ala Glu Arg Thr
 65 70 75 80
 Gly Tyr Leu Leu Lys Ile Ala Thr Glu Ile Glu Ser Arg Ser Glu Ala
 85 90 95
 Leu Ala Leu Thr Asn Thr Arg Glu Asn Gly Ser Pro Ile Ser Glu Thr
 100 105 110
 Arg Gly Ala Ala Ser Asn Ala Ala Gly Ile Phe Arg Tyr Phe Ala Thr
 115 120 125
 Leu Ala Pro Trp Leu Asp Gly Glu Asp Ile Arg Pro Phe Pro Ala Gly
 130 135 140
 Ser Ala Glu Ser Ile Val Asp Lys Asp Pro Ile Gly Val Cys Ala Leu
 145 150 155 160
 Ile Ala Pro Trp Asn Phe Pro Ile Asn Leu Val Val Ile Lys Leu Ala
 165 170 175
 Pro Ala Leu Leu Ala Gly Cys Thr Val Ile Ile Lys Pro Ala Ser Pro
 180 185 190
 Thr Pro Leu Ser Ile Arg Phe Ile Ile Glu Ala Ile Glu Ala Ala Gly
 195 200 205
 Val Pro Ala Gly Val Val Asn Leu Leu Thr Gly Ser Gly Arg Phe Gly
 210 215 220

Asp Ala Leu Val Arg His Pro Gly Val Asp Lys Val Ala Phe Thr Gly
 225 230 235 240
 Ser Thr Pro Val Gly Lys Lys Ile Ala Ala Ala Cys Gly Glu Leu Leu
 245 250 255
 Arg Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Ser Ala Ile Ile Leu
 260 265 270
 Pro Asp Ala Asp Met Ser Val Leu Ser Thr Arg Leu Ile Arg Ser Cys
 275 280 285
 Met Arg Asn Thr Gly Gln Thr Cys Tyr Ile Ser Thr Arg Ile Ile Ala
 290 295 300
 Pro Ser Ser Arg Tyr Ala Glu Val Val Gln Thr Val Ala Ser Thr Ile
 305 310 315 320
 Ala Ala Gly Arg Gln Gly Asp Pro Tyr Asp Glu Glu Thr Val Phe Gly
 325 330 335
 Pro Val Ala Ser Ala Ser Gln Tyr Ser Thr Val Met Ser Tyr Ile Asp
 340 345 350
 Ser Ala Arg Glu Glu Gly Ala Arg Val Val Ala Gly Gly Thr Arg Ser
 355 360 365
 Ile Ser Leu Ser Glu Gly Leu Glu Ser Gly Glu Phe Ile Gln Pro Thr
 370 375 380
 Val Phe Ala Asp Val Thr Pro Asp Met Arg Ile Ser Arg Glu Glu Ile
 385 390 395 400
 Phe Gly Pro Val Ile Ser Ile Leu Lys Tyr Asp Asp Thr Asn Gly Val
 405 410 415
 Ser Glu Ala Ile Ala Leu Ala Asn Asn Thr Lys Phe Gly Leu Gly Gly
 420 425 430
 Leu Val Phe Gly Ala Asp Glu Glu Gln Ala Leu Glu Val Ala Arg Gln
 435 440 445
 Val Asp Ser Gly Ser Val Gly Ile Asn Phe Phe Gly Ser Asn His Ser
 450 455 460
 Ala Pro Phe Gly Gly Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly
 465 470 475 480
 Ile Glu Gly Leu Ser Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr
 485 490 495
 Ile

<210> 183

<211> 750

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(727)

<223> FRXA00689

<400> 183

actccgacca gtgactttag agctaggcgg aaaatcttcc gcgattatcc ttcctgatgc 60

agacatgtca gtactctcga cgcgggtgat tcgatcctgt atg cgc aac act gga 115
 Met Arg Asn Thr Gly
 1 5

caa acc tgc tac atc agt acc cgg att att gcc cct agc tca cgc tat 163
 Gln Thr Cys Tyr Ile Ser Thr Arg Ile Ile Ala Pro Ser Ser Arg Tyr
 10 15 20

gcg gaa gtc gta caa aca gtg gca agc act atc gct gca ggt aga caa 211
 Ala Glu Val Val Gln Thr Val Ala Ser Thr Ile Ala Ala Gly Arg Gln
 25 30 35

ggt gac ccc tat gat gaa gaa acg gtt ttt ggg cca gtt gcc agc gcc 259
 Gly Asp Pro Tyr Asp Glu Glu Thr Val Phe Gly Pro Val Ala Ser Ala
 40 45 50

tct cag tac tca acc gtc atg tct tac att gac tcc gca cga gag gaa 307
 Ser Gln Tyr Ser Thr Val Met Ser Tyr Ile Asp Ser Ala Arg Glu Glu
 55 60 65

ggt gca cga gtg gtt gca ggt gga acc cgg tca atc agc ctt tct gaa 355
 Gly Ala Arg Val Val Ala Gly Gly Thr Arg Ser Ile Ser Leu Ser Glu
 70 75 80 85

ggt tta gaa tca ggc gag ttt atc caa cca acc gtg ttt gcc gat gtc 403
 Gly Leu Glu Ser Gly Glu Phe Ile Gln Pro Thr Val Phe Ala Asp Val
 90 95 100

acc ccc gac atg cgg ata tca cgc gaa gaa atc ttc ggc cct gtt att 451
 Thr Pro Asp Met Arg Ile Ser Arg Glu Glu Ile Phe Gly Pro Val Ile
 105 110 115

tcc atc cta aag tac gac gat aca aac ggt gtt tcc gaa gca atc gca 499
 Ser Ile Leu Lys Tyr Asp Asp Thr Asn Gly Val Ser Glu Ala Ile Ala
 120 125 130

cta gcc aac aac acg aaa ttc ggt ctc ggt ggc ttg gta ttt ggt gcg 547
 Leu Ala Asn Asn Thr Lys Phe Gly Leu Gly Gly Leu Val Phe Gly Ala
 135 140 145

gat gag gaa caa gca cta gaa gtc gcc cgt caa gtg gat tct ggt tcc 595
 Asp Glu Glu Gln Ala Leu Glu Val Ala Arg Gln Val Asp Ser Gly Ser
 150 155 160 165

gta ggc atc aac ttc ttc ggt tcc aac cat tcc gcc cca ttt gga gga 643
 Val Gly Ile Asn Phe Phe Gly Ser Asn His Ser Ala Pro Phe Gly Gly
 170 175 180

cgc cac gaa tcc ggt atg gga gtg gaa tac ggc atc gaa ggc ctc agt 691
 Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly Ile Glu Gly Leu Ser
 185 190 195

gct tac ctg aca tac aag agt att cac cga acc att tagttactga 737
 Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr Ile

200

205

aagttctcag cta

750

<210> 184

<211> 209

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 184

Met Arg Asn Thr Gly Gln Thr Cys Tyr Ile Ser Thr Arg Ile Ile Ala
 1 5 10 15

Pro Ser Ser Arg Tyr Ala Glu Val Val Gln Thr Val Ala Ser Thr Ile
 20 25 30

Ala Ala Gly Arg Gln Gly Asp Pro Tyr Asp Glu Glu Thr Val Phe Gly
 35 40 45

Pro Val Ala Ser Ala Ser Gln Tyr Ser Thr Val Met Ser Tyr Ile Asp
 50 55 60

Ser Ala Arg Glu Glu Gly Ala Arg Val Val Ala Gly Gly Thr Arg Ser
 65 70 75 80

Ile Ser Leu Ser Glu Gly Leu Glu Ser Gly Glu Phe Ile Gln Pro Thr
 85 90 95

Val Phe Ala Asp Val Thr Pro Asp Met Arg Ile Ser Arg Glu Glu Ile
 100 105 110

Phe Gly Pro Val Ile Ser Ile Leu Lys Tyr Asp Asp Thr Asn Gly Val
 115 120 125

Ser Glu Ala Ile Ala Leu Ala Asn Asn Thr Lys Phe Gly Leu Gly Gly
 130 135 140

Leu Val Phe Gly Ala Asp Glu Glu Gln Ala Leu Glu Val Ala Arg Gln
 145 150 155 160

Val Asp Ser Gly Ser Val Gly Ile Asn Phe Phe Gly Ser Asn His Ser
 165 170 175

Ala Pro Phe Gly Gly Arg His Glu Ser Gly Met Gly Val Glu Tyr Gly
 180 185 190

Ile Glu Gly Leu Ser Ala Tyr Leu Thr Tyr Lys Ser Ile His Arg Thr
 195 200 205

Ile

<210> 185

<211> 878

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(855)

<223> RXN03128

<400> 185

aac gga ctc gcc att ccc gac att gga ttt ggt gta ttc caa acc cca	48
Asn Gly Leu Ala Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro	
1 5 10 15	
ccc gat gaa acc cga aac tcc gtt aac gct gct ctt gaa gcc ggc tat	96
Pro Asp Glu Thr Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr	
20 25 30	
cgc cac atc gac acc gcc gcc gca tac ggc aat gaa cgt gaa gtc ggt	144
Arg His Ile Asp Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly	
35 40 45	
gaa gca atc gca gca tcc ggc att ggc cgc gac gag atc acc atc gaa	192
Glu Ala Ile Ala Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu	
50 55 60	
acc aaa atc tgg gtg acc gac tac ggc ttc gag gaa act ctc cac gca	240
Thr Lys Ile Trp Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala	
65 70 75 80	
ttc gac aag gcc aca ggc aag ctt ggt gtc gat aca ctg gac att ttg	288
Phe Asp Lys Ala Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu	
85 90 95	
atc ttg cac cag gca gtg cca agc agc ttt gat cgc acc atc gcc gcc	336
Ile Leu His Gln Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala	
100 105 110	
tac aag gcg cta gag aag ctg ctt ttc gac ggc gcg gtg cgg gca atc	384
Tyr Lys Ala Leu Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile	
115 120 125	
gga gtc agt aat ttc atg cca gag cac ctg gac aaa ctc ctt ttg gaa	432
Gly Val Ser Asn Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu	
130 135 140	
acc tcc att gtc cca gct ctg aac caa atc gaa tgc cac ccc tac ttc	480
Thr Ser Ile Val Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe	
145 150 155 160	
cag cag cgt gac gtg ctt gcc cgc aat gag cag ctt ggc att ttg act	528
Gln Gln Arg Asp Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr	
165 170 175	
cag gcg tgg tca cca atc ggt ggc atc acc ttc tac cgc gac gga cag	576
Gln Ala Trp Ser Pro Ile Gly Gly Ile Thr Phe Tyr Arg Asp Gly Gln	
180 185 190	
ctt cca agc act cta gaa aat gag gtc atc gct gga atc gcc gca gaa	624
Leu Pro Ser Thr Leu Glu Asn Glu Val Ile Ala Gly Ile Ala Ala Glu	
195 200 205	
gtt ggc aaa aca cca gct caa gta atg ctg cgc tgg cac cta cag cgt	672
Val Gly Lys Thr Pro Ala Gln Val Met Leu Arg Trp His Leu Gln Arg	
210 215 220	
aga cgt cac gca att cca aag tct gtg acc cca tca cgc att gtg gaa	720

Arg Arg His Ala Ile Pro Lys Ser Val Thr Pro Ser Arg Ile Val Glu
 225 230 235 240

aac ttt gag atc ttt gat ttc gaa ctc tcc gat gag caa cta cag caa 768
 Asn Phe Glu Ile Phe Asp Phe Glu Leu Ser Asp Glu Gln Leu Gln Gln
 245 250 255

atc gat gcc ctc aac acc gat ctg cgc ggt ggc cca gaa cca gag aac 816
 Ile Asp Ala Leu Asn Thr Asp Leu Arg Gly Gly Pro Glu Pro Glu Asn
 260 265 270

atc acc atg gaa aac tac tac cga gaa atc cca gaa gcc taaaggccct 865
 Ile Thr Met Glu Asn Tyr Tyr Arg Glu Ile Pro Glu Ala
 275 280 285

tagaggcgaa tgt 878

<210> 186

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Asn Gly Leu Ala Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro
 1 5 10 15

Pro Asp Glu Thr Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr
 20 25 30

Arg His Ile Asp Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly
 35 40 45

Glu Ala Ile Ala Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu
 50 55 60

Thr Lys Ile Trp Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala
 65 70 75 80

Phe Asp Lys Ala Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu
 85 90 95

Ile Leu His Gln Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala
 100 105 110

Tyr Lys Ala Leu Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile
 115 120 125

Gly Val Ser Asn Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu
 130 135 140

Thr Ser Ile Val Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe
 145 150 155 160

Gln Gln Arg Asp Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr
 165 170 175

Gln Ala Trp Ser Pro Ile Gly Gly Ile Thr Phe Tyr Arg Asp Gly Gln
 180 185 190

Leu Pro Ser Thr Leu Glu Asn Glu Val Ile Ala Gly Ile Ala Ala Glu

195	200	205
Val Gly Lys Thr Pro Ala Gln Val Met Leu Arg Trp His Leu Gln Arg		
210	215	220
Arg Arg His Ala Ile Pro Lys Ser Val Thr Pro Ser Arg Ile Val Glu		
225	230	235
Asn Phe Glu Ile Phe Asp Phe Glu Leu Ser Asp Glu Gln Leu Gln Gln		
245	250	255
Ile Asp Ala Leu Asn Thr Asp Leu Arg Gly Gly Pro Glu Pro Glu Asn		
260	265	270
Ile Thr Met Glu Asn Tyr Tyr Arg Glu Ile Pro Glu Ala		
275	280	285

<210> 187

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(522)

<223> FRXA02192

<400> 187

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Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro Pro Asp Glu Thr	
1 5 10 15	
cga aac tcc gtt aac gct gct ctt gaa gcc ggc tat cgc cac atc gac	96
Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr Arg His Ile Asp	
20 25 30	
acc gcg gcc gca tac ggc aat gaa cgt gaa gtc ggt gaa gca atc gca	144
Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly Glu Ala Ile Ala	
35 40 45	
gca tcc ggc att ggc cgc gac gag atc acc atc gaa acc aaa atc tgg	192
Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu Thr Lys Ile Trp	
50 55 60	
gtg acc gac tac ggc ttc gag gaa act ctc cac gca ttc gac aag gcc	240
Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala Phe Asp Lys Ala	
65 70 75 80	
aca ggc aag ctt ggt gtc gat aca ctg gac att ttg atc ttg cac cag	288
Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu Ile Leu His Gln	
85 90 95	
gca gtg cca agc agc ttt gat cgc acc atc gcc gcc tac aag gcg cta	336
Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala Tyr Lys Ala Leu	
100 105 110	
gag aag ctg ctt ttc gac ggc gcg gtg cgg gca atc gga gtc agt aat	384
Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile Gly Val Ser Asn	
115 120 125	

ttc atg cca gag cac ctg gac aaa ctc ctt ttg gaa acc tcc att gtc 432
 Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu Thr Ser Ile Val
 130 135 140

cca gct ctg aac caa atc gaa tgc cac ccc tac ttc cag cag cgt gac 480
 Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe Gln Gln Arg Asp
 145 150 155 160

gtg ctt gcc cgc aat gag cag ctt ggc att ttg act cag gcg 522
 Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr Gln Ala
 165 170

<210> 188

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 188

Ile Pro Asp Ile Gly Phe Gly Val Phe Gln Thr Pro Pro Asp Glu Thr
 1 5 10 15

Arg Asn Ser Val Asn Ala Ala Leu Glu Ala Gly Tyr Arg His Ile Asp
 20 25 30

Thr Ala Ala Ala Tyr Gly Asn Glu Arg Glu Val Gly Glu Ala Ile Ala
 35 40 45

Ala Ser Gly Ile Gly Arg Asp Glu Ile Thr Ile Glu Thr Lys Ile Trp
 50 55 60

Val Thr Asp Tyr Gly Phe Glu Glu Thr Leu His Ala Phe Asp Lys Ala
 65 70 75 80

Thr Gly Lys Leu Gly Val Asp Thr Leu Asp Ile Leu Ile Leu His Gln
 85 90 95

Ala Val Pro Ser Ser Phe Asp Arg Thr Ile Ala Ala Tyr Lys Ala Leu
 100 105 110

Glu Lys Leu Leu Phe Asp Gly Ala Val Arg Ala Ile Gly Val Ser Asn
 115 120 125

Phe Met Pro Glu His Leu Asp Lys Leu Leu Leu Glu Thr Ser Ile Val
 130 135 140

Pro Ala Leu Asn Gln Ile Glu Cys His Pro Tyr Phe Gln Gln Arg Asp
 145 150 155 160

Val Leu Ala Arg Asn Glu Gln Leu Gly Ile Leu Thr Gln Ala
 165 170

<210> 189

<211> 1039

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1039)

<223> RXA02351

<400> 189

tgacacttta cagactggtt ttcaactaat gacaccgaaa gaaatacacc tcaacctttt 60

tgctttcggg	gccgggcacc	acgcggcggc	gtggcgagcg	gtg	gag	gga	agc	gtc	115
				Val	Glu	Gly	Ser	Val	
				1				5	
gaa aag ctg	ggt tta att	tcc tgg tgg	gag gaa ctc	gcg	cg	acc	gct	163	
Glu Lys Leu	Gly Leu Ile	Ser Trp Trp	Glu Glu Leu	Ala Arg	Thr	Ala			
	10		15		20				
gag cgg ggc	aag ctg gat	gcg gtc ttt	ttg gcc gat	ggg	cag	gcg	att	211	
Glu Arg Gly	Lys Leu Asp	Ala Val Phe	Leu Ala Asp	Gly Gln	Ala	Ile			
	25		30		35				
aat ccg gtc	ggt ctg gag	aat ggg ccg	ggc tgg ttt	ttg	gag	ccg	gtg	259	
Asn Pro Val	Gly Leu Glu	Asn Gly Pro	Gly Trp Phe	Leu Glu	Pro	Val			
	40		45		50				
acc gcg ttg	act gcg atg	gcg cgg gcg	acg aac aat	att	ggg	ttg	atc	307	
Thr Ala Leu	Thr Ala Met	Ala Arg Ala	Thr Asn Asn	Ile Gly	Leu	Ile			
	55		60		65				
agc aca att	tcc agt acg	ttt tgg cag	ccg ttt cat	gcg	gcg	ccg	atg	355	
Ser Thr Ile	Ser Ser Thr	Phe Trp Gln	Pro Phe His	Ala Ala	Arg	Met			
	70		75		80		85		
atc gcc agc	ttg gat cat	att tcc ggt	ggg cgt gct	gga	atc	aat	gtg	403	
Ile Ala Ser	Leu Asp His	Ile Ser Gly	Gly Arg Ala	Gly Ile	Asn	Val			
	90		95		100				
gtg aca tcc	atg acc gat	gcg gag gcg	cgt aac cac	ggg	atg	gat	gcg	451	
Val Thr Ser	Met Thr Asp	Ala Glu Ala	Arg Asn His	Gly Met	Asp	Ala			
	105		110		115				
ttg ccg ggt	cac gat gtt	cg	tat gcg	cg	gct gcg	gaa	ttt	att	gaa
Leu Pro Gly	His Asp Val	Arg Tyr	Ala Arg	Ala	Ala	Glu	Phe	Ile	Glu
	120		125		130				
acc atc act	gcg ctg tgg	gat tct tgg	cct gcg gaa	agt	ttg	gtg	atg	547	
Thr Ile Thr	Ala Leu Trp	Asp Ser Trp	Pro Ala Glu	Ser Leu	Val	Met			
	135		140		145				
gat cgt gct	gga aaa ttt	gcg gac tcc	tcc ctc att	aaa	tct	atc	gat	595	
Asp Arg Ala	Gly Lys Phe	Ala Ala Asp	Ser Ser Leu	Ile Lys	Ser	Ile	Asp		
150		155		160		165			
cat gat ggt	gag ttc ttc	caa gtc gct	ggt ccg ctg	aat	atc	ccc	agt	643	
His Asp Gly	Glu Phe Phe	Gln Val Ala	Gly Pro Leu	Asn Ile	Pro	Ser			
	170		175		180				
cct ccg cag	ggt cga ccc	gta ctt ttt	cag gct gga	tcc	tca	ccg	caa	691	
Pro Pro Gln	Gly Arg Pro	Val Leu Phe	Gln Ala Gly	Ser Ser	Pro	Gln			
	185		190		195				
gga ccg gaa	atc gct gcg	aaa tac gcc	gag gca att	tac	tct	gtg	gcg	739	
Gly Arg Glu	Ile Ala Ala	Lys Tyr Ala	Glu Ala Ile	Tyr Ser	Val	Ala			
	200		205		210				

tgg gat ttg gag caa gcg caa gat tat cgc tct gat att cat gct cgt 787
 Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser Asp Ile His Ala Arg
 215 220 225

 gcc act gcc cag ggt cgc gag ccc atg ccg gtg ctt cct ggt ttg gtg 835
 Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val Leu Pro Gly Leu Val
 230 235 240 245

 act ttt gtt ggc acg acc gtg gaa gaa gcg cgt gca aaa cag cag gct 883
 Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg Ala Lys Gln Gln Ala
 250 255 260

 ctt aat gcg ttg ctg ccg gtc aaa gac tca cta aat cag ttg agt ttc 931
 Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu Asn Gln Leu Ser Phe
 265 270 275

 ttt gtg ggt caa gat tgc tcg acg tgg gat ttg gat gca cct ccc cca 979
 Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu Asp Ala Pro Pro Pro
 280 285 290

 cca ctg cca ccg cta gaa gag ttt tcc ggt cct aaa ggc agg tac gaa 1027
 Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro Lys Gly Arg Tyr Glu
 295 300 305

 acg gtc ctg cgg 1039
 Thr Val Leu Arg
 310

<210> 190
 <211> 313
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30

 Asp Gly Gln Ala Ile Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp
 35 40 45

 Phe Leu Glu Pro Val Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn
 50 55 60

 Asn Ile Gly Leu Ile Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe
 65 70 75 80

 His Ala Ala Arg Met Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg
 85 90 95

 Ala Gly Ile Asn Val Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn
 100 105 110

 His Gly Met Asp Ala Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala
 115 120 125

 Ala Glu Phe Ile Glu Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala
 130 135 140

Glu Ser Leu Val Met Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu
 145 150 155 160
 Ile Lys Ser Ile Asp His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro
 165 170 175
 Leu Asn Ile Pro Ser Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala
 180 185 190
 Gly Ser Ser Pro Gln Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala
 195 200 205
 Ile Tyr Ser Val Ala Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser
 210 215 220
 Asp Ile His Ala Arg Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val
 225 230 235 240
 Leu Pro Gly Leu Val Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg
 245 250 255
 Ala Lys Gln Gln Ala Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu
 260 265 270
 Asn Gln Leu Ser Phe Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu
 275 280 285
 Asp Ala Pro Pro Pro Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro
 290 295 300
 Lys Gly Arg Tyr Glu Thr Val Leu Arg
 305 310

<210> 191
 <211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> RXN00905

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 tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
 Met Thr Gln Phe Glu
 1 5
 aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20
 ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
 25 30 35
 cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259

Pro	Asn	Leu	Leu	Glu	Asp	Tyr	Ala	Gly	Ala	Lys	Glu	Trp	Val	Lys	Glu		
	40						45					50					
aca	ctg	acc	aac	gca	ggt	ctc	acc	gtc	agc	gaa	ttc	gct	gcc	gaa	gat	307	
Thr	Leu	Thr	Asn	Ala	Gly	Leu	Thr	Val	Ser	Glu	Phe	Ala	Ala	Glu	Asp		
	55					60					65						
gga	acc	acc	aac	ttc	atc	ggc	acc	cgc	aag	ggc	tcc	gaa	ggt	gca	cca	355	
Gly	Thr	Thr	Asn	Phe	Ile	Gly	Thr	Arg	Lys	Gly	Ser	Glu	Gly	Ala	Pro		
	70				75					80					85		
aag	gta	ctg	ctg	tac	agc	cac	ttc	gac	gtt	gtc	cca	tcc	ggc	cct	ttg	403	
Lys	Val	Leu	Leu	Tyr	Ser	His	Phe	Asp	Val	Val	Pro	Ser	Gly	Pro	Leu		
				90					95					100			
gat	ctc	tgg	gac	acc	aat	cct	ttt	gaa	ctc	acc	gag	cgc	gac	gct	ggc	451	
Asp	Leu	Trp	Asp	Thr	Asn	Pro	Phe	Glu	Leu	Thr	Glu	Arg	Asp	Ala	Gly		
			105					110					115				
cac	ggc	acc	cgc	tgg	tac	ggc	cgc	ggc	gcc	gct	gac	tgc	aag	ggc	aac	499	
His	Gly	Thr	Arg	Trp	Tyr	Gly	Arg	Gly	Ala	Ala	Asp	Cys	Lys	Gly	Asn		
			120				125					130					
ctg	gtc	atg	cac	ctc	gca	gca	ctg	cgc	gcc	gtc	gaa	gcc	agc	ggc	gac	547	
Leu	Val	Met	His	Leu	Ala	Ala	Leu	Arg	Ala	Val	Glu	Ala	Ser	Gly	Asp		
	135					140					145						
acc	aca	ctc	aac	ctc	acc	tac	gtg	gtc	gag	ggc	tcc	gag	gaa	atg	gga	595	
Thr	Thr	Leu	Asn	Leu	Thr	Tyr	Val	Val	Glu	Gly	Ser	Glu	Glu	Met	Gly		
	150				155				160					165			
ggc	gga	gcg	ctc	agc	gcg	ctc	atc	aag	gac	aag	cct	gag	ctt	ttc	gac	643	
Gly	Gly	Ala	Leu	Ser	Ala	Leu	Ile	Lys	Asp	Lys	Pro	Glu	Leu	Phe	Asp		
			170					175						180			
gca	gat	gtc	atc	ttg	att	gca	gac	agc	gga	aac	gct	tcc	gtg	ggc	acc	691	
Ala	Asp	Val	Ile	Leu	Ile	Ala	Asp	Ser	Gly	Asn	Ala	Ser	Val	Gly	Thr		
			185					190					195				
cca	acc	ttg	acc	act	acc	ctg	cgc	ggt	ggc	gga	cag	gtc	acc	gtc	acc	739	
Pro	Thr	Leu	Thr	Thr	Thr	Leu	Arg	Gly	Gly	Gly	Gln	Val	Thr	Val	Thr		
		200					205					210					
gtg	gac	acc	ctt	gaa	ggc	gct	gtt	cac	tcc	ggc	cag	aac	ggt	ggc	gct	787	
Val	Asp	Thr	Leu	Glu	Gly	Ala	Val	His	Ser	Gly	Gln	Asn	Gly	Gly	Ala		
	215					220					225						
gcc	cca	gat	gct	gtt	gct	gct	ctc	gtg	cgc	gtt	ctg	gat	act	ttg	cgc	835	
Ala	Pro	Asp	Ala	Val	Ala	Ala	Leu	Val	Arg	Val	Leu	Asp	Thr	Leu	Arg		
	230				235					240				245			
gat	gaa	cac	gga	cgc	acc	gtt	atc	gac	ggc	tgt	caa	cac	cac	cgc	aaa	883	
Asp	Glu	His	Gly	Arg	Thr	Val	Ile	Asp	Gly	Cys	Gln	His	His	Arg	Lys		
			250					255						260			
ctg	gaa	ggg	cga	gcc	tta	tgatccagag	actttccgca	gcg								924	
Leu	Glu	Gly	Arg	Ala	Leu												
			265														

<210> 192

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

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Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn
 1           5           10           15

Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn
          20           25           30

Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
          35           40           45

Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
 50           55           60

Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
 65           70           75           80

Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
          85           90           95

Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
          100          105          110

Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
          115          120          125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
          130          135          140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
          145          150          155          160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys
          165          170          175

Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn
          180          185          190

Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly
          195          200          205

Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly
          210          215          220

Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val
          225          230          235          240

Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys
          245          250          255

Gln His His Arg Lys Leu Glu Gly Arg Ala Leu
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<210> 193

<211> 716

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(693)

<223> FRXA00905

<400> 193

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 gaa aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa	96
Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu	
20 25 30	
 gat gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca	144
Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala	
35 40 45	
 cca aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct	192
Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro	
50 55 60	
 ttg gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct	240
Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala	
65 70 75 80	
 ggc cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc	288
Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly	
85 90 95	
 aac ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc	336
Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly	
100 105 110	
 gac acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg	384
Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met	
115 120 125	
 gga ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc	432
Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe	
130 135 140	
 gac gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc	480
Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly	
145 150 155 160	
 acc cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc	528
Thr Pro Thr Leu Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val	
165 170 175	
 acc gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc	576
Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly	
180 185 190	
 gct gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg	624
Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu	
195 200 205	
 cgc gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc	672
Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg	

210

215

220

aaa ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg
 Lys Leu Glu Gly Arg Ala Leu
 225 230

716

<210> 194

<211> 231

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 194

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Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu
 20 25 30

Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala
 35 40 45

Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro
 50 55 60

Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala
 65 70 75 80

Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly
 85 90 95

Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly
 100 105 110

Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met
 115 120 125

Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe
 130 135 140

Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly
 145 150 155 160

Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val
 165 170 175

Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly
 180 185 190

Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu
 195 200 205

Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg
 210 215 220

Lys Leu Glu Gly Arg Ala Leu
 225 230

<210> 195

<211> 627

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(604)

<223> RXA00906

<400> 195

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gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115
                               Met Asn Thr Asp Ala
                               1           5

ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163
Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro
          10           15           20

tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211
Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val
          25           30           35

gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259
Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg
          40           45           50

cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307
Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala
          55           60           65

ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355
Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val
          70           75           80           85

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403
Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His
          90           95           100

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451
Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp
          105           110           115

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499
Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser
          120           125           130

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547
Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val
          135           140           145

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595
Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu
          150           155           160           165

gtc aac cca taagcagaat tggcactcta cgg 627
Val Asn Pro

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<210> 196

<211> 168
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 196

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Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn
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Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly
          20             25             30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser
      35             40             45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
  50             55             60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
  65             70             75             80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
          85             90             95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
      100             105             110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
      115             120             125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu
  130             135             140

Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys
  145             150             155             160

Thr Glu Leu Ile Glu Val Asn Pro
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<210> 197
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(223)

<223> RXA00907

<400> 197

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actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt    115
                               Leu Ala Leu Tyr Gly
                               1             5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac    163
Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
          10             15             20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc    211
  
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Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
 25 30 35

aac tac acc aag tagacccaaa agcaggcgtt aac 246
 Asn Tyr Thr Lys
 40

<210> 198
 <211> 41
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 198
 Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala
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 Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu
 20 25 30
 Ala Leu Phe Leu Leu Asn Tyr Thr Lys
 35 40

<210> 199
 <211> 1386
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1363)
 <223> RXA02101

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 Met Ser Arg Ile Ser
 1 5
 gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163
 Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala
 10 15 20
 tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag 211
 Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu
 25 30 35
 acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259
 Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val
 40 45 50
 att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307
 Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly
 55 60 65
 tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355
 Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp
 70 75 80 85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt	403
Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg	
90 95 100	
atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc	451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly	
105 110 115	
cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat	499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp	
120 125 130	
gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca	547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro	
135 140 145	
tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta	595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu	
150 155 160 165	
gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc	643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val	
170 175 180	
ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct	691
Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala	
185 190 195	
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Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
200 205 210	
tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att	787
Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat	835
Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac	883
Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt	979
Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
280 285 290	
ggg gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac	1027
Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr	
295 300 305	
ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act	1075
Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr	
310 315 320 325	
gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct	1123

Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala
 330 335 340

tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc 1171
 Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe
 345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag 1219
 Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln
 360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc 1267
 Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala
 375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct 1315
 Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala
 390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac 1363
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taatcatcta gttttctgcg acg 1386

<210> 200

<211> 421

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 200

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 20 25 30

Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg
 35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala
 50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met
 65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro
 85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val
 100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala
 115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile
 130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met
 145 150 155 160

Val Ala Gly Gly Leu Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe
 165 170 175
 Gly Gln His Val Val Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro
 180 185 190
 Gly Gly Ala Leu Ala Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly
 195 200 205
 Arg Ser Ala His Gly Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr
 210 215 220
 Val Ala Ala Met Ile Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu
 225 230 235 240
 Val Ser Pro Glu Asp Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser
 245 250 255
 Gly Asn Thr Asn Asn Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn
 260 265 270
 Cys Arg Phe Tyr Asn Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile
 275 280 285
 Glu Arg Val Val Arg Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu
 290 295 300
 Pro Val Ile Glu Tyr Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro
 305 310 315 320
 Val Val Phe Asp Thr Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu
 325 330 335
 Asp Ser Ile Asp Ala Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser
 340 345 350
 Ile Pro Lys Ala Phe Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val
 355 360 365
 Thr Pro Arg Asp Gln Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala
 370 375 380
 Ser Asp Val Pro Ala Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala
 385 390 395 400
 Pro Thr Met Ser Ala Ala Thr Arg Ala Ala Ala Ala Ala Leu Leu Thr
 405 410 415
 Tyr Leu Gly Thr Asn
 420

<210> 201
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1366)

<223> RXN02565

<400> 201

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                                         Val Asn Asp Leu Thr
                                         1       5
cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
          10              15              20
ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
          25              30              35
ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
          40              45              50
gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
          55              60              65
cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
          70              75              80              85
att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
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gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
          105              110              115
ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
          120              125              130
gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
          135              140              145
tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
          150              155              160              165
gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643
Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg
          170              175              180
att cac gtc aat ggc gat gct ggt cat ggt tcc att cct ttc gac cgt 691
Ile His Val Asn Gly Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg
          185              190              195
gac agc gct att gtc aag atc ggt gaa gtc gcc cgc cga atc gct gcc 739
Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala Arg Arg Ile Ala Ala
          200              205              210

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gcc gat ctg aag gta gcc aag gac gat atc tgg caa ggc ttc gtc caa 787
 Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp Gln Gly Phe Val Gln
 215 220 225

gcg cac cgt ttc gac cca gaa acg gag cag gcg ctt ctt agc ggg acc 835
 Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala Leu Leu Ser Gly Thr
 230 235 240 245

tcc cct gag gcc tac gca gag ttc ggc gga ctc tcc cgc ttc gcc cac 883
 Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu Ser Arg Phe Ala His
 250 255 260

gcg gtg tct cat ctc acg atc gcc caa act gtg gtt cgt gca ggt caa 931
 Ala Val Ser His Leu Thr Ile Ala Gln Thr Val Val Arg Ala Gly Gln
 265 270 275

gcc atc aat gta ttg cca tcg cat gcg tac ttg gaa ctg gat atc cgt 979
 Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu Glu Leu Asp Ile Arg
 280 285 290

acc ctt cca ggc caa acc aat gac tat gtt gat gac acc ctg cgt gct 1027
 Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp Asp Thr Leu Arg Ala
 295 300 305

gct ctg ggc gat ctt gcc gat gaa gta gaa atc gaa cac ctc atc tct 1075
 Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile Glu His Leu Ile Ser
 310 315 320 325

gaa gaa gca acg gtg agc cca act gat tcc agg ttg tat aac acc ttg 1123
 Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg Leu Tyr Asn Thr Leu
 330 335 340

gaa aaa gtt ctt ggt gat ttc ttc ccc gat gcg cct gtg gtc cca att 1171
 Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro Ile
 345 350 355

att tcc tct ggt ggc tct gac ctg cgc ttt ggt cgt cga cta ggc ggt 1219
 Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly Gly
 360 365 370

gtt ggt tat ggt ttt gca gtt cat gca cgt gaa cga act ttg gcg gaa 1267
 Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala Glu
 375 380 385

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat 1315
 Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp
 390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta 1363
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 410 415 420

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 Gly

<210> 202

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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 20 25 30
 Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
 35 40 45
 Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
 50 55 60
 Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
 65 70 75 80
 Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
 85 90 95
 Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
 100 105 110
 Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
 115 120 125
 Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
 130 135 140
 Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
 145 150 155 160
 Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
 165 170 175
 Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
 180 185 190
 Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
 195 200 205
 Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320

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<211> 365
<212> DNA
<213> Corynebacterium glutamicum
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<222> (1)..(342)  
<223> FRXA02565
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Ala	Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile		
1				5					10					15			
tct	gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	96	
Ser	Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr		
			20					25					30				
ttg	gaa	aaa	gtt	ctt	ggt	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	144	
Leu	Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro		
		35					40					45					
att	att	tcc	tct	ggt	ggc	tct	gac	ctg	cgc	ttt	ggt	cgt	cga	cta	ggc	192	
Ile	Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly		
	50					55					60						
ggt	gtt	ggt	tat	ggt	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	240	
Gly	Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala		
65					70					75				80			
gaa	gca	atg	ggg	caa	ctt	cac	tcc	cat	gac	gag	gcg	ctg	tac	ctg	gaa	288	
Glu	Ala	Met	Gly	Gln	Leu	His	Ser	His	Asp	Glu	Ala	Leu	Tyr	Leu	Glu		
				85					90					95			
gat	ctt	gaa	ctg	act	gtt	cgg	ggt	tat	gac	tcc	gtc	gtg	cgt	gaa	ttc	336	
Asp	Leu	Glu	Leu	Thr	Val	Arg	Gly	Tyr	Asp	Ser	Val	Val	Arg	Glu	Phe		
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cta ggc taaaaacatg aagcaggagt ctt
Leu Gly

365

<210> 204
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 204
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20 25 30
Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro
35 40 45
Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly
50 55 60
Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala
65 70 75 80
Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu
85 90 95
Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe
100 105 110
Leu Gly

<210> 205
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(738)
<223> FRXA02567

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gaa att aga aac gcg gaa agc cta gaa cgt ttc ttt gaa gga acc ccc 96
Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro
20 25 30
aac gtt aaa atc acc aag ctg gaa ccg cat ccg ggc cgg acc tca att 144
Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro Gly Arg Thr Ser Ile
35 40 45
atc gtg act gtt cca ggc agc gat cca gat gct gag cct tta aca ctg 192

Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu
 50 55 60

ctt gga cat act gat gtt gtg cct gtt gat ctg cct aaa tgg act aaa 240
 Leu Gly His Thr Asp Val Val Pro Val Asp Leu Pro Lys Trp Thr Lys
 65 70 75 80

gat cca ttc ggt gcg gag att tcg gat gga cag att tgg ggt aga ggg 288
 Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly
 85 90 95

tcc gtc gat atg ctc ttt att acc gca acc caa gcg gcc gtc acc cgt 336
 Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln Ala Ala Val Thr Arg
 100 105 110

caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg ctg aca ttc gtt ggc 384
 Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr Leu Thr Phe Val Gly
 115 120 125

gtt gct gat gag gaa gcc cgc ggc gga ctc gga gcg aag tgg ctt tcc 432
 Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser
 130 135 140

gaa gaa cac caa aac ctc ttc agc tgg aaa aac tgc ctc tcc gaa tcc 480
 Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser
 145 150 155 160

ggc gga tcg cac ctt cca gtc cac gac ggc agc gac gca gta gta att 528
 Gly Gly Ser His Leu Pro Val His Asp Gly Ser Asp Ala Val Val Ile
 165 170 175

aac gtt gga gaa aaa ggt gca gct caa cgt cgt att cac gtc aat ggc 576
 Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg Ile His Val Asn Gly
 180 185 190

gat gct ggt cat ggt tcc att cct ttc gac cgt gac agc gct att gtc 624
 Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg Asp Ser Ala Ile Val
 195 200 205

aag atc ggt gaa gtc gcc cgc cga atc gct gcc gcc gat ctg aag gta 672
 Lys Ile Gly Glu Val Ala Arg Arg Ile Ala Ala Ala Asp Leu Lys Val
 210 215 220

gcc aag gac gat atc tgg caa ggc ttc gtc caa gcg cac cgt ttc gac 720
 Ala Lys Asp Asp Ile Trp Gln Gly Phe Val Gln Ala His Arg Phe Asp
 225 230 235 240

cca gaa acg gag cag gcg 738
 Pro Glu Thr Glu Gln Ala
 245

<210> 206

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Leu Ile Arg Asn Ala Cys Val Asn Asp Leu Thr Pro Asp Ser Gly Gln
 1 5 10 15

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			20					25		30					
Asn	Val	Lys	Ile	Thr	Lys	Leu	Glu	Pro	His	Pro	Gly	Arg	Thr	Ser	Ile
			35					40		45					
Ile	Val	Thr	Val	Pro	Gly	Ser	Asp	Pro	Asp	Ala	Glu	Pro	Leu	Thr	Leu
			50					55		60					
Leu	Gly	His	Thr	Asp	Val	Val	Pro	Val	Asp	Leu	Pro	Lys	Trp	Thr	Lys
			65					70		75					
Asp	Pro	Phe	Gly	Ala	Glu	Ile	Ser	Asp	Gly	Gln	Ile	Trp	Gly	Arg	Gly
			85					90		95					
Ser	Val	Asp	Met	Leu	Phe	Ile	Thr	Ala	Thr	Gln	Ala	Ala	Val	Thr	Arg
			100					105		110					
Gln	Val	Ala	Arg	Glu	Gly	Gly	Leu	Arg	Gly	Thr	Leu	Thr	Phe	Val	Gly
			115					120		125					
Val	Ala	Asp	Glu	Glu	Ala	Arg	Gly	Gly	Leu	Gly	Ala	Lys	Trp	Leu	Ser
			130					135		140					
Glu	Glu	His	Gln	Asn	Leu	Phe	Ser	Trp	Lys	Asn	Cys	Leu	Ser	Glu	Ser
			145					150		155					
Gly	Gly	Ser	His	Leu	Pro	Val	His	Asp	Gly	Ser	Asp	Ala	Val	Val	Ile
			165					170		175					
Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg	Ile	His	Val	Asn	Gly
			180					185		190					
Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg	Asp	Ser	Ala	Ile	Val
			195					200		205					
Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala	Ala	Asp	Leu	Lys	Val
			210					215		220					
Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln	Ala	His	Arg	Phe	Asp
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Pro	Glu	Thr	Glu	Gln	Ala										
			245												

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<210> 207
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<213> Corynebacterium glutamicum
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Val Met Glu Ile Gly

1															5				
gtg	cag	gtt	gcc	tca	tgg	atg	gac	cgc	cac	cat	gac	gag	gtc	ata	aag				163
Val	Gln	Val	Ala	Ser	Trp	Met	Asp	Arg	His	His	Asp	Glu	Val	Ile	Lys				
			10					15						20					
tgg	cgc	agg	cat	ttg	cac	agc	cat	cct	gag	ctc	tcc	cac	atg	gaa	tac				211
Trp	Arg	Arg	His	Leu	His	Ser	His	Pro	Glu	Leu	Ser	His	Met	Glu	Tyr				
			25					30					35						
cgc	acg	act	gag	tat	ttg	gcc	tcg	gtt	ctg	aaa	gat	cac	ggc	atg	gaa				259
Arg	Thr	Thr	Glu	Tyr	Leu	Ala	Ser	Val	Leu	Lys	Asp	His	Gly	Met	Glu				
		40					45					50							
cca	cac	ctg	ttc	cca	gga	acc	ggt	ttg	atg	gtg	gat	atc	gga	cca	gaa				307
Pro	His	Leu	Phe	Pro	Gly	Thr	Gly	Leu	Met	Val	Asp	Ile	Gly	Pro	Glu				
	55					60					65								
ggg	gac	tcc	cgc	ctg	gcg	ttt	cgc	gct	gat	atc	gat	gcc	ctt	ccg	ctg				355
Gly	Asp	Ser	Arg	Leu	Ala	Phe	Arg	Ala	Asp	Ile	Asp	Ala	Leu	Pro	Leu				
70					75				80					85					
ctt	gaa	tca	acc	ggc	tta	gag	ttc	tct	tcc	aca	gcc	act	ggc	gtt	gcg				403
Leu	Glu	Ser	Thr	Gly	Leu	Glu	Phe	Ser	Ser	Thr	Ala	Thr	Gly	Val	Ala				
			90					95					100						
cat	gcc	tgc	gga	cat	gac	gtg	cac	acg	gtg	atc	gct	ttg	gca	ctt	gcc				451
His	Ala	Cys	Gly	His	Asp	Val	His	Thr	Val	Ile	Ala	Leu	Ala	Leu	Ala				
			105					110					115						
tgt	gca	ctg	aac	acc	atc	gaa	ctg	ccc	atc	ggc	att	cgg	gtg	att	ttc				499
Cys	Ala	Leu	Asn	Thr	Ile	Glu	Leu	Pro	Ile	Gly	Ile	Arg	Val	Ile	Phe				
	120						125					130							
cag	ccg	gca	gaa	gaa	gtc	atg	act	ggt	ggc	gca	acg	gac	gtc	att	gcc				547
Gln	Pro	Ala	Glu	Glu	Val	Met	Thr	Gly	Gly	Ala	Thr	Asp	Val	Ile	Ala				
	135					140					145								
cac	ggt	ggc	ctt	gat	ggt	gtg	gat	gcg	att	tac	gcc	atc	cac	gtt	gaa				595
His	Gly	Gly	Leu	Asp	Gly	Val	Asp	Ala	Ile	Tyr	Ala	Ile	His	Val	Glu				
150					155				160					165					
ccc	aaa	ttg	aag	gtc	ggt	cgc	gtc	ggt	gta	cgc	gct	ggc	gcg	att	act				643
Pro	Lys	Leu	Lys	Val	Gly	Arg	Val	Gly	Val	Arg	Ala	Gly	Ala	Ile	Thr				
			170					175						180					
tct	gcc	tca	gat	gtg	atc	gaa	atc	aga	gtc	aag	ggt	gaa	gga	gga	cat				691
Ser	Ala	Ser	Asp	Val	Ile	Glu	Ile	Arg	Val	Lys	Gly	Glu	Gly	Gly	His				
			185					190					195						
agc	gca	cgt	cca	cac	ctc	tcc	gct	gat	gtt	gtt	tac	gcc	ttg	agc	aaa				739
Ser	Ala	Arg	Pro	His	Leu	Ser	Ala	Asp	Val	Val	Tyr	Ala	Leu	Ser	Lys				
		200					205					210							
ttg	gtc	gtt	gat	ctt	ccc	ggt	ttg	ctg	tcc	agg	cgc	gtc	gat	cca	cgc				787
Leu	Val	Val	Asp	Leu	Pro	Gly	Leu	Leu	Ser	Arg	Arg	Val	Asp	Pro	Arg				
	215					220					225								
acc	ggc	acc	gtg	ctt	gtt	ttc	ggc	acc	atc	aac	gcc	ggc	tat	gcg	ccc				835
Thr	Gly	Thr	Val	Leu	Val	Phe	Gly	Thr	Ile	Asn	Ala	Gly	Tyr	Ala	Pro				
230					235				240					245					

aac gcg atc cca gat tcc ggc atc gtg tca ggc acc ttg cgt aca gcc 883
 Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala
 250 255 260

gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg 931
 Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val
 265 270 275

gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat 979
 Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn
 280 285 290

ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg 1027
 Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu
 295 300 305

gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg 1075
 Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro
 310 315 320 325

cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca 1123
 Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro
 330 335 340

gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa 1171
 Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln
 345 350 355

gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt 1219
 Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val
 360 365 370

ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct 1267
 Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser
 375 380 385

gaa gct ttc tta aat tcc taatgggggt agtgtgtagg gct 1308
 Glu Ala Phe Leu Asn Ser
 390 395

<210> 208
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 208
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 Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
 20 25 30
 Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
 35 40 45
 Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
 50 55 60
 Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile

65	70	75	80
Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr	85	90	95
Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile	100	105	110
Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly	115	120	125
Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala	130	135	140
Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr	145	150	155
Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg	165	170	175
Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys	180	185	190
Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val	195	200	205
Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg	210	215	220
Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn	225	230	235
Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly	245	250	255
Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu	260	265	270
Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His	275	280	285
Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val	290	295	300
Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser	305	310	315
Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr	325	330	335
Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly	340	345	350
His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu	355	360	365
Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln	370	375	380
Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser	385	390	395


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<210> 209
<211> 1308
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1285)  
<223> FRXA02855
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<400> 209

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Val Met Glu Ile Gly
1 5

gtg cag gtt gcc tca tgg atg gac cgc cac cat gac gag gtc ata aag 163
Val Gln Val Ala Ser Trp Met Asp Arg His His Asp Glu Val Ile Lys
10 15 20

tgg	cgc	agg	cat	ttg	cac	agc	cat	cct	gag	ctc	tcc	cac	atg	gaa	tac	211
Trp	Arg	Arg	His	Leu	His	Ser	His	Pro	Glu	Leu	Ser	His	Met	Glu	Tyr	
			25					30					35			

cgc acg act gag tat ttg gcc tcg gtt ctg aaa gat cac ggc atg gaa 259
 Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys Asp His Gly Met Glu
 40 45 50

cca cac ctg ttc cca gga acc ggt ttg atg gtg gat atc gga cca gaa 307
Pro His Leu Phe Pro Gly Thr Gly Leu Met Val Asp Ile Gly Pro Glu
55 60 65

ggg gac tcc cgc ctg gcg ttt cgc gct gat atc gat gcc ctt ccg ctg 355
Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile Asp Ala Leu Pro Leu
70 75 80 85

ctt gaa tca acc ggc tta gag ttc tct tcc aca gcc act ggc gtt gcg 403
Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr Ala Thr Gly Val Ala
90 95 100

cat gcc tgc gga cat gac gtg cac acg gtg atc gct ttg gca ctt gcc 451
His Ala Cys Gly His Asp Val His Thr Val Ile Ala Leu Ala Leu Ala
105 110 115

tgt gca ctg aac acc atc gaa ctg ccc atc gcc att cgg gtg att ttc 499
Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly Ile Arg Val Ile Phe
 120 125 130

cag ccg gca gaa gaa gtc atg act ggt ggc gca acg gac gtc att gcc 547
Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala Thr Asp Val Ile Ala
135 140 145

cac ggt ggc ctt gat ggt gtg gat gcg att tac gcc atc cac gtt gaa 595
 His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr Ala Ile His Val Glu
 150 155 160 165

ccc aaa ttg aag gtc ggt cgc gtc ggt gta cgc gct ggc gcg att act 643
Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg Ala Gly Ala Ile Thr

170										175										180										
tct gcc tca gat gtg atc gaa atc aga gtc aag ggt gaa gga gga cat	691																													
Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys Gly Glu Gly Gly His																														
185 190 195																														
agc gca cgt cca cac ctc tcc gct gat gtt gtt tac gcc ttg agc aaa	739																													
Ser Ala Arg Pro His Leu Ser Ala Asp Val Val Tyr Ala Leu Ser Lys																														
200 205 210																														
ttg gtc gtt gat ctt ccc ggt ttg ctg tcc agg cgc gtc gat cca cgc	787																													
Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg Arg Val Asp Pro Arg																														
215 220 225																														
acc ggc acc gtg ctt gtt ttc ggc acc atc aac gcc ggc tat gcg ccc	835																													
Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn Ala Gly Tyr Ala Pro																														
230 235 240 245																														
aac gcg atc cca gat tcc ggc atc gtg tca ggc acc ttg cgt aca gcc	883																													
Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala																														
250 255 260																														
gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg	931																													
Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val																														
265 270 275																														
gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat	979																													
Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn																														
280 285 290																														
ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg	1027																													
Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu																														
295 300 305																														
gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg	1075																													
Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro																														
310 315 320 325																														
cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca	1123																													
Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro																														
330 335 340																														
gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa	1171																													
Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln																														
345 350 355																														
gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt	1219																													
Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val																														
360 365 370																														
ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct	1267																													
Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser																														
375 380 385																														
gaa gct ttc tta aat tcc taatgggggt agtgtgtagg gct	1308																													
Glu Ala Phe Leu Asn Ser																														
390 395																														

<210> 210

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

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Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
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Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
      20           25           30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
      35           40           45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
      50           55           60

Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile
      65           70           75           80

Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr
      85           90           95

Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile
      100          105          110

Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly
      115          120          125

Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala
      130          135          140

Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr
      145          150          155          160

Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg
      165          170          175

Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys
      180          185          190

Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val
      195          200          205

Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg
      210          215          220

Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn
      225          230          235          240

Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly
      245          250          255

Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu
      260          265          270

Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His
      275          280          285

Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val
      290          295          300

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Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser
305 310 315 320

Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr
325 330 335

Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly
340 345 350

His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu
355 360 365

Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln
370 375 380

Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser
385 390 395

<210> 211

<211> 1509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> RXA00026

<400> 211

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Met Ser Thr Asp Asn
1 5

ttt tct cca caa gtt ccg tcg act gtg tat ttg gat tac atg gag caa 163
Phe Ser Pro Gln Val Pro Ser Thr Val Tyr Leu Asp Tyr Met Glu Gln
10 15 20

ggg att gcc gcg cgc aaa gcg gag gca gaa tct aac gcc agc acg aag 211
Gly Ile Ala Ala Arg Lys Ala Glu Ala Glu Ser Asn Ala Ser Thr Lys
25 30 35

ggg gag agc ccg gat tat cca ggc cag cag gtt att tgg cgc ctg atc 259
Gly Glu Ser Pro Asp Tyr Pro Gly Gln Gln Val Ile Trp Arg Leu Ile
40 45 50

cag gaa gca ggg gag tcg ttg cgt gat gaa ctg cgc aca ctg gct ttc 307
Gln Glu Ala Gly Glu Ser Leu Arg Asp Glu Leu Arg Thr Leu Ala Phe
55 60 65

acg ctg cac gac cat ccg gaa gaa gcg ttc gag gag gtg ttc gcc acc 355
Thr Leu His Asp His Pro Glu Glu Ala Phe Glu Glu Val Phe Ala Thr
70 75 80 85

gag gaa atc aca aaa ctt ctg caa aat cat ggt ttt gag gtt cag agt 403
Glu Glu Ile Thr Lys Leu Leu Gln Asn His Gly Phe Glu Val Gln Ser
90 95 100

gga gtt tat ggt gtt aaa acc gct cta gaa act agt ttt gaa acc cct 451

Gly Val Tyr Gly Val Lys Thr Ala Leu Glu Thr Ser Phe Glu Thr Pro	
105 110 115	
ggt tat gat cca gcg cag cac cca agc att gcg atc ttg gcg gaa tac	499
Gly Tyr Asp Pro Ala Gln His Pro Ser Ile Ala Ile Leu Ala Glu Tyr	
120 125 130	
gat gcc ctt cca gag atc ggc cat gca tgc ggg cac aat atc atc gca	547
Asp Ala Leu Pro Glu Ile Gly His Ala Cys Gly His Asn Ile Ile Ala	
135 140 145	
gca gct ggt gtt ggc gca ttt tta gct gtc acc aac atg atc aaa act	595
Ala Ala Gly Val Gly Ala Phe Leu Ala Val Thr Asn Met Ile Lys Thr	
150 155 160 165	
gcc gaa gtg aaa ggc gtg gat cac ctc gac ttt gaa ggc cgg atc gtg	643
Ala Glu Val Lys Gly Val Asp His Leu Asp Phe Glu Gly Arg Ile Val	
170 175 180	
ctg ttg gga aca cct gct gag gag ggg cat tcc ggc aag gaa tac atg	691
Leu Leu Gly Thr Pro Ala Glu Glu Gly His Ser Gly Lys Glu Tyr Met	
185 190 195	
atc cga aat ggc gca ttc gat ggc att gat gcg tcg att atg atg cac	739
Ile Arg Asn Gly Ala Phe Asp Gly Ile Asp Ala Ser Ile Met Met His	
200 205 210	
ccc ttt ggc ttc gat ctg gcg gag cat gtt tgg gtg ggc aga cgt acc	787
Pro Phe Gly Phe Asp Leu Ala Glu His Val Trp Val Gly Arg Arg Thr	
215 220 225	
atg acg gcg acg ttc cac ggt gtc tct gca cac gcg tct tcg cag cct	835
Met Thr Ala Thr Phe His Gly Val Ser Ala His Ala Ser Ser Gln Pro	
230 235 240 245	
ttc atg ggt aaa aat gcc ctc gac gct gca agt ttg gcg tac cag ggc	883
Phe Met Gly Lys Asn Ala Leu Asp Ala Ala Ser Leu Ala Tyr Gln Gly	
250 255 260	
ttc gga gtt ttg cgt cag caa atg cca ccg agc gac cgc ctt cac gcc	931
Phe Gly Val Leu Arg Gln Gln Met Pro Pro Ser Asp Arg Leu His Ala	
265 270 275	
att att acg gaa ggc gga aac cgg cca agc atc att cca gac act gca	979
Ile Ile Thr Glu Gly Gly Asn Arg Pro Ser Ile Ile Pro Asp Thr Ala	
280 285 290	
acg atg tcg ctg tac gtg cgt tct ttg ttg ccg gaa gca ctc aaa gac	1027
Thr Met Ser Leu Tyr Val Arg Ser Leu Leu Pro Glu Ala Leu Lys Asp	
295 300 305	
ata tcg aaa cgc gtg gat gat gtg ctc gat ggg gcg gcc ttg atg gcg	1075
Ile Ser Lys Arg Val Asp Asp Val Leu Asp Gly Ala Ala Leu Met Ala	
310 315 320 325	
ggg gtt ggc gtc gaa aag caa tgg gat gtg cac cca gct agc ttg ccc	1123
Gly Val Gly Val Glu Lys Gln Trp Asp Val His Pro Ala Ser Leu Pro	
330 335 340	
gtg cgc aac aat cat gtg ttg gcg cgg cgt tgg gca aaa acg cag aat	1171
Val Arg Asn Asn His Val Leu Ala Arg Arg Trp Ala Lys Thr Gln Asn	

	345	350	355	
ctg cgt ggt cga acg gcg ctt tcg gag ggt att ttg ccc gac act ctg				1219
Leu Arg Gly Arg Thr Ala Leu Ser Glu Gly Ile Leu Pro Asp Thr Leu				
	360	365	370	
gca gca tcg act gat ttt ggc aat gtc tcg cac ctg gtt ccg ggc att				1267
Ala Ala Ser Thr Asp Phe Gly Asn Val Ser His Leu Val Pro Gly Ile				
	375	380	385	
cat ccg atg gtg aaa att tct ccg gaa aac gtt gcg ctc cac acc aag				1315
His Pro Met Val Lys Ile Ser Pro Glu Asn Val Ala Leu His Thr Lys				
	390	395	400	405
gaa ttc gcc gct tat gcg cgc acg gaa gag gcc atc gac gca gcc gtc				1363
Glu Phe Ala Ala Tyr Ala Arg Thr Glu Glu Ala Ile Asp Ala Ala Val				
	410	415	420	
gac gcc gca atc ggg ctg gcg caa gtc gcc gtt gac gcg ctt gca gat				1411
Asp Ala Ala Ile Gly Leu Ala Gln Val Ala Val Asp Ala Leu Ala Asp				
	425	430	435	
ccg caa atg ctt atc gac gcg acc ctc gag ttc acc aac tcc ggc gac				1459
Pro Gln Met Leu Ile Asp Ala Thr Leu Glu Phe Thr Asn Ser Gly Asp				
	440	445	450	
gta ctt aaa gta ggg gac tat ttg gct taggcaacga ctccgaaacc				1506
Val Leu Lys Val Gly Asp Tyr Leu Ala				
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ttc				1509

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<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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20	25	30		
Asn Ala Ser Thr Lys Gly Glu Ser Pro Asp Tyr Pro Gly Gln Gln Val				
35	40	45		
Ile Trp Arg Leu Ile Gln Glu Ala Gly Glu Ser Leu Arg Asp Glu Leu				
50	55	60		
Arg Thr Leu Ala Phe Thr Leu His Asp His Pro Glu Glu Ala Phe Glu				
65	70	75	80	
Glu Val Phe Ala Thr Glu Glu Ile Thr Lys Leu Leu Gln Asn His Gly				
85	90	95		
Phe Glu Val Gln Ser Gly Val Tyr Gly Val Lys Thr Ala Leu Glu Thr				
100	105	110		
Ser Phe Glu Thr Pro Gly Tyr Asp Pro Ala Gln His Pro Ser Ile Ala				

115	120	125
Ile Leu Ala Glu Tyr Asp Ala Leu Pro Glu Ile Gly His Ala Cys Gly 130 135 140		
His Asn Ile Ile Ala Ala Gly Val Gly Ala Phe Leu Ala Val Thr 145 150 155 160		
Asn Met Ile Lys Thr Ala Glu Val Lys Gly Val Asp His Leu Asp Phe 165 170 175		
Glu Gly Arg Ile Val Leu Leu Gly Thr Pro Ala Glu Glu Gly His Ser 180 185 190		
Gly Lys Glu Tyr Met Ile Arg Asn Gly Ala Phe Asp Gly Ile Asp Ala 195 200 205		
Ser Ile Met Met His Pro Phe Gly Phe Asp Leu Ala Glu His Val Trp 210 215 220		
Val Gly Arg Arg Thr Met Thr Ala Thr Phe His Gly Val Ser Ala His 225 230 235 240		
Ala Ser Ser Gln Pro Phe Met Gly Lys Asn Ala Leu Asp Ala Ala Ser 245 250 255		
Leu Ala Tyr Gln Gly Phe Gly Val Leu Arg Gln Gln Met Pro Pro Ser 260 265 270		
Asp Arg Leu His Ala Ile Ile Thr Glu Gly Gly Asn Arg Pro Ser Ile 275 280 285		
Ile Pro Asp Thr Ala Thr Met Ser Leu Tyr Val Arg Ser Leu Leu Pro 290 295 300		
Glu Ala Leu Lys Asp Ile Ser Lys Arg Val Asp Asp Val Leu Asp Gly 305 310 315 320		
Ala Ala Leu Met Ala Gly Val Gly Val Glu Lys Gln Trp Asp Val His 325 330 335		
Pro Ala Ser Leu Pro Val Arg Asn Asn His Val Leu Ala Arg Arg Trp 340 345 350		
Ala Lys Thr Gln Asn Leu Arg Gly Arg Thr Ala Leu Ser Glu Gly Ile 355 360 365		
Leu Pro Asp Thr Leu Ala Ala Ser Thr Asp Phe Gly Asn Val Ser His 370 375 380		
Leu Val Pro Gly Ile His Pro Met Val Lys Ile Ser Pro Glu Asn Val 385 390 395 400		
Ala Leu His Thr Lys Glu Phe Ala Ala Tyr Ala Arg Thr Glu Glu Ala 405 410 415		
Ile Asp Ala Ala Val Asp Ala Ala Ile Gly Leu Ala Gln Val Ala Val 420 425 430		
Asp Ala Leu Ala Asp Pro Gln Met Leu Ile Asp Ala Thr Leu Glu Phe 435 440 445		

Thr Asn Ser Gly Asp Val Leu Lys Val Gly Asp Tyr Leu Ala
 450 455 460

<210> 213
 <211> 954
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (101)..(931)
 <223> RXA01971

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 Met Ser Lys Lys Lys
 1 5
 cct cgc ccc att ccg gtt cct gcc caa ttt atc cct ggt ctg att gat 163
 Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile Pro Gly Leu Ile Asp
 10 15 20
 gcg cat aca cat ttg gca tcg tgt gga gga gat ctt gca ggg ttg gtg 211
 Ala His Thr His Leu Ala Ser Cys Gly Gly Asp Leu Ala Gly Leu Val
 25 30 35
 gaa agg gcc aag gag gcg ggc gtc gaa aag ctt tgt acc gtc ggt gat 259
 Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu Cys Thr Val Gly Asp
 40 45 50
 ggt ttg gct gag gcc gag ctt gcg ctg gag gcc gcg caa cag ttt ggc 307
 Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala Ala Gln Gln Phe Gly
 55 60 65
 aat gtg ttt gct gcg tgt gcg att cat ccg acg aag gct gat cag ttg 355
 Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr Lys Ala Asp Gln Leu
 70 75 80 85
 gat ggg gct gcg cgt gcg cgg ctg acg cag atg gcg gcg gat ccg aat 403
 Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met Ala Ala Asp Pro Asn
 90 95 100
 tgt gtg gcc att ggt gag act ggt ttg gat tcg tat tgg atc aag cac 451
 Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser Tyr Trp Ile Lys His
 105 110 115
 gat cca gag gac acg gcg gcg ttg gat gtg caa gag gag gcg ctg cgc 499
 Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln Glu Glu Ala Leu Arg
 120 125 130
 tgg cat att gat ttg gca att agt gcg gat aag ccg ttg atg att cac 547
 Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys Pro Leu Met Ile His
 135 140 145
 aat cgt gag gcg gat gct gat ttg atg cga gtg ttg gcg gat gct cca 595
 Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val Leu Ala Asp Ala Pro
 150 155 160 165

cct cca aaa gat acg att ctg cat tgt ttt tct tcg ccg ttg gac gtg 643
 Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser Ser Pro Leu Asp Val
 170 175 180

gcg aag gaa gcg ttg gat cgt gga tat gtg ttg agt ttt gcg ggc aat 691
 Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu Ser Phe Ala Gly Asn
 185 190 195

gtg acg ttt aag cgt aat gag gag ttg cgg gag gct gct cgt att gcg 739
 Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu Ala Ala Arg Ile Ala
 200 205 210

ccg att tcc cag att ttg att gaa acc gat gcg ccg tat atg acg ccg 787
 Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala Pro Tyr Met Thr Pro
 215 220 225

gag ccg ttt cgg ggg agt agg aat gag ccg tcg ttg att ggt cat acg 835
 Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser Leu Ile Gly His Thr
 230 235 240 245

gcg cta tgc att gcg gag gtt cgg ggg atg gct gtg gag gat gtt gcg 883
 Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala Val Glu Asp Val Ala
 250 255 260

gcg gct ttg aat gag aat ttt gat cgc gtt tat ggg gtc aca aat cta 931
 Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr Gly Val Thr Asn Leu
 265 270 275

taacgtgagg tagctcacag tca 954

<210> 214

<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 214

Met Ser Lys Lys Lys Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile
 1 5 10 15

Pro Gly Leu Ile Asp Ala His Thr His Leu Ala Ser Cys Gly Gly Asp
 20 25 30

Leu Ala Gly Leu Val Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu
 35 40 45

Cys Thr Val Gly Asp Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala
 50 55 60

Ala Gln Gln Phe Gly Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr
 65 70 75 80

Lys Ala Asp Gln Leu Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met
 85 90 95

Ala Ala Asp Pro Asn Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser
 100 105 110

Tyr Trp Ile Lys His Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln
 115 120 125

Glu Glu Ala Leu Arg Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys
 130 135 140
 Pro Leu Met Ile His Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val
 145 150 155 160
 Leu Ala Asp Ala Pro Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser
 165 170 175
 Ser Pro Leu Asp Val Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu
 180 185 190
 Ser Phe Ala Gly Asn Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu
 195 200 205
 Ala Ala Arg Ile Ala Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala
 210 215 220
 Pro Tyr Met Thr Pro Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser
 225 230 235 240
 Leu Ile Gly His Thr Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala
 245 250 255
 Val Glu Asp Val Ala Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr
 260 265 270
 Gly Val Thr Asn Leu
 275

<210> 215
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXA01802

<400> 215
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 gaaatcttcg cgggtgttta gacaaccogg atgtgacaga atg ggc gat caa gac 115
 Met Gly Asp Gln Asp
 1 5
 ata atc gga aag gaa tcc aaa caa atg gac ttt cgc ctc gtc gcg aca 163
 Ile Ile Gly Lys Glu Ser Lys Gln Met Asp Phe Arg Leu Val Ala Thr
 10 15 20
 gac atg gac ggc aca ctt tta aac acc cac cac gaa gtc cca gag aaa 211
 Asp Met Asp Gly Thr Leu Leu Asn Thr His His Glu Val Pro Glu Lys
 25 30 35
 ttt tgg gac atc ctg gaa caa atg cgt gcc aaa gga atc gcc ttc gca 259
 Phe Trp Asp Ile Leu Glu Gln Met Arg Ala Lys Gly Ile Ala Phe Ala
 40 45 50

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cca gcc agc ggc cgt caa tta gcc acc ttg caa aaa caa ttc ggg cac 307
Pro Ala Ser Gly Arg Gln Leu Ala Thr Leu Gln Lys Gln Phe Gly His
    55                      60                      65

gcg ggt gaa ccc att tct tac atc gca gaa aac ggc acc gtg gta gtc 355
Ala Gly Glu Pro Ile Ser Tyr Ile Ala Glu Asn Gly Thr Val Val Val
    70                      75                      80                      85

cac gac ggc gaa att atc tcc ctg acc acc atc gac tcc gac acc gta 403
His Asp Gly Glu Ile Ile Ser Leu Thr Thr Ile Asp Ser Asp Thr Val
                      90                      95                      100

cac tcc atc atc gat gcc gtg cgc gca tcc gac atc gat atg gga gta 451
His Ser Ile Ile Asp Ala Val Arg Ala Ser Asp Ile Asp Met Gly Val
                      105                      110                      115

gtg gtc tgc cga cca gaa cgc gcc tac gtc gaa cgc aac gac gaa gct 499
Val Val Cys Arg Pro Glu Arg Ala Tyr Val Glu Arg Asn Asp Glu Ala
                      120                      125                      130

ttc cgc gcc gaa ggc ctg aaa tac tac gtc tcc atc gag gaa gtc caa 547
Phe Arg Ala Glu Gly Leu Lys Tyr Tyr Val Ser Ile Glu Glu Val Gln
                      135                      140                      145

gac ctc cac gaa gca gtc aac aat gaa gta atc aag gta gcg atc ttt 595
Asp Leu His Glu Ala Val Asn Asn Glu Val Ile Lys Val Ala Ile Phe
    150                      155                      160                      165

aca ttc caa gat gcc gaa aag gac tgt gcc ccc atc atc cgc gca gcc 643
Thr Phe Gln Asp Ala Glu Lys Asp Cys Ala Pro Ile Ile Arg Ala Ala
                      170                      175                      180

tcc ccc aac gcc aac gtt gtt gtc tcc ggc cag cac tgg gtc gat gtc 691
Ser Pro Asn Ala Asn Val Val Val Ser Gly Gln His Trp Val Asp Val
                      185                      190                      195

atg gat cct tca gcc aac aag ggc caa gct ttg gct gct ctc cgc gat 739
Met Asp Pro Ser Ala Asn Lys Gly Gln Ala Leu Ala Ala Leu Arg Asp
                      200                      205                      210

gcc ctc gga ttg gaa gaa tcc caa act ctc gtg ttt ggc gac tac ctc 787
Ala Leu Gly Leu Glu Glu Ser Gln Thr Leu Val Phe Gly Asp Tyr Leu
                      215                      220                      225

aac gac act gaa ttg atc aag gcc gcc ggc aag tct tac gcc atg tcc 835
Asn Asp Thr Glu Leu Ile Lys Ala Ala Gly Lys Ser Tyr Ala Met Ser
    230                      235                      240                      245

aat gcc cac ccg gac att ttg gaa ttg gcc gac gaa att gca cca tcc 883
Asn Ala His Pro Asp Ile Leu Glu Leu Ala Asp Glu Ile Ala Pro Ser
                      250                      255                      260

aac att gaa gag ggc gtt att gtg gtg ctg gag aag ttg ctt aac ggt 931
Asn Ile Glu Glu Gly Val Ile Val Val Leu Glu Lys Leu Leu Asn Gly
                      265                      270                      275

taacgattgc aggcagcagg ttc 954

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<210> 216

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Met Gly Asp Gln Asp Ile Ile Gly Lys Glu Ser Lys Gln Met Asp Phe
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Arg Leu Val Ala Thr Asp Met Asp Gly Thr Leu Leu Asn Thr His His
          20             25             30

Glu Val Pro Glu Lys Phe Trp Asp Ile Leu Glu Gln Met Arg Ala Lys
          35             40             45

Gly Ile Ala Phe Ala Pro Ala Ser Gly Arg Gln Leu Ala Thr Leu Gln
 50             55             60

Lys Gln Phe Gly His Ala Gly Glu Pro Ile Ser Tyr Ile Ala Glu Asn
 65             70             75             80

Gly Thr Val Val Val His Asp Gly Glu Ile Ile Ser Leu Thr Thr Ile
          85             90             95

Asp Ser Asp Thr Val His Ser Ile Ile Asp Ala Val Arg Ala Ser Asp
          100             105             110

Ile Asp Met Gly Val Val Val Cys Arg Pro Glu Arg Ala Tyr Val Glu
          115             120             125

Arg Asn Asp Glu Ala Phe Arg Ala Glu Gly Leu Lys Tyr Tyr Val Ser
          130             135             140

Ile Glu Glu Val Gln Asp Leu His Glu Ala Val Asn Asn Glu Val Ile
          145             150             155             160

Lys Val Ala Ile Phe Thr Phe Gln Asp Ala Glu Lys Asp Cys Ala Pro
          165             170             175

Ile Ile Arg Ala Ala Ser Pro Asn Ala Asn Val Val Val Ser Gly Gln
          180             185             190

His Trp Val Asp Val Met Asp Pro Ser Ala Asn Lys Gly Gln Ala Leu
          195             200             205

Ala Ala Leu Arg Asp Ala Leu Gly Leu Glu Glu Ser Gln Thr Leu Val
          210             215             220

Phe Gly Asp Tyr Leu Asn Asp Thr Glu Leu Ile Lys Ala Ala Gly Lys
          225             230             235             240

Ser Tyr Ala Met Ser Asn Ala His Pro Asp Ile Leu Glu Leu Ala Asp
          245             250             255

Glu Ile Ala Pro Ser Asn Ile Glu Glu Gly Val Ile Val Val Leu Glu
          260             265             270

Lys Leu Leu Asn Gly
          275

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<210> 217

<211> 1066

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1066)

<223> RXN00866

<400> 217

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ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115
                                         Met Asn Asp Ser Arg
                                         1 5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt 163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly
          10          15          20

cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc 211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser
          25          30          35

tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg 259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg
          40          45          50

gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln
          55          60          65

aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn
          70          75          80          85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly
          90          95          100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln
          105          110          115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys
          120          125          130

tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag 547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys
          135          140          145

gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa 595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu
          150          155          160          165

atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc 643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile
          170          175          180

gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac 691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp

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185	190	195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc			739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val			
200	205	210	
gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att			787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile			
215	220	225	
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt			835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg			
230	235	240	245
ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt			883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg			
250	255	260	
ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg			931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro			
265	270	275	
ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt			979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu			
280	285	290	
ggg ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac			1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp			
295	300	305	
atc aag ctg gat cag act cct cct gat gga cgc cca act			1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr			
310	315	320	

<210> 218

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
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Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20						25					30		

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55					60				

Ser	Gln	Gly	Ser	Gln	Asn	Ala	Gln	Gly	Ser	Gln	Asn	Arg	Glu	Ser	Gly
65					70				75					80	

Asn	Asn	Asn	Arg	Asn	Arg	Ser	Asn	Asn	Asn	Arg	Arg	Gly	Gly	Arg	Gly
			85					90						95	

Arg	Arg	Gly	Ser	Gly	Asn	Ala	Asn	Glu	Gly	Ala	Asn	Asn	Asn	Ser	Gly
			100					105					110		

Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
 115 120 125
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
 130 135 140
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
 145 150 155 160
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
 165 170 175
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
 180 185 190
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
 245 250 255
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
 290 295 300
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg
 305 310 315 320
 Pro Thr

<210> 219
 <211> 1045
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1045)
 <223> FRXA00866

<400> 219
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 ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115
 Met Asn Asp Ser Arg
 1 5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt	163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly	
10 15 20	
cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc	211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser	
25 30 35	
tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg	259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg	
40 45 50	
gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag	307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln	
55 60 65	
aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac	355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn	
70 75 80 85	
cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga	403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly	
90 95 100	
aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag	451
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln	
105 110 115	
ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag	499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys	
120 125 130	
tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag	547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys	
135 140 145	
gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa	595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu	
150 155 160 165	
atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc	643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile	
170 175 180	
gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac	691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp	
185 190 195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc	739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val	
200 205 210	
gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att	787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile	
215 220 225	
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt	835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg	
230 235 240 245	
ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt	883

Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg
 250 255 260

ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg 931
 Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro
 265 270 275

ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt 979
 Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu
 280 285 290

ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac 1027
 Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp
 295 300 305

atc aag ctg gat cag act 1045
 Ile Lys Leu Asp Gln Thr
 310 315

<210> 220
 <211> 315
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 220
 Met Asn Asp Ser Arg Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly
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Pro Pro Glu Ala Gly Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln
 20 25 30

Ala Pro Asp Ala Ser Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala
 35 40 45

Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp
 50 55 60

Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly
 65 70 75 80

Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly
 85 90 95

Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly
 100 105 110

Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
 115 120 125

Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
 130 135 140

Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
 145 150 155 160

Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
 165 170 175

Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
 180 185 190

Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
 245 250 255
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
 290 295 300
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr
 305 310 315

<210> 221
 <211> 789
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXA02410

<400> 221
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 Met Asp Met Gly Pro
 1 5
 ggt gtc ctt gca gca gtt caa gaa att caa gat cct gct gat gcg cat 163
 Gly Val Leu Ala Ala Val Gln Glu Ile Gln Asp Pro Ala Asp Ala His
 10 15 20
 gtt att ttc tcc cat ttg cac acc gat cac tgc gct gat ttt gcg tcc 211
 Val Ile Phe Ser His Leu His Thr Asp His Cys Ala Asp Phe Ala Ser
 25 30 35
 ttg atg gtg tgg cgc agg ttc cac cca acg ctg gcc gcc aag agc cgc 259
 Leu Met Val Trp Arg Arg Phe His Pro Thr Leu Ala Ala Lys Ser Arg
 40 45 50
 aat ctt ttg ttt gga cct gaa gat acc ccc aac agg ctt ggt cgt ttg 307
 Asn Leu Leu Phe Gly Pro Glu Asp Thr Pro Asn Arg Leu Gly Arg Leu
 55 60 65
 agc tcc gat gag cct gat ggc gtt gac gat atg tca gat act ttt gct 355
 Ser Ser Asp Glu Pro Asp Gly Val Asp Asp Met Ser Asp Thr Phe Ala

70	75	80	85	
ttc gac gcc tgg gaa gag cgc aag cca gag ctc att gat aat ttc acg	403			
Phe Asp Ala Trp Glu Glu Arg Lys Pro Glu Leu Ile Asp Asn Phe Thr				
90 95 100				
gtc acg ccg ttc cgc gtt gtg cac ccc att gag acc tac gcg ctt cgc	451			
Val Thr Pro Phe Arg Val Val His Pro Ile Glu Thr Tyr Ala Leu Arg				
105 110 115				
gta gag gag cac cgc acc ggc gcc tca att acg tat tcc ggt gac agc	499			
Val Glu Glu His Arg Thr Gly Ala Ser Ile Thr Tyr Ser Gly Asp Ser				
120 125 130				
gcg tac acc gaa gcg ctt atc gac gcc gcc cgc aac gtt gac att ttc	547			
Ala Tyr Thr Glu Ala Leu Ile Asp Ala Ala Arg Asn Val Asp Ile Phe				
135 140 145				
ttg tgc gag gca act tgg ggc acc tct tgc gat gac aaa gca cca gga	595			
Leu Cys Glu Ala Thr Trp Gly Thr Ser Cys Asp Asp Lys Ala Pro Gly				
150 155 160 165				
atg cat atg tgt ggc caa gac gcc gga aga att gcg gca gca gct ggc	643			
Met His Met Cys Gly Gln Asp Ala Gly Arg Ile Ala Ala Ala Ala Gly				
170 175 180				
gta aag aaa ctg att atc act cat gtt cca cca tgg att gat gca gag	691			
Val Lys Lys Leu Ile Ile Thr His Val Pro Pro Trp Ile Asp Ala Glu				
185 190 195				
gcc aca gtg gca gca gct gcg gaa cac ttt gat ggt cct atc gaa ttg	739			
Ala Thr Val Ala Ala Ala Ala Glu His Phe Asp Gly Pro Ile Glu Leu				
200 205 210				
gca cga tca gga atg gtt atc gag ttt tagtccgttt gtactaataa	786			
Ala Arg Ser Gly Met Val Ile Glu Phe				
215 220				
ggt	789			
<210> 222				
<211> 222				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 222				
Met Asp Met Gly Pro Gly Val Leu Ala Ala Val Gln Glu Ile Gln Asp				
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Pro Ala Asp Ala His Val Ile Phe Ser His Leu His Thr Asp His Cys				
20 25 30				
Ala Asp Phe Ala Ser Leu Met Val Trp Arg Arg Phe His Pro Thr Leu				
35 40 45				
Ala Ala Lys Ser Arg Asn Leu Leu Phe Gly Pro Glu Asp Thr Pro Asn				
50 55 60				
Arg Leu Gly Arg Leu Ser Ser Asp Glu Pro Asp Gly Val Asp Asp Met				
65 70 75 80				

Ser Asp Thr Phe Ala Phe Asp Ala Trp Glu Glu Arg Lys Pro Glu Leu
85 90 95

Ile Asp Asn Phe Thr Val Thr Pro Phe Arg Val Val His Pro Ile Glu
100 105 110

Thr Tyr Ala Leu Arg Val Glu Glu His Arg Thr Gly Ala Ser Ile Thr
115 120 125

Tyr Ser Gly Asp Ser Ala Tyr Thr Glu Ala Leu Ile Asp Ala Ala Arg
130 135 140

Asn Val Asp Ile Phe Leu Cys Glu Ala Thr Trp Gly Thr Ser Cys Asp
145 150 155 160

Asp Lys Ala Pro Gly Met His Met Cys Gly Gln Asp Ala Gly Arg Ile
165 170 175

Ala Ala Ala Ala Gly Val Lys Lys Leu Ile Ile Thr His Val Pro Pro
180 185 190

Trp Ile Asp Ala Glu Ala Thr Val Ala Ala Ala Ala Glu His Phe Asp
195 200 205

Gly Pro Ile Glu Leu Ala Arg Ser Gly Met Val Ile Glu Phe
210 215 220

<210> 223

<211> 455

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(432)

<223> RXA00961

<400> 223

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Leu Glu Asn Trp Arg Ile Gly Arg Met Leu Leu Leu Gly Asp Ala Ala
1 5 10 15

cac gca ccc ctc cag tac ctc gcc tca ggc gcg gtc atg gcc atg gaa 96
His Ala Pro Leu Gln Tyr Leu Ala Ser Gly Ala Val Met Ala Met Glu
20 25 30

gac gcc gag gct gtc gcc ctc ttc gct gcc gac gct gcg cgt gct ggc 144
Asp Ala Glu Ala Val Ala Leu Phe Ala Ala Asp Ala Ala Arg Ala Gly
35 40 45

aac ctc gat tgg gaa gag gta ctc gca gag gtg gaa gct gaa cgc cga 192
Asn Leu Asp Trp Glu Glu Val Leu Ala Glu Val Glu Ala Glu Arg Arg
50 55 60

cca cgc tgc agc cgc atc caa acc gta ggc cgt ttc tgg gga gag ctc 240
Pro Arg Cys Ser Arg Ile Gln Thr Val Gly Arg Phe Trp Gly Glu Leu
65 70 75 80

tgg cat gtg gaa ggc acc gca cgt ctc atc cgc aac gaa gtt ttc cgc 288

Trp His Val Glu Gly Thr Ala Arg Leu Ile Arg Asn Glu Val Phe Arg
 85 90 95
 caa gca gac cgc aat ggc tgg ttc atc tat gca gac tgg ctg tgg ggt 336
 Gln Ala Asp Arg Asn Gly Trp Phe Ile Tyr Ala Asp Trp Leu Trp Gly
 100 105 110
 tac gat gca tcc aag cgt gcc cac atc gcc aac cct gag ctc gga gaa 384
 Tyr Asp Ala Ser Lys Arg Ala His Ile Ala Asn Pro Glu Leu Gly Glu
 115 120 125
 atg cca caa gca ctg aag gaa tgg cgc tac gcc ctc ctc gaa cag aaa 432
 Met Pro Gln Ala Leu Lys Glu Trp Arg Tyr Ala Leu Leu Glu Gln Lys
 130 135 140
 tagcagcctc acctgttaag gga 455

 <210> 224
 <211> 144
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 224
 Leu Glu Asn Trp Arg Ile Gly Arg Met Leu Leu Leu Gly Asp Ala Ala
 1 5 10 15
 His Ala Pro Leu Gln Tyr Leu Ala Ser Gly Ala Val Met Ala Met Glu
 20 25 30
 Asp Ala Glu Ala Val Ala Leu Phe Ala Ala Asp Ala Ala Arg Ala Gly
 35 40 45
 Asn Leu Asp Trp Glu Glu Val Leu Ala Glu Val Glu Ala Glu Arg Arg
 50 55 60
 Pro Arg Cys Ser Arg Ile Gln Thr Val Gly Arg Phe Trp Gly Glu Leu
 65 70 75 80
 Trp His Val Glu Gly Thr Ala Arg Leu Ile Arg Asn Glu Val Phe Arg
 85 90 95
 Gln Ala Asp Arg Asn Gly Trp Phe Ile Tyr Ala Asp Trp Leu Trp Gly
 100 105 110
 Tyr Asp Ala Ser Lys Arg Ala His Ile Ala Asn Pro Glu Leu Gly Glu
 115 120 125
 Met Pro Gln Ala Leu Lys Glu Trp Arg Tyr Ala Leu Leu Glu Gln Lys
 130 135 140

<210> 225
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 <212> DNA
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 <220>

<221> CDS

<222> (101)..(1093)

<223> RXA00111

<400> 225

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ccggcgccat cactggcgac cactaaaaaa ggagacttcg atg gcc ttt ttt agc 115
 Met Ala Phe Phe Ser
 1 5

ttt tcg acg tct ccc ctc acc cgc ctc atc ccc ggc agc cgc tcc aaa 163
 Phe Ser Thr Ser Pro Leu Thr Arg Leu Ile Pro Gly Ser Arg Ser Lys
 10 15 20

gcc aca ggc gcc aaa cgg cgc ctg agc agc aca atc gcg tcg att gaa 211
 Ala Thr Gly Ala Lys Arg Arg Leu Ser Ser Thr Ile Ala Ser Ile Glu
 25 30 35

cgc tcc ccc ggc atc att gcc cta gac gga ccg ttc acc cac gat cac 259
 Arg Ser Pro Gly Ile Ile Ala Leu Asp Gly Pro Phe Thr His Asp His
 40 45 50

gtc tcc gta cgt ggc att cgc ctc cat tta gca gag gca ggc tcc ccc 307
 Val Ser Val Arg Gly Ile Arg Leu His Leu Ala Glu Ala Gly Ser Pro
 55 60 65

acc aaa ccc ctg gtt ctt ctg atc cac ggg gct ttc ggc ggt tgg tac 355
 Thr Lys Pro Leu Val Leu Leu Ile His Gly Ala Phe Gly Gly Trp Tyr
 70 75 80 85

gac tac cgc gaa gtc atc ggc cca ctc gca gat gcc ggc ttc cac gtc 403
 Asp Tyr Arg Glu Val Ile Gly Pro Leu Ala Asp Ala Gly Phe His Val
 90 95 100

gcc gcc atc gat cta cgc ggc tac ggc atg tcc gac aaa ccc cca aca 451
 Ala Ala Ile Asp Leu Arg Gly Tyr Gly Met Ser Asp Lys Pro Pro Thr
 105 110 115

ggc tac gac ctc cgc cac gca gcc gga gaa ctc agc agc gtt atc gca 499
 Gly Tyr Asp Leu Arg His Ala Ala Gly Glu Leu Ser Ser Val Ile Ala
 120 125 130

gct ctc ggc cac gat gac gca ctt ctt gtc ggc tcc gac acc ggc gcc 547
 Ala Leu Gly His Asp Asp Ala Leu Leu Val Gly Ser Asp Thr Gly Ala
 135 140 145

agc atc gcc tgg gct atc gct tcc atg tac ccc gaa cgg gtc cgc ggc 595
 Ser Ile Ala Trp Ala Ile Ala Ser Met Tyr Pro Glu Arg Val Arg Gly
 150 155 160 165

cta att tcc ctc ggc gcg atc cac ccc ctt gac atg cga cgc gcc atc 643
 Leu Ile Ser Leu Gly Ala Ile His Pro Leu Asp Met Arg Arg Ala Ile
 170 175 180

cga cga aaa ccc cac cta cac gtc tct gac ctc agc cga ctt gct cct 691
 Arg Arg Lys Pro His Leu His Val Ser Asp Leu Ser Arg Leu Ala Pro
 185 190 195

ttt cgg ttg ccc tca ttc ctg cat aac ctc ttc cac ttc gga atc acc 739
 Phe Arg Leu Pro Ser Phe Leu His Asn Leu Phe His Phe Gly Ile Thr

200	205	210	
agc gaa gct cga cgt gag atc gtc aac aac acg tcc tcg tcc tac cag Ser Glu Ala Arg Arg Glu Ile Val Asn Asn Thr Ser Ser Ser Tyr Gln 215 220 225			787
cgc agc aac gca ttc aca gag aca gtg ctc ctc cgc aaa aaa gca cta Arg Ser Asn Ala Phe Thr Glu Thr Val Leu Leu Arg Lys Lys Ala Leu 230 235 240 245			835
tcg atc gac cac acc atc acc ccg atc atc cgc acc aac cgc tac ctc Ser Ile Asp His Thr Ile Thr Pro Ile Ile Arg Thr Asn Arg Tyr Leu 250 255 260			883
gtt ggg tcg atc ccc agc aaa aca gtc tcc gca ccg gtg tgg ctg ctc Val Gly Ser Ile Pro Ser Lys Thr Val Ser Ala Pro Val Trp Leu Leu 265 270 275			931
aga acc aac act cga cgc tgg gaa cat cta gcc aat act gcg cgc act Arg Thr Asn Thr Arg Arg Trp Glu His Leu Ala Asn Thr Ala Arg Thr 280 285 290			979
cga acg aca ggg cca ttc acc acc atc gcg atc ccc ggc ggc tac gaa Arg Thr Thr Gly Pro Phe Thr Thr Ile Ala Ile Pro Gly Gly Tyr Glu 295 300 305			1027
ctc ccc tac ctc gag aac cct tcc gaa ttt gca gca acc atc gca gag Leu Pro Tyr Leu Glu Asn Pro Ser Glu Phe Ala Ala Thr Ile Ala Glu 310 315 320 325			1075
ttc gcg cgc acc acg ttt taagcactgt ggctgaggcg ctg Phe Ala Arg Thr Thr Phe 330			1116
<210> 226			
<211> 331			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 226			
Met Ala Phe Phe Ser Phe Ser Thr Ser Pro Leu Thr Arg Leu Ile Pro 1 5 10 15			
Gly Ser Arg Ser Lys Ala Thr Gly Ala Lys Arg Arg Leu Ser Ser Thr 20 25 30			
Ile Ala Ser Ile Glu Arg Ser Pro Gly Ile Ile Ala Leu Asp Gly Pro 35 40 45			
Phe Thr His Asp His Val Ser Val Arg Gly Ile Arg Leu His Leu Ala 50 55 60			
Glu Ala Gly Ser Pro Thr Lys Pro Leu Val Leu Leu Ile His Gly Ala 65 70 75 80			
Phe Gly Gly Trp Tyr Asp Tyr Arg Glu Val Ile Gly Pro Leu Ala Asp 85 90 95			
Ala Gly Phe His Val Ala Ala Ile Asp Leu Arg Gly Tyr Gly Met Ser 100 105 110			

Asp	Lys	Pro	Pro	Thr	Gly	Tyr	Asp	Leu	Arg	His	Ala	Ala	Gly	Glu	Leu
		115					120					125			
Ser	Ser	Val	Ile	Ala	Ala	Leu	Gly	His	Asp	Asp	Ala	Leu	Leu	Val	Gly
	130					135					140				
Ser	Asp	Thr	Gly	Ala	Ser	Ile	Ala	Trp	Ala	Ile	Ala	Ser	Met	Tyr	Pro
145					150					155					160
Glu	Arg	Val	Arg	Gly	Leu	Ile	Ser	Leu	Gly	Ala	Ile	His	Pro	Leu	Asp
				165					170					175	
Met	Arg	Arg	Ala	Ile	Arg	Arg	Lys	Pro	His	Leu	His	Val	Ser	Asp	Leu
			180					185					190		
Ser	Arg	Leu	Ala	Pro	Phe	Arg	Leu	Pro	Ser	Phe	Leu	His	Asn	Leu	Phe
		195					200					205			
His	Phe	Gly	Ile	Thr	Ser	Glu	Ala	Arg	Arg	Glu	Ile	Val	Asn	Asn	Thr
	210					215					220				
Ser	Ser	Ser	Tyr	Gln	Arg	Ser	Asn	Ala	Phe	Thr	Glu	Thr	Val	Leu	Leu
225					230					235					240
Arg	Lys	Lys	Ala	Leu	Ser	Ile	Asp	His	Thr	Ile	Thr	Pro	Ile	Ile	Arg
				245					250					255	
Thr	Asn	Arg	Tyr	Leu	Val	Gly	Ser	Ile	Pro	Ser	Lys	Thr	Val	Ser	Ala
			260				265						270		
Pro	Val	Trp	Leu	Leu	Arg	Thr	Asn	Thr	Arg	Arg	Trp	Glu	His	Leu	Ala
		275					280					285			
Asn	Thr	Ala	Arg	Thr	Arg	Thr	Thr	Gly	Pro	Phe	Thr	Thr	Ile	Ala	Ile
	290					295					300				
Pro	Gly	Gly	Tyr	Glu	Leu	Pro	Tyr	Leu	Glu	Asn	Pro	Ser	Glu	Phe	Ala
305					310					315					320
Ala	Thr	Ile	Ala	Glu	Phe	Ala	Arg	Thr	Thr	Phe					
				325					330						

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<210> 227
<211> 1020
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(997)  
<223> RXA01932
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<400> 227
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tcaaccaaat ttcttgcccta aggcttctag gattgtcggt atg ctc ctt cac cca 115
                                     Met Leu Leu His Pro
                                     1       5

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gat gcg cag ttt tat atc gat acc ttg ccc act ctc agc gcg gag gag	163
Asp Ala Gln Phe Tyr Ile Asp Thr Leu Pro Thr Leu Ser Ala Glu Glu	
10 15 20	
cag gtg agt ttt ggt aaa gac gct cct gtt tca gag gct gat gca acc	211
Gln Val Ser Phe Gly Lys Asp Ala Pro Val Ser Glu Ala Asp Ala Thr	
25 30 35	
cat gtg gcg aca gat caa gat att gct ggg gtg ccg gtg agg gtt tat	259
His Val Ala Thr Asp Gln Asp Ile Ala Gly Val Pro Val Arg Val Tyr	
40 45 50	
acg cct tta tct ggg gct ggg gat ttg ccg tgt ttg gtg tac ttc cac	307
Thr Pro Leu Ser Gly Ala Gly Asp Leu Pro Cys Leu Val Tyr Phe His	
55 60 65	
ggc ggt ggc tgg tcc ggc ggc acc ctc aac atg atc gat gcc acg gtt	355
Gly Gly Gly Trp Ser Gly Gly Thr Leu Asn Met Ile Asp Ala Thr Val	
70 75 80 85	
cac tct cta gtg gtt ggc ctg ccg atc atc gcc atc agc gtg gac tac	403
His Ser Leu Val Val Gly Leu Pro Ile Ile Ala Ile Ser Val Asp Tyr	
90 95 100	
cga ctt gca ccc gca cac cca ttt cca gcg gct atc gac gac gcg ttt	451
Arg Leu Ala Pro Ala His Pro Phe Pro Ala Ala Ile Asp Asp Ala Phe	
105 110 115	
gca gtg gtc agt gcc gta ttg gat ggg gtg tct ggg ctg agt att gat	499
Ala Val Val Ser Ala Val Leu Asp Gly Val Ser Gly Leu Ser Ile Asp	
120 125 130	
act tcc cga gtg gca att ggc ggt gac agt gcc ggt gga aat att gcc	547
Thr Ser Arg Val Ala Ile Gly Gly Asp Ser Ala Gly Gly Asn Ile Ala	
135 140 145	
gcg gtt act gca caa cag ctg cgt gaa cgg gct gtg ggt tct act cct	595
Ala Val Thr Ala Gln Gln Leu Arg Glu Arg Ala Val Gly Ser Thr Pro	
150 155 160 165	
gta ttg gct cac cag gtg ctt att ttt ccg gta act gat gtt tcc act	643
Val Leu Ala His Gln Val Leu Ile Phe Pro Val Thr Asp Val Ser Thr	
170 175 180	
aca tct acg ccg agc tat ctc aca ttt ggc aaa gat tgc tac ctg aca	691
Thr Ser Thr Pro Ser Tyr Leu Thr Phe Gly Lys Asp Cys Tyr Leu Thr	
185 190 195	
aag gac gcg atg gaa cgc tac atc gaa caa tat gcc gat ggg cac gac	739
Lys Asp Ala Met Glu Arg Tyr Ile Glu Gln Tyr Ala Asp Gly His Asp	
200 205 210	
cgc acc gac cct cga ctc tca ccg cta ctg gca tct gat ttg agc gac	787
Arg Thr Asp Pro Arg Leu Ser Pro Leu Leu Ala Ser Asp Leu Ser Asp	
215 220 225	
ctc cca ccc acc acc att gtg tac ggc gaa tgc gac gtg tta gcc cat	835
Leu Pro Pro Thr Thr Ile Val Tyr Gly Glu Cys Asp Val Leu Ala His	
230 235 240 245	
gaa gtg cga gcc tat gga caa gct cta cta gag gct gga aat tcc gtg	883

Glu Val Arg Ala Tyr Gly Gln Ala Leu Leu Glu Ala Gly Asn Ser Val
 250 255 260

acg atg act gaa ttc aaa gga cag atc cac gcc ttt att aac cta ggg 931
 Thr Met Thr Glu Phe Lys Gly Gln Ile His Ala Phe Ile Asn Leu Gly
 265 270 275

gga atc agt tcc gat gcg cgg gct gct cga cga ctc atc cgc gcc gaa 979
 Gly Ile Ser Ser Asp Ala Arg Ala Ala Arg Arg Leu Ile Arg Ala Glu
 280 285 290

ttg gaa gca gca ctt tgt taaagggtga gatttaacat tcg 1020
 Leu Glu Ala Ala Leu Cys
 295

<210> 228

<211> 299

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Leu Leu His Pro Asp Ala Gln Phe Tyr Ile Asp Thr Leu Pro Thr
 1 5 10 15

Leu Ser Ala Glu Glu Gln Val Ser Phe Gly Lys Asp Ala Pro Val Ser
 20 25 30

Glu Ala Asp Ala Thr His Val Ala Thr Asp Gln Asp Ile Ala Gly Val
 35 40 45

Pro Val Arg Val Tyr Thr Pro Leu Ser Gly Ala Gly Asp Leu Pro Cys
 50 55 60

Leu Val Tyr Phe His Gly Gly Gly Trp Ser Gly Gly Thr Leu Asn Met
 65 70 75 80

Ile Asp Ala Thr Val His Ser Leu Val Val Gly Leu Pro Ile Ile Ala
 85 90 95

Ile Ser Val Asp Tyr Arg Leu Ala Pro Ala His Pro Phe Pro Ala Ala
 100 105 110

Ile Asp Asp Ala Phe Ala Val Val Ser Ala Val Leu Asp Gly Val Ser
 115 120 125

Gly Leu Ser Ile Asp Thr Ser Arg Val Ala Ile Gly Gly Asp Ser Ala
 130 135 140

Gly Gly Asn Ile Ala Ala Val Thr Ala Gln Gln Leu Arg Glu Arg Ala
 145 150 155 160

Val Gly Ser Thr Pro Val Leu Ala His Gln Val Leu Ile Phe Pro Val
 165 170 175

Thr Asp Val Ser Thr Thr Ser Thr Pro Ser Tyr Leu Thr Phe Gly Lys
 180 185 190

Asp Cys Tyr Leu Thr Lys Asp Ala Met Glu Arg Tyr Ile Glu Gln Tyr
 195 200 205

Ala Asp Gly His Asp Arg Thr Asp Pro Arg Leu Ser Pro Leu Leu Ala
 210 215 220

Ser Asp Leu Ser Asp Leu Pro Pro Thr Thr Ile Val Tyr Gly Glu Cys
 225 230 235 240

Asp Val Leu Ala His Glu Val Arg Ala Tyr Gly Gln Ala Leu Leu Glu
 245 250 255

Ala Gly Asn Ser Val Thr Met Thr Glu Phe Lys Gly Gln Ile His Ala
 260 265 270

Phe Ile Asn Leu Gly Gly Ile Ser Ser Asp Ala Arg Ala Ala Arg Arg
 275 280 285

Leu Ile Arg Ala Glu Leu Glu Ala Ala Leu Cys
 290 295

<210> 229
 <211> 1131
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1108)
 <223> RXA02574

<400> 229
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 gagctccccc tccaccctc ccgcaccgac cgcgaggat ttg gcg cgc gcg caa 115
 Leu Ala Arg Ala Gln
 1 5

atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
 10 15 20

gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
 25 30 35

ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
 40 45 50

ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
 55 60 65

gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
 70 75 80 85

ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
 90 95 100

gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451

Glu Gln Val	Glu Asp Leu Ala	Glu Ile Leu Gly Thr Gly	Leu Ala Ala	
105		110	115	
cat ggt gtg	aca gtt aac ttt	gca cct gtt gta gat gta	gat gct tgg	499
His Gly Val	Thr Val Asn Phe	Ala Pro Val Val Asp Val	Asp Ala Trp	
120		125	130	
ggt ctc ccc	gtc gtt ggc gat	cgt tcc ttt tcc aac gac	cca gcc gta	547
Gly Leu Pro	Val Val Gly Asp	Arg Ser Phe Ser Asn Asp	Pro Ala Val	
135		140	145	
gca gct act	tat gcc aca gct	ttt gca aag ggc tta agc	aaa gta gga	595
Ala Ala Thr	Tyr Ala Thr Ala	Phe Ala Lys Gly Leu Ser	Lys Val Gly	
150		155	160	165
att acc cca	gta ttc aaa cat	ttc cca ggt cac ggt	cgt gca agt ggc	643
Ile Thr Pro	Val Phe Lys His	Phe Pro Gly His Gly	Arg Ala Ser Gly	
	170	175	180	
gat tcg cac	acc caa gat gtg	gtg acc ccc gca ctt	gat gag ctt aaa	691
Asp Ser His	Thr Gln Asp Val	Val Thr Pro Ala Leu	Asp Glu Leu Lys	
	185	190	195	
act tac gac	ctc atc cct tat	ggt caa gca ctt tct	gaa act gac gga	739
Thr Tyr Asp	Leu Ile Pro Tyr	Gly Gln Ala Leu Ser	Glu Thr Asp Gly	
200		205	210	
gcc gtc atg	gtg ggc cac atg	att gtt cca ggt	ctt ggc acc gac gga	787
Ala Val Met	Val Gly His Met	Ile Val Pro Gly Leu	Gly Thr Asp Gly	
215		220	225	
gtt cca tcc	tct atc gac ccc	gcc acc tat caa ctg	ctc cgc agt ggc	835
Val Pro Ser	Ser Ile Asp Pro	Ala Thr Tyr Gln Leu	Leu Arg Ser Gly	
230		235	240	245
gat tac cca	ggt ggc gtg cct	ttc gat ggc gtg	atc tac acc gac gat	883
Asp Tyr Pro	Gly Gly Val Pro	Phe Asp Gly Val Ile	Tyr Thr Asp Asp	
	250	255	260	
ctc tct gga	atg agt gcc att	tcc gcc acc cat	tca ccc gca gaa gca	931
Leu Ser Gly	Met Ser Ala Ile	Ser Ala Thr His Ser	Pro Ala Glu Ala	
	265	270	275	
gtg ctt gcc	tcc ctc aaa gca	ggc gca gac caa gca	cta tgg atc gac	979
Val Leu Ala	Ser Leu Lys Ala	Gly Ala Asp Gln Ala	Leu Trp Ile Asp	
280		285	290	
tat ggg tcg	ttg ggc tcc gcg	att gat cgc gtt	gat gct gcc gtt agc	1027
Tyr Gly Ser	Leu Gly Ser Ala	Ile Asp Arg Val Asp	Ala Ala Val Ser	
295		300	305	
agc ggt gaa	tac cct caa gaa	caa atg ctg gca	tct gcg tta aga gtc	1075
Ser Gly Glu	Tyr Pro Gln Glu	Gln Met Leu Ala Ser	Ala Leu Arg Val	
310		315	320	325
caa ttg ctc	tac atc aca cgt	ctc gaa caa aag	tgaagttacc agtccgtaac	1128
Gln Leu Leu	Tyr Ile Thr Arg	Leu Glu Gln Lys		
	330	335		
ccc				1131

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<211> 336

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 230

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Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu
 20 25 30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn
 35 40 45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
 50 55 60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65 70 75 80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
 85 90 95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
 100 105 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
 115 120 125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
 130 135 140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
 145 150 155 160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
 165 170 175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
 180 185 190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
 195 200 205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
 210 215 220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
 225 230 235 240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
 245 250 255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
 260 265 270

Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
 275 280 285

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val
 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala
 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
 325 330 335

<210> 231
 <211> 1599
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1576)
 <223> RXN00983

<400> 231
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ggaggccggc tgcattggtg tcgacgccga tgaacgctcc gtg act gca ggt gaa 115
 Val Thr Ala Gly Glu
 1 5

acc acc act atg aat gtc acg ttg acc aat cct ttc gac aac gca att 163
 Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro Phe Asp Asn Ala Ile
 10 15 20

ttt gac cga gca gtc tcc ctt gaa cgt ccc gaa gga tgg caa gct gag 211
 Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu Gly Trp Gln Ala Glu
 25 30 35

gat gtt cgt gtg tcg atc cca tct gga gaa tct gtc aca atc cca gtc 259
 Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser Val Thr Ile Pro Val
 40 45 50

cag gtc aca gca ccg ctg gta gcc gac aac ggt gaa ctt cca gtg gag 307
 Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly Glu Leu Pro Val Glu
 55 60 65

gtg tcc att ctt gat gga gca gac cgc tac acg ggt cgt ctc aat ctc 355
 Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr Gly Arg Leu Asn Leu
 70 75 80 85

act gtt cag ggt ggg caa gaa cct gca cca act tca gtg aag gtg agc 403
 Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr Ser Val Lys Val Ser
 90 95 100

att cca aat ctc aag gac act tat gta gca ggg gag aag atc agc att 451
 Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly Glu Lys Ile Ser Ile
 105 110 115

aac ttt gcg gtc aac aac ccg ttt gac gtt acg gtt aat tcg gtg cca 499
 Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr Val Asn Ser Val Pro
 120 125 130

agc ctg ggg gaa ggc gag aac tgg atg cct gca aac cta cgc gga ttt	547
Ser Leu Gly Glu Gly Glu Asn Trp Met Pro Ala Asn Leu Arg Gly Phe	
135 140 145	
gat cca gag cag ggt act ccc aac tgt cgt tac aag aat tta ggc gcg	595
Asp Pro Glu Gln Gly Thr Pro Asn Cys Arg Tyr Lys Asn Leu Gly Ala	
150 155 160 165	
aat aag agc tat gac tgc acc aca act acc tat gaa gtc agc gat ttg	643
Asn Lys Ser Tyr Asp Cys Thr Thr Thr Thr Tyr Glu Val Ser Asp Leu	
170 175 180	
gat gta gaa cgc gga tac gtg gat att cca acg gta tgg acg ttt act	691
Asp Val Glu Arg Gly Tyr Val Asp Ile Pro Thr Val Trp Thr Phe Thr	
185 190 195	
aac tcc gca ggc gaa acg gta tgg tcc aaa aac gtt gat gtg cct cga	739
Asn Ser Ala Gly Glu Thr Val Trp Ser Lys Asn Val Asp Val Pro Arg	
200 205 210	
gtt gaa ctc aat gga aca cag gat gct gtc act gat gca atc gta acg	787
Val Glu Leu Asn Gly Thr Gln Asp Ala Val Thr Asp Ala Ile Val Thr	
215 220 225	
gtt gat ccc atc aac cca gtt cat tcc aac ggc cag agc caa act gtt	835
Val Asp Pro Ile Asn Pro Val His Ser Asn Gly Gln Ser Gln Thr Val	
230 235 240 245	
gag gtc cag gct aat gtc acc tca gag gga gat ctg cca gct gga tct	883
Glu Val Gln Ala Asn Val Thr Ser Glu Gly Asp Leu Pro Ala Gly Ser	
250 255 260	
aag gtg gcc ttt tat cta gat tca tcg ccc att gat acc gca gct gtt	931
Lys Val Ala Phe Tyr Leu Asp Ser Ser Pro Ile Asp Thr Ala Ala Val	
265 270 275	
gat gcg gaa ggg cat gcc agc atc tcg att gat gtg gac aac atc gca	979
Asp Ala Glu Gly His Ala Ser Ile Ser Ile Asp Val Asp Asn Ile Ala	
280 285 290	
agc gag cag cct gaa cgc aca ttt gag gtt cgc gcc cga ctc gtc gtt	1027
Ser Glu Gln Pro Glu Arg Thr Phe Glu Val Arg Ala Arg Leu Val Val	
295 300 305	
cca gaa gat gca cca cga tca atc gcg cgt gat gcc ttg gca cgt ttt	1075
Pro Glu Asp Ala Pro Arg Ser Ile Ala Arg Asp Ala Leu Ala Arg Phe	
310 315 320 325	
aca gtc ctg tct gaa caa gtg cag cag aac tcc ttg gtg atc atg aat	1123
Thr Val Leu Ser Glu Gln Val Gln Gln Asn Ser Leu Val Ile Met Asn	
330 335 340	
cat cca gat gtg ttt tct gat gga caa aca aag act att gtc atc gca	1171
His Pro Asp Val Phe Ser Asp Gly Gln Thr Lys Thr Ile Val Ile Ala	
345 350 355	
gcg aag gcg aca gca cac gat gga tcg ccg gtg gct atc ggt act ctc	1219
Ala Lys Ala Thr Ala His Asp Gly Ser Pro Val Ala Ile Gly Thr Leu	
360 365 370	

att gca ttt cgc gtc aac ggt att gag cgg gac gtg gtt cca act aac 1267
 Ile Ala Phe Arg Val Asn Gly Ile Glu Arg Asp Val Val Pro Thr Asn
 375 380 385

gcg caa gga aca gca aag ctt cag cta gac ctc aag cca gta aat act 1315
 Ala Gln Gly Thr Ala Lys Leu Gln Leu Asp Leu Lys Pro Val Asn Thr
 390 395 400 405

gaa gac gag gaa tat gaa gta aca gtt gaa gcc gag ctg gat gaa ttg 1363
 Glu Asp Glu Glu Tyr Glu Val Thr Val Glu Ala Glu Leu Asp Glu Leu
 410 415 420

act gct cag acc acg ttc aaa gta ctt gct ggt gag gaa gag gaa ccc 1411
 Thr Ala Gln Thr Thr Phe Lys Val Leu Ala Gly Glu Glu Glu Glu Pro
 425 430 435

acc agc acc gaa gaa caa ccg tca gaa act gag cag cct tct gaa cct 1459
 Thr Ser Thr Glu Glu Gln Pro Ser Glu Thr Glu Gln Pro Ser Glu Pro
 440 445 450

gaa gag gaa tcg act ggt gtt gct gga agc tct aac ggt ggc agt ttt 1507
 Glu Glu Glu Ser Thr Gly Val Ala Gly Ser Ser Asn Gly Gly Ser Phe
 455 460 465

gtc gcg ctt tta gcg ctg ctg gca gcg ctt ggt ggc atc gtc ggt gca 1555
 Val Ala Leu Leu Ala Leu Leu Ala Ala Leu Gly Gly Ile Val Gly Ala
 470 475 480 485

gtc ctc gga ttg ctt aag ttg taggtggctg ggggcgtcga aaa 1599
 Val Leu Gly Leu Leu Lys Leu
 490

<210> 232

<211> 492

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Val Thr Ala Gly Glu Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro
 1 5 10 15

Phe Asp Asn Ala Ile Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu
 20 25 30

Gly Trp Gln Ala Glu Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser
 35 40 45

Val Thr Ile Pro Val Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly
 50 55 60

Glu Leu Pro Val Glu Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr
 65 70 75 80

Gly Arg Leu Asn Leu Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr
 85 90 95

Ser Val Lys Val Ser Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly
 100 105 110

Glu Lys Ile Ser Ile Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr

115	120	125
Val Asn Ser Val Pro Ser Leu Gly Glu Gly Glu Asn Trp Met Pro Ala		
130	135	140
Asn Leu Arg Gly Phe Asp Pro Glu Gln Gly Thr Pro Asn Cys Arg Tyr		
145	150	155
Lys Asn Leu Gly Ala Asn Lys Ser Tyr Asp Cys Thr Thr Thr Tyr		
165	170	175
Glu Val Ser Asp Leu Asp Val Glu Arg Gly Tyr Val Asp Ile Pro Thr		
180	185	190
Val Trp Thr Phe Thr Asn Ser Ala Gly Glu Thr Val Trp Ser Lys Asn		
195	200	205
Val Asp Val Pro Arg Val Glu Leu Asn Gly Thr Gln Asp Ala Val Thr		
210	215	220
Asp Ala Ile Val Thr Val Asp Pro Ile Asn Pro Val His Ser Asn Gly		
225	230	235
Gln Ser Gln Thr Val Glu Val Gln Ala Asn Val Thr Ser Glu Gly Asp		
245	250	255
Leu Pro Ala Gly Ser Lys Val Ala Phe Tyr Leu Asp Ser Ser Pro Ile		
260	265	270
Asp Thr Ala Ala Val Asp Ala Glu Gly His Ala Ser Ile Ser Ile Asp		
275	280	285
Val Asp Asn Ile Ala Ser Glu Gln Pro Glu Arg Thr Phe Glu Val Arg		
290	295	300
Ala Arg Leu Val Val Pro Glu Asp Ala Pro Arg Ser Ile Ala Arg Asp		
305	310	315
Ala Leu Ala Arg Phe Thr Val Leu Ser Glu Gln Val Gln Gln Asn Ser		
325	330	335
Leu Val Ile Met Asn His Pro Asp Val Phe Ser Asp Gly Gln Thr Lys		
340	345	350
Thr Ile Val Ile Ala Ala Lys Ala Thr Ala His Asp Gly Ser Pro Val		
355	360	365
Ala Ile Gly Thr Leu Ile Ala Phe Arg Val Asn Gly Ile Glu Arg Asp		
370	375	380
Val Val Pro Thr Asn Ala Gln Gly Thr Ala Lys Leu Gln Leu Asp Leu		
385	390	395
Lys Pro Val Asn Thr Glu Asp Glu Glu Tyr Glu Val Thr Val Glu Ala		
405	410	415
Glu Leu Asp Glu Leu Thr Ala Gln Thr Thr Phe Lys Val Leu Ala Gly		
420	425	430
Glu Glu Glu Glu Pro Thr Ser Thr Glu Glu Gln Pro Ser Glu Thr Glu		
435	440	445

Gln Pro Ser Glu Pro Glu Glu Glu Ser Thr Gly Val Ala Gly Ser Ser
 450 455 460

Asn Gly Gly Ser Phe Val Ala Leu Leu Ala Leu Leu Ala Ala Leu Gly
 465 470 475 480

Gly Ile Val Gly Ala Val Leu Gly Leu Leu Lys Leu
 485 490

<210> 233

<211> 1297

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1297)

<223> FRXA00983

<400> 233

gtgagaaaac agtggctcaa atatcgacat cttctactca cagttcaacc tgcgtggct 60

ggaggccggc tgcattggtg tcgacgccga tgaaacgtcc gtg act gca ggt gaa 115
 Val Thr Ala Gly Glu
 1 5

acc acc act atg aat gtc acg ttg acc aat cct ttc gac aac gca att 163
 Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro Phe Asp Asn Ala Ile
 10 15 20

ttt gac cga gca gtc tcc ctt gaa cgt ccc gaa gga tgg caa gct gag 211
 Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu Gly Trp Gln Ala Glu
 25 30 35

gat gtt cgt gtg tcg atc cca tct gga gaa tct gtc aca atc cca gtc 259
 Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser Val Thr Ile Pro Val
 40 45 50

cag gtc aca gca ccg ctg gta gcc gac aac ggt gaa ctt cca gtg gag 307
 Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly Glu Leu Pro Val Glu
 55 60 65

gtg tcc att ctt gat gga gca gac cgc tac acg ggt cgt ctc aat ctc 355
 Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr Gly Arg Leu Asn Leu
 70 75 80 85

act gtt cag ggt ggg caa gaa cct gca cca act tca gtg aag gtg agc 403
 Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr Ser Val Lys Val Ser
 90 95 100

att cca aat ctc aag gac act tat gta gca ggg gag aag atc agc att 451
 Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly Glu Lys Ile Ser Ile
 105 110 115

aac ttt gcg gtc aac aac ccg ttt gac gtt acg gtt aat tcg gtg cca 499
 Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr Val Asn Ser Val Pro
 120 125 130

agc ctg ggg gaa ggc gag aac tgg atg cct gca aac cta cgc gga ttt 547

Ser	Leu	Gly	Glu	Gly	Glu	Asn	Trp	Met	Pro	Ala	Asn	Leu	Arg	Gly	Phe		
135						140					145						
gat	cca	gag	cag	ggt	act	ccc	aac	tgt	cgt	tac	aag	aat	tta	ggc	gcg	595	
Asp	Pro	Glu	Gln	Gly	Thr	Pro	Asn	Cys	Arg	Tyr	Lys	Asn	Leu	Gly	Ala		
150				155					160					165			
aat	aag	agc	tat	gac	tgc	acc	aca	act	acc	tat	gaa	gtc	agc	gat	ttg	643	
Asn	Lys	Ser	Tyr	Asp	Cys	Thr	Thr	Thr	Thr	Tyr	Glu	Val	Ser	Asp	Leu		
				170					175					180			
gat	gta	gaa	cgc	gga	tac	gtg	gat	att	cca	acg	gta	tgg	acg	ttt	act	691	
Asp	Val	Glu	Arg	Gly	Tyr	Val	Asp	Ile	Pro	Thr	Val	Trp	Thr	Phe	Thr		
				185				190						195			
aac	tcc	gca	ggc	gaa	acg	gta	tgg	tcc	aaa	aac	ggt	gat	gtg	cct	cga	739	
Asn	Ser	Ala	Gly	Glu	Thr	Val	Trp	Ser	Lys	Asn	Val	Asp	Val	Pro	Arg		
	200						205					210					
gtt	gaa	ctc	aat	gga	aca	cag	gat	gct	gtc	act	gat	gca	atc	gta	acg	787	
Val	Glu	Leu	Asn	Gly	Thr	Gln	Asp	Ala	Val	Thr	Asp	Ala	Ile	Val	Thr		
	215					220					225						
gtt	gat	ccc	atc	aac	cca	gtt	cat	tcc	aac	ggc	cag	agc	caa	act	gtt	835	
Val	Asp	Pro	Ile	Asn	Pro	Val	His	Ser	Asn	Gly	Gln	Ser	Gln	Thr	Val		
230				235						240				245			
gag	gtc	cag	gct	aat	gtc	acc	tca	gag	gga	gat	ctg	cca	gct	gga	tct	883	
Glu	Val	Gln	Ala	Asn	Val	Thr	Ser	Glu	Gly	Asp	Leu	Pro	Ala	Gly	Ser		
				250					255					260			
aag	gtg	gcc	ttt	tat	cta	gat	tca	tcg	ccc	att	gat	acc	gca	gct	gtt	931	
Lys	Val	Ala	Phe	Tyr	Leu	Asp	Ser	Ser	Pro	Ile	Asp	Thr	Ala	Ala	Val		
			265					270					275				
gat	gcg	gaa	ggg	cat	gcc	agc	atc	tcg	att	gat	gtg	gac	aac	atc	gca	979	
Asp	Ala	Glu	Gly	His	Ala	Ser	Ile	Ser	Ile	Asp	Val	Asp	Asn	Ile	Ala		
		280					285					290					
agc	gag	cag	cct	gaa	cgc	aca	ttt	gag	gtt	cgc	gcc	cga	ctc	gtc	gtt	1027	
Ser	Glu	Gln	Pro	Glu	Arg	Thr	Phe	Glu	Val	Arg	Ala	Arg	Leu	Val	Val		
	295					300					305						
cca	gaa	gat	gca	cca	cga	tca	atc	gcg	cgt	gat	gcc	ttg	gca	cgt	ttt	1075	
Pro	Glu	Asp	Ala	Pro	Arg	Ser	Ile	Ala	Arg	Asp	Ala	Leu	Ala	Arg	Phe		
310					315					320					325		
aca	gtc	ctg	tct	gaa	caa	gtg	cag	cag	aac	tcc	ttg	gtg	atc	atg	aat	1123	
Thr	Val	Leu	Ser	Glu	Gln	Val	Gln	Gln	Asn	Ser	Leu	Val	Ile	Met	Asn		
				330					335					340			
cat	cca	gat	gtg	ttt	tct	gat	gga	caa	aca	aag	act	att	gtc	atc	gca	1171	
His	Pro	Asp	Val	Phe	Ser	Asp	Gly	Gln	Thr	Lys	Thr	Ile	Val	Ile	Ala		
			345					350					355				
gcg	aag	gcg	aca	gca	cac	gat	gga	tcg	ccg	gcg	gct	atc	ggg	act	ctc	1219	
Ala	Lys	Ala	Thr	Ala	His	Asp	Gly	Ser	Pro	Ala	Ala	Ile	Gly	Thr	Leu		
		360					365					370					
att	gca	ttt	cgc	gtc	aac	ggg	att	gag	cgg	gac	gtg	gtt	cca	act	aac	1267	
Ile	Ala	Phe	Arg	Val	Asn	Gly	Ile	Glu	Arg	Asp	Val	Val	Pro	Thr	Asn		

375

380

385

gcg caa gga aca gca aag ctt cag cta gac
 Ala Gln Gly Thr Ala Lys Leu Gln Leu Asp
 390 395

1297

<210> 234

<211> 399

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Val Thr Ala Gly Glu Thr Thr Thr Met Asn Val Thr Leu Thr Asn Pro
 1 5 10 15

Phe Asp Asn Ala Ile Phe Asp Arg Ala Val Ser Leu Glu Arg Pro Glu
 20 25 30

Gly Trp Gln Ala Glu Asp Val Arg Val Ser Ile Pro Ser Gly Glu Ser
 35 40 45

Val Thr Ile Pro Val Gln Val Thr Ala Pro Leu Val Ala Asp Asn Gly
 50 55 60

Glu Leu Pro Val Glu Val Ser Ile Leu Asp Gly Ala Asp Arg Tyr Thr
 65 70 75 80

Gly Arg Leu Asn Leu Thr Val Gln Gly Gly Gln Glu Pro Ala Pro Thr
 85 90 95

Ser Val Lys Val Ser Ile Pro Asn Leu Lys Asp Thr Tyr Val Ala Gly
 100 105 110

Glu Lys Ile Ser Ile Asn Phe Ala Val Asn Asn Pro Phe Asp Val Thr
 115 120 125

Val Asn Ser Val Pro Ser Leu Gly Glu Gly Glu Asn Trp Met Pro Ala
 130 135 140

Asn Leu Arg Gly Phe Asp Pro Glu Gln Gly Thr Pro Asn Cys Arg Tyr
 145 150 155 160

Lys Asn Leu Gly Ala Asn Lys Ser Tyr Asp Cys Thr Thr Thr Tyr
 165 170 175

Glu Val Ser Asp Leu Asp Val Glu Arg Gly Tyr Val Asp Ile Pro Thr
 180 185 190

Val Trp Thr Phe Thr Asn Ser Ala Gly Glu Thr Val Trp Ser Lys Asn
 195 200 205

Val Asp Val Pro Arg Val Glu Leu Asn Gly Thr Gln Asp Ala Val Thr
 210 215 220

Asp Ala Ile Val Thr Val Asp Pro Ile Asn Pro Val His Ser Asn Gly
 225 230 235 240

Gln Ser Gln Thr Val Glu Val Gln Ala Asn Val Thr Ser Glu Gly Asp
 245 250 255

Leu Pro Ala Gly Ser Lys Val Ala Phe Tyr Leu Asp Ser Ser Pro Ile
 260 265 270
 Asp Thr Ala Ala Val Asp Ala Glu Gly His Ala Ser Ile Ser Ile Asp
 275 280 285
 Val Asp Asn Ile Ala Ser Glu Gln Pro Glu Arg Thr Phe Glu Val Arg
 290 295 300
 Ala Arg Leu Val Val Pro Glu Asp Ala Pro Arg Ser Ile Ala Arg Asp
 305 310 315 320
 Ala Leu Ala Arg Phe Thr Val Leu Ser Glu Gln Val Gln Gln Asn Ser
 325 330 335
 Leu Val Ile Met Asn His Pro Asp Val Phe Ser Asp Gly Gln Thr Lys
 340 345 350
 Thr Ile Val Ile Ala Ala Lys Ala Thr Ala His Asp Gly Ser Pro Ala
 355 360 365
 Ala Ile Gly Thr Leu Ile Ala Phe Arg Val Asn Gly Ile Glu Arg Asp
 370 375 380
 Val Val Pro Thr Asn Ala Gln Gly Thr Ala Lys Leu Gln Leu Asp
 385 390 395

<210> 235
 <211> 440
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(417)
 <223> RXA00984

<400> 235
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 Gln Arg Gly Thr Pro Val Leu Leu Gly Glu Thr Pro Trp Met Lys Thr
 1 5 10 15
 aaa atc gtg gaa ctc agc gat gga acc ctg atg aac aac agt cgt tca 96
 Lys Ile Val Glu Leu Ser Asp Gly Thr Leu Met Asn Asn Ser Arg Ser
 20 25 30
 tca gga gcc gat act tac cgc aag gtg tct tat tcc acc gac ggc ggc 144
 Ser Gly Ala Asp Thr Tyr Arg Lys Val Ser Tyr Ser Thr Asp Gly Gly
 35 40 45
 gtc act tgg acc gag cca act ctt gat acc cag ctg ccg gat cct cgc 192
 Val Thr Trp Thr Glu Pro Thr Leu Asp Thr Gln Leu Pro Asp Pro Arg
 50 55 60
 aac aat gct tcc ctg att cga gta ttc ccg aca gca cct gag gga agt 240
 Asn Asn Ala Ser Leu Ile Arg Val Phe Pro Thr Ala Pro Glu Gly Ser
 65 70 75 80
 gcg cag gca aag gtt ctg ctg ttc tcc aac act gcc acc acg agt ggc 288
 Ala Gln Ala Lys Val Leu Leu Phe Ser Asn Thr Ala Thr Thr Ser Gly

85 90 95
 cgc acc aat ggc acc gtc cgc atg tgc tgt gat gat ggt cag acc tgg 336
 Arg Thr Asn Gly Thr Val Arg Met Ser Cys Asp Asp Gly Gln Thr Trp
 100 105 110
 ccg gtg tct aag gtg ttt gaa cca gga gca atc caa tat acc tgc atg 384
 Pro Val Ser Lys Val Phe Glu Pro Gly Ala Ile Gln Tyr Thr Ser Met
 115 120 125
 gca acg ctt ccc aac ggt gac atc ggc atg ctg tgagaaaaca gtggctcaaa 437
 Ala Thr Leu Pro Asn Gly Asp Ile Gly Met Leu
 130 135
 tat 440

<210> 236
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 236
 Gln Arg Gly Thr Pro Val Leu Leu Gly Glu Thr Pro Trp Met Lys Thr
 1 5 10 15
 Lys Ile Val Glu Leu Ser Asp Gly Thr Leu Met Asn Asn Ser Arg Ser
 20 25 30
 Ser Gly Ala Asp Thr Tyr Arg Lys Val Ser Tyr Ser Thr Asp Gly Gly
 35 40 45
 Val Thr Trp Thr Glu Pro Thr Leu Asp Thr Gln Leu Pro Asp Pro Arg
 50 55 60
 Asn Asn Ala Ser Leu Ile Arg Val Phe Pro Thr Ala Pro Glu Gly Ser
 65 70 75 80
 Ala Gln Ala Lys Val Leu Leu Phe Ser Asn Thr Ala Thr Thr Ser Gly
 85 90 95
 Arg Thr Asn Gly Thr Val Arg Met Ser Cys Asp Asp Gly Gln Thr Trp
 100 105 110
 Pro Val Ser Lys Val Phe Glu Pro Gly Ala Ile Gln Tyr Thr Ser Met
 115 120 125
 Ala Thr Leu Pro Asn Gly Asp Ile Gly Met Leu
 130 135

<210> 237
 <211> 832
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(832)
 <223> RXN02513

<400> 237

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ggggaggcat gtctatgccc ccaattagac atctgacatc atg ctt cca atc tgg 115
Met Leu Pro Ile Trp
1 5

atg ggt ctt cca ttc aag aaa gca ggt gct ttg tct cgg cgt aaa gca 163
Met Gly Leu Pro Phe Lys Lys Ala Gly Ala Leu Ser Arg Arg Lys Ala
10 15 20

gta ttc tca gcg ctt ggt gca gcc gca ctc atg ggc gca gca cta ccc 211
Val Phe Ser Ala Leu Gly Ala Ala Ala Leu Met Gly Ala Ala Leu Pro
25 30 35

acc atc cca acg gcc caa gct caa aca ccc acg ggc tac gga ttc gat 259
Thr Ile Pro Thr Ala Gln Ala Gln Thr Pro Thr Gly Tyr Gly Phe Asp
40 45 50

gca aca gca agc atc agc gaa gaa cca gag ttt tca aca caa caa ctc 307
Ala Thr Ala Ser Ile Ser Glu Glu Pro Glu Phe Ser Thr Gln Gln Leu
55 60 65

gct gac ggc gga act ctc gga ttt gat tgc tac cgc atc cca tcg ctt 355
Ala Asp Gly Gly Thr Leu Gly Phe Asp Cys Tyr Arg Ile Pro Ser Leu
70 75 80 85

ggc gtc gca ccc aac ggc aac gtc ctc gca tcg tgg gat ggt cgc cca 403
Gly Val Ala Pro Asn Gly Asn Val Leu Ala Ser Trp Asp Gly Arg Pro
90 95 100

aac aac tgt tca gat gct cca caa ccc aac tcc atc gtg ggc aag gta 451
Asn Asn Cys Ser Asp Ala Pro Gln Pro Asn Ser Ile Val Gly Lys Val
105 110 115

tcg acc gac aac gga gca acc tgg ggc gaa cag cac gac att tcc gca 499
Ser Thr Asp Asn Gly Ala Thr Trp Gly Glu Gln His Asp Ile Ser Ala
120 125 130

ggt atc acc gcc gaa ccc aaa act ggc tat tcc gat ccc agc atc gtt 547
Gly Ile Thr Ala Glu Pro Lys Thr Gly Tyr Ser Asp Pro Ser Ile Val
135 140 145

gtg gac tgg gag agg ggc gat gtc ttt aac ttc cac gtg aag tca ttc 595
Val Asp Trp Glu Arg Gly Asp Val Phe Asn Phe His Val Lys Ser Phe
150 155 160 165

gat gca gga tac ttc acc tcc caa cca ggc acg gac ccg gat gat cgc 643
Asp Ala Gly Tyr Phe Thr Ser Gln Pro Gly Thr Asp Pro Asp Asp Arg
170 175 180

aac gtt gcc cat gtt gcc tac gcc aaa tca tca gat aac ggc tca acc 691
Asn Val Ala His Val Ala Tyr Ala Lys Ser Ser Asp Asn Gly Ser Thr
185 190 195

tgg gtt gca gac acc gtc att act gat caa gtg gtt gct cat gac acc 739
Trp Val Ala Asp Thr Val Ile Thr Asp Gln Val Val Ala His Asp Thr
200 205 210

tgg gac agc cga ttt gcc aca tcc gga aac ggc atc caa ctg caa tac 787
Trp Asp Ser Arg Phe Ala Thr Ser Gly Asn Gly Ile Gln Leu Gln Tyr

Val Thr Arg Met


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<210> 239
<211> 824
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (93) .. (824)
<223> FRXA02513
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<400> 239																
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atgtctatgc ccccaattag acatctgaca tcatg ctt cca atc tgg atg ggt 113																
Met Leu Pro Ile Trp Met Gly																
1 5																
ctt cca ttc aag aaa gca ggg gct ttg tct cgg cgt aaa gca gta ttc 161																
Leu Pro Phe Lys Lys Ala Gly Ala Leu Ser Arg Arg Lys Ala Val Phe																
10 15 20																
tca gcg ctt ggt gca gac gca ctc atg ggc gca gca cta ccc acc atc 209																
Ser Ala Leu Gly Ala Asp Ala Leu Met Gly Ala Ala Leu Pro Thr Ile																
25 30 35																
cca acg gcc caa gct caa aca ccc acg ggc tac gga ttc gat gca aca 257																
Pro Thr Ala Gln Ala Gln Thr Pro Thr Gly Tyr Gly Phe Asp Ala Thr																
40 45 50 55																
gca agc atc agc gaa gaa cca gag ttt tca aca caa caa ctc gct gac 305																
Ala Ser Ile Ser Glu Glu Pro Glu Phe Ser Thr Gln Gln Leu Ala Asp																
60 65 70																
ggc gga act ctc gga ttt gat tgc tac cgc atc cca tcg ctt ggc gtc 353																
Gly Gly Thr Leu Gly Phe Asp Cys Tyr Arg Ile Pro Ser Leu Gly Val																
75 80 85																
gca ccc aac ggc aac gtc ctc gca tcg tgg gat ggt cgc cca aac aac 401																
Ala Pro Asn Gly Asn Val Leu Ala Ser Trp Asp Gly Arg Pro Asn Asn																
90 95 100																
tgt tca gat gct cca caa ccc aac tcc atc gtg ggc aag gta tcg acc 449																
Cys Ser Asp Ala Pro Gln Pro Asn Ser Ile Val Gly Lys Val Ser Thr																
105 110 115																
gac aac gga gca acc tgg ggc gaa cag cac gac att tcc gca ggt atc 497																
Asp Asn Gly Ala Thr Trp Gly Glu Gln His Asp Ile Ser Ala Gly Ile																
120 125 130 135																
acc gcc gaa ccc aaa act ggc tat tcc gat ccc agc atc gtt gtg gac 545																
Thr Ala Glu Pro Lys Thr Gly Tyr Ser Asp Pro Ser Ile Val Val Asp																
140 145 150																
tgg gag agg ggc gat gtc ttt aac ttc cac gtg aag tca ttc gat gca 593																
Trp Glu Arg Gly Asp Val Phe Asn Phe His Val Lys Ser Phe Asp Ala																
155 160 165																
gga tac ttc acc tcc caa cca ggc acg gac ccg gat gat cgc aac gtt 641																
Gly Tyr Phe Thr Ser Gln Pro Gly Thr Asp Pro Asp Arg Asn Val																
170 175 180																

gcc cat gtt gcc tac gcc aaa tca tca gat aac ggc tca acc tgg gtt 689
 Ala His Val Ala Tyr Ala Lys Ser Ser Asp Asn Gly Ser Thr Trp Val
 185 190 195

gca gac acc gtc att act gat caa gtg gtt gct cat gac acc tgg gac 737
 Ala Asp Thr Val Ile Thr Asp Gln Val Val Ala His Asp Thr Trp Asp
 200 205 210 215

agc cga ttt gcc aca tcc gga aac ggc atc caa ctg caa tac ggc gcg 785
 Ser Arg Phe Ala Thr Ser Gly Asn Gly Ile Gln Leu Gln Tyr Gly Ala
 220 225 230

tac aag gga cga ttg gtc cag cca tgc gta act cgc atg 824
 Tyr Lys Gly Arg Leu Val Gln Pro Ser Val Thr Arg Met
 235 240

<210> 240

<211> 244

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

Met Leu Pro Ile Trp Met Gly Leu Pro Phe Lys Lys Ala Gly Ala Leu
 1 5 10 15

Ser Arg Arg Lys Ala Val Phe Ser Ala Leu Gly Ala Asp Ala Leu Met
 20 25 30

Gly Ala Ala Leu Pro Thr Ile Pro Thr Ala Gln Ala Gln Thr Pro Thr
 35 40 45

Gly Tyr Gly Phe Asp Ala Thr Ala Ser Ile Ser Glu Glu Pro Glu Phe
 50 55 60

Ser Thr Gln Gln Leu Ala Asp Gly Gly Thr Leu Gly Phe Asp Cys Tyr
 65 70 75 80

Arg Ile Pro Ser Leu Gly Val Ala Pro Asn Gly Asn Val Leu Ala Ser
 85 90 95

Trp Asp Gly Arg Pro Asn Asn Cys Ser Asp Ala Pro Gln Pro Asn Ser
 100 105 110

Ile Val Gly Lys Val Ser Thr Asp Asn Gly Ala Thr Trp Gly Glu Gln
 115 120 125

His Asp Ile Ser Ala Gly Ile Thr Ala Glu Pro Lys Thr Gly Tyr Ser
 130 135 140

Asp Pro Ser Ile Val Val Asp Trp Glu Arg Gly Asp Val Phe Asn Phe
 145 150 155 160

His Val Lys Ser Phe Asp Ala Gly Tyr Phe Thr Ser Gln Pro Gly Thr
 165 170 175

Asp Pro Asp Asp Arg Asn Val Ala His Val Ala Tyr Ala Lys Ser Ser
 180 185 190

Asp Asn Gly Ser Thr Trp Val Ala Asp Thr Val Ile Thr Asp Gln Val

195

200

205

Val Ala His Asp Thr Trp Asp Ser Arg Phe Ala Thr Ser Gly Asn Gly
 210 215 220

Ile Gln Leu Gln Tyr Gly Ala Tyr Lys Gly Arg Leu Val Gln Pro Ser
 225 230 235 240

Val Thr Arg Met

<210> 241

<211> 733

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA00903

<400> 241

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 gccctattac caagtagatg tattcagctc cgagccgttc atg gga aac ccg ctt 115
 Met Gly Asn Pro Leu
 1 5
 gct gtc atc gcc gat gct gat gac tta agt gcc gaa caa atg gcc cga 163
 Ala Val Ile Ala Asp Ala Asp Leu Ser Ala Glu Gln Met Ala Arg
 10 15 20
 atc gct agg tgg aca aac ctc tca gaa acc aca ttt ctt tta aag cca 211
 Ile Ala Arg Trp Thr Asn Leu Ser Glu Thr Thr Phe Leu Leu Lys Pro
 25 30 35
 acc caa gaa ggt gct gac tac cgg gta cgc att ttc acc cca acc ggt 259
 Thr Gln Glu Gly Ala Asp Tyr Arg Val Arg Ile Phe Thr Pro Thr Gly
 40 45 50
 gag ctc ccc ttc gct gga cac cca aca ctc gga acc gcc cac gtg ttt 307
 Glu Leu Pro Phe Ala Gly His Pro Thr Leu Gly Thr Ala His Val Phe
 55 60 65
 agg gaa ctg cac ggt gaa cag gga acc cag ttg gtt cag gaa tgt gtc 355
 Arg Glu Leu His Gly Glu Gln Gly Thr Gln Leu Val Gln Glu Cys Val
 70 75 80 85
 gcc ggt tta gtt gct gtg cgc gct att gac ggg cca gca agt gga ttg 403
 Ala Gly Leu Val Ala Val Arg Ala Ile Asp Gly Pro Ala Ser Gly Leu
 90 95 100
 gct ttt cag gct cca ccc aca ctc aaa gac ggg cca ttg gat gct tcc 451
 Ala Phe Gln Ala Pro Pro Thr Leu Lys Asp Gly Pro Leu Asp Ala Ser
 105 110 115
 gac cta gac gca gct tgt gag gct tta gga atc agc ccc gac ttc att 499
 Asp Leu Asp Ala Ala Cys Glu Ala Leu Gly Ile Ser Pro Asp Phe Ile
 120 125 130

cga gcc cac caa tgg gta gac aac ggc ccc ggc tgg gca gta gtg gag 547
 Arg Ala His Gln Trp Val Asp Asn Gly Pro Gly Trp Ala Val Val Glu
 135 140 145

 cta ccg agc gcc caa cac gta ttg gat ctg gaa ccc gat ttc agt gca 595
 Leu Pro Ser Ala Gln His Val Leu Asp Leu Glu Pro Asp Phe Ser Ala
 150 155 160 165

 cat cca aca ttg aaa ctc gga gtg att ggg gcc tat ccc gaa ggg gct 643
 His Pro Thr Leu Lys Leu Gly Val Ile Gly Ala Tyr Pro Glu Gly Ala
 170 175 180

 ccc cac gcc ttt gaa gta cgg gca ttc gct caa gga atc ggt gaa gac 691
 Pro His Ala Phe Glu Val Arg Ala Phe Ala Gln Gly Ile Gly Glu Asp
 185 190 195

 cca gtt aca gga agc ctc aat gca ttc att gcg cag tgg cta 733
 Pro Val Thr Gly Ser Leu Asn Ala Phe Ile Ala Gln Trp Leu
 200 205 210

<210> 242

<211> 211

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 242

Met Gly Asn Pro Leu Ala Val Ile Ala Asp Ala Asp Asp Leu Ser Ala
 1 5 10 15

 Glu Gln Met Ala Arg Ile Ala Arg Trp Thr Asn Leu Ser Glu Thr Thr
 20 25 30

 Phe Leu Leu Lys Pro Thr Gln Glu Gly Ala Asp Tyr Arg Val Arg Ile
 35 40 45

 Phe Thr Pro Thr Gly Glu Leu Pro Phe Ala Gly His Pro Thr Leu Gly
 50 55 60

 Thr Ala His Val Phe Arg Glu Leu His Gly Glu Gln Gly Thr Gln Leu
 65 70 75 80

 Val Gln Glu Cys Val Ala Gly Leu Val Ala Val Arg Ala Ile Asp Gly
 85 90 95

 Pro Ala Ser Gly Leu Ala Phe Gln Ala Pro Pro Thr Leu Lys Asp Gly
 100 105 110

 Pro Leu Asp Ala Ser Asp Leu Asp Ala Ala Cys Glu Ala Leu Gly Ile
 115 120 125

 Ser Pro Asp Phe Ile Arg Ala His Gln Trp Val Asp Asn Gly Pro Gly
 130 135 140

 Trp Ala Val Val Glu Leu Pro Ser Ala Gln His Val Leu Asp Leu Glu
 145 150 155 160

 Pro Asp Phe Ser Ala His Pro Thr Leu Lys Leu Gly Val Ile Gly Ala
 165 170 175

 Tyr Pro Glu Gly Ala Pro His Ala Phe Glu Val Arg Ala Phe Ala Gln

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180          185          190
Gly Ile Gly Glu Asp Pro Val Thr Gly Ser Leu Asn Ala Phe Ile Ala
195          200          205

Gln Trp Leu
210

<210> 243
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXA01224

<400> 243
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acggaagtca tcctatggca ggcgcgccta ggatggtgcc atg agc atc ctt gac 115
Met Ser Ile Leu Asp
1 5

acg ttg aaa act ccc gtg att gtc gcc ccg atg gct ggc ggc ccg tcc 163
Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met Ala Gly Gly Pro Ser
10 15 20

act ccc gcg ttg gtc aat gca gca gca gag gca ggt tcc ctc ggg ttc 211
Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala Gly Ser Leu Gly Phe
25 30 35

ttg gct ggt ggc gtc atg cct ctt gag cag ctg aaa cag gaa ttg tca 259
Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu Lys Gln Glu Leu Ser
40 45 50

gag gta aaa ggc gtc ttt ggc gtc aac ctg ttt cgc ccg cag acg gat 307
Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe Arg Pro Gln Thr Asp
55 60 65

gcg cct aag cct tca gac att gat gag ctg gcg gga ttg ttg tcc tcg 355
Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala Gly Leu Leu Ser Ser
70 75 80 85

gcg ttt cgg caa ttt ggc ctc gat gag ccg acg gtg cct acg ccg gat 403
Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr Val Pro Thr Pro Asp
90 95 100

ttg agc aat ggg tgg gag gct aaa ttt gag gcc gtt ctt gcc gct aag 451
Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala Val Leu Ala Ala Lys
105 110 115

ccc gcc gtt ttt tcc tgc acc ttt ggt att ttt agc gct gaa gaa ttc 499
Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe Ser Ala Glu Glu Phe
120 125 130

gcc cgg atc aaa gcc acc gga att gag gcg tgg gtg acg gtg acc aat 547
Ala Arg Ile Lys Ala Thr Gly Ile Glu Ala Trp Val Thr Val Thr Asn
135 140 145

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ccg gag gac gcg ctg gct gcg cag aaa gct ggc gcc aac gcg ctt gtc 595
 Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly Ala Asn Ala Leu Val
 150 155 160 165

 gtg caa ggc ccc gag gcg ggt ggg cac cgc tct acc tgg tcc att gaa 643
 Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser Thr Trp Ser Ile Glu
 170 175 180

 gtg gag ccg gac gag cgc gac ctg aaa acc ctc ctc gca gct gtc aaa 691
 Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu Leu Ala Ala Val Lys
 185 190 195

 caa gcg ggc gtt tac ctc ccg ctc atc gca gcc ggc ggc ctt tca acc 739
 Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala Gly Gly Leu Ser Thr
 200 205 210

 tcc gca gac gtg gca gca att tta gaa gcc ggc gcc agc gct gcc tcc 787
 Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly Ala Ser Ala Ala Ser
 215 220 225

 tgt ggt tcc gcc ttt ttg ctt agc gac gaa gcc ggc acc agc tca ctt 835
 Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala Gly Thr Ser Ser Leu
 230 235 240 245

 aac cgc gag atc ttg gac gcc gcc cca gca ctt ggt ttg gaa tcg gtg 883
 Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu Gly Leu Glu Ser Val
 250 255 260

 tca tct cgc gca ttt tcg ggc cgt tat gcc agg gga gtg gaa acc agg 931
 Ser Ser Arg Ala Phe Ser Gly Arg Tyr Ala Arg Gly Val Glu Thr Arg
 265 270 275

 ttc acc cgt tcg aac gag ggg tta ccc ccg ttg tac cca tac ctc aac 979
 Phe Thr Arg Ser Asn Glu Gly Leu Pro Pro Leu Tyr Pro Tyr Leu Asn
 280 285 290

 cca atg atc aca tct tta cgt aag gtg gcg gga agt gca ggc aac tgg 1027
 Pro Met Ile Thr Ser Leu Arg Lys Val Ala Gly Ser Ala Gly Asn Trp
 295 300 305

 gat tac gcc tac tgc ctg gta gga gtc ggc ctg gaa tcg att gcg aag 1075
 Asp Tyr Ala Tyr Cys Leu Val Gly Val Gly Leu Glu Ser Ile Ala Lys
 310 315 320 325

 ggt agt gca aag cag ata ctg gaa tca tta aca cct tcc gct ttg ggc 1123
 Gly Ser Ala Lys Gln Ile Leu Glu Ser Leu Thr Pro Ser Ala Leu Gly
 330 335 340

 taatgttggg gggagtgcctt tca 1146

<210> 244

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Ser Ile Leu Asp Thr Leu Lys Thr Pro Val Ile Val Ala Pro Met
 1 5 10 15

Ala Gly Gly Pro Ser Thr Pro Ala Leu Val Asn Ala Ala Ala Glu Ala
 20 25 30
 Gly Ser Leu Gly Phe Leu Ala Gly Gly Val Met Pro Leu Glu Gln Leu
 35 40 45
 Lys Gln Glu Leu Ser Glu Val Lys Gly Val Phe Gly Val Asn Leu Phe
 50 55 60
 Arg Pro Gln Thr Asp Ala Pro Lys Pro Ser Asp Ile Asp Glu Leu Ala
 65 70 75 80
 Gly Leu Leu Ser Ser Ala Phe Arg Gln Phe Gly Leu Asp Glu Pro Thr
 85 90 95
 Val Pro Thr Pro Asp Leu Ser Asn Gly Trp Glu Ala Lys Phe Glu Ala
 100 105 110
 Val Leu Ala Ala Lys Pro Ala Val Phe Ser Cys Thr Phe Gly Ile Phe
 115 120 125
 Ser Ala Glu Glu Phe Ala Arg Ile Lys Ala Thr Gly Ile Glu Ala Trp
 130 135 140
 Val Thr Val Thr Asn Pro Glu Asp Ala Leu Ala Ala Gln Lys Ala Gly
 145 150 155 160
 Ala Asn Ala Leu Val Val Gln Gly Pro Glu Ala Gly Gly His Arg Ser
 165 170 175
 Thr Trp Ser Ile Glu Val Glu Pro Asp Glu Arg Asp Leu Lys Thr Leu
 180 185 190
 Leu Ala Ala Val Lys Gln Ala Gly Val Tyr Leu Pro Leu Ile Ala Ala
 195 200 205
 Gly Gly Leu Ser Thr Ser Ala Asp Val Ala Ala Ile Leu Glu Ala Gly
 210 215 220
 Ala Ser Ala Ala Ser Cys Gly Ser Ala Phe Leu Leu Ser Asp Glu Ala
 225 230 235 240
 Gly Thr Ser Ser Leu Asn Arg Glu Ile Leu Asp Ala Ala Pro Ala Leu
 245 250 255
 Gly Leu Glu Ser Val Ser Ser Arg Ala Phe Ser Gly Arg Tyr Ala Arg
 260 265 270
 Gly Val Glu Thr Arg Phe Thr Arg Ser Asn Glu Gly Leu Pro Pro Leu
 275 280 285
 Tyr Pro Tyr Leu Asn Pro Met Ile Thr Ser Leu Arg Lys Val Ala Gly
 290 295 300
 Ser Ala Gly Asn Trp Asp Tyr Ala Tyr Cys Leu Val Gly Val Gly Leu
 305 310 315 320
 Glu Ser Ile Ala Lys Gly Ser Ala Lys Gln Ile Leu Glu Ser Leu Thr
 325 330 335
 Pro Ser Ala Leu Gly

340

<210> 245
 <211> 723
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(700)
 <223> RXA01571

<400> 245
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 cgctcgtagg cgcttttgat ttttcggtag gctaactggg gtg agt atc tca gta 115
 Val Ser Ile Ser Val
 1 5
 aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc 163
 Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile
 10 15 20
 att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa 211
 Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val Val Ile Asp Ile Lys
 25 30 35
 gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg 259
 Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp
 40 45 50
 ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt 307
 Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val
 55 60 65
 gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc 355
 Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg
 70 75 80 85
 gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc 403
 Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys
 90 95 100
 gtc gca gga ttt gaa aac aac tgc ctt cgc gga aac gtc gga acc tac 451
 Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly Asn Val Gly Thr Tyr
 105 110 115
 aac tct aac gac gtc gac ggc acc atc acc caa ggc ggc tac gct gaa 499
 Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln Gly Gly Tyr Ala Glu
 120 125 130
 aag gta gtg gtc aac gaa cgt ttc ctg tgc agc atc cca gag gaa ctt 547
 Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser Ile Pro Glu Glu Leu
 135 140 145
 aac ttc gat gtc gca gca cca ctg ctg tgc gca ggc atc acc acc tac 595
 Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr
 150 155 160 165
 tcc cca atc gct cgc tgg aac gtt aaa gaa ggc gac aaa gta gca gtc 643

Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val
 170 175 180

atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc 691
 Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser
 185 190 195

caa ggg tgc tgaggttacc gttctgtccc gtt 723
 Gln Gly Cys
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<210> 246
 <211> 200
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 246
 Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro
 1 5 10 15

Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val
 20 25 30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
 35 40 45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
 50 55 60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
 65 70 75 80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
 85 90 95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
 100 105 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
 115 120 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys
 195 200

<210> 247
 <211> 1338
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1315)

<223> RXN02478

<400> 247

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gacatcgtcg aagcgcctctc cagcggcaac atcgacgatt atcgcagcgc cgtgctcgct 60
cactacgcgc cgttttcgccg catgatttcc aacatgctcg atg cgc act agc ctc 115
                                     Met Arg Thr Ser Leu
                                     1 5
att gcg cgc ggg ttg tac cgc att ccc gcg ctg gtc tgg gat cag ggt 163
Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu Val Trp Asp Gln Gly
          10          15          20
ctt tta acg ctt ttc gac gcc cgc ctc agt gtt gac gac ctc ccc gca 211
Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val Asp Asp Leu Pro Ala
          25          30          35
ccc atc gac gtg gtg tca gcg cga tcc tca gac ggc atc acc tgg acc 259
Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp Gly Ile Thr Trp Thr
          40          45          50
acc cca gaa cca gca atc gtc gaa act gaa cac cgc ggt gtg ggc gat 307
Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His Arg Gly Val Gly Asp
          55          60          65
gtc tgc ctt gtc acg ggc gat ctg tgc ttc cac gga ttg tcc aac ctc 355
Val Cys Leu Val Thr Gly Asp Leu Cys Phe His Gly Leu Ser Asn Leu
          70          75          80          85
gca gga ttt ttt gag gat ccc acc gac ctt gaa ccc cgg ctg gcg cgc 403
Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu Pro Arg Leu Ala Arg
          90          95          100
cgg gat gtg agt ggg tgg acg tcg ata agc atg gcc cac tat ttt gcg 451
Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met Ala His Tyr Phe Ala
          105          110          115
gat gtt gat gcc gcg ttc gcc tcg tcg ggg acg gga ctt gtc ctg gcg 499
Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr Gly Leu Val Leu Ala
          120          125          130
gat ggg cgg tgg att cag agt ttt gtg gtg cgg cgc ggg cgc gag att 547
Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg Arg Gly Arg Glu Ile
          135          140          145
tcg ctt cgg att ctg cgc agc gat ggc cac atc acc gat att gcc ggc 595
Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile Thr Asp Ile Ala Gly
          150          155          160          165
ggt aac gaa tcc gcg atg acg cag ctg ccg agc ggt cgg att gtg ctg 643
Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser Gly Arg Ile Val Leu
          170          175          180
cat tcc agg ggg gtg gga cac cgt ctg agc agt gtg tcc gat gat ttc 691
His Ser Arg Gly Val Gly His Arg Leu Ser Ser Val Ser Asp Asp Phe
          185          190          195

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ggg gag aca ttc act ccg ctg gag cct gtg cct gaa cta atc gac ccc 739
Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro Glu Leu Ile Asp Pro
      200                      205                      210

ggc tgc aac ggc cac gtg ttc tac tgg aaa gcg gct gga atg ctc gcc 787
Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala Ala Gly Met Leu Ala
      215                      220                      225

gca acg cac ctg gcg gac cct gat ctg cga cgc cac ttg gtg gtt gat 835
Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg His Leu Val Val Asp
      230                      235                      240                      245

tta tcc agc gac gaa gga gcg acc tgg gcg cat cgc atc acc atc gag 883
Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His Arg Ile Thr Ile Glu
      250                      255                      260

cgc gaa gaa gcc gcc tat tca acc gct gcg gaa atg ccc aac gga gat 931
Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu Met Pro Asn Gly Asp
      265                      270                      275

gtt gcc gtg gtg tgg gaa gca gag gga acg cgc gcg ata aaa tgc acg 979
Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg Ala Ile Lys Cys Thr
      280                      285                      290

gtg atc agc gta aat gat att tcg ctg cgg atc gat gag ccc att tcc 1027
Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile Asp Glu Pro Ile Ser
      295                      300                      305

gat gcc ata tcc ctc cgc cat gtg gtg atc aac gat gac cat gac ggc 1075
Asp Ala Ile Ser Leu Arg His Val Val Ile Asn Asp Asp His Asp Gly
      310                      315                      320                      325

atc gaa gtc gca ctg cct gac gca tcg caa tgg ggt gaa ggt gta ttc 1123
Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp Gly Glu Gly Val Phe
      330                      335                      340

aaa att gtg tcc aat cca gac gcg agc acc caa aaa atc cgc act cga 1171
Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln Lys Ile Arg Thr Arg
      345                      350                      355

ggc aag ccc gcg cga cag acc ctg gaa att ggg gat gaa ttg gtt ttt 1219
Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly Asp Glu Leu Val Phe
      360                      365                      370

gat atc cgc aag ggt gga gaa gtg gct tac ggc gtc acg gtt cct tat 1267
Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly Val Thr Val Pro Tyr
      375                      380                      385

gat ggt cgc tcg ttg ggg gaa gtt aaa cag gat ttt gga gtg ggg ctg 1315
Asp Gly Arg Ser Leu Gly Glu Val Lys Gln Asp Phe Gly Val Gly Leu
      390                      395                      400                      405

tagaggccga ttgctgtcc ttt 1338

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<210> 248

<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

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Met Arg Thr Ser Leu Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu
 1           5           10           15

Val Trp Asp Gln Gly Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val
          20           25           30

Asp Asp Leu Pro Ala Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp
      35           40           45

Gly Ile Thr Trp Thr Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His
 50           55           60

Arg Gly Val Gly Asp Val Cys Leu Val Thr Gly Asp Leu Cys Phe His
 65           70           75           80

Gly Leu Ser Asn Leu Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu
          85           90           95

Pro Arg Leu Ala Arg Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met
      100           105           110

Ala His Tyr Phe Ala Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr
      115           120           125

Gly Leu Val Leu Ala Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg
 130           135           140

Arg Gly Arg Glu Ile Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile
 145           150           155           160

Thr Asp Ile Ala Gly Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser
          165           170           175

Gly Arg Ile Val Leu His Ser Arg Gly Val Gly His Arg Leu Ser Ser
      180           185           190

Val Ser Asp Asp Phe Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro
      195           200           205

Glu Leu Ile Asp Pro Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala
 210           215           220

Ala Gly Met Leu Ala Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg
 225           230           235           240

His Leu Val Val Asp Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His
          245           250           255

Arg Ile Thr Ile Glu Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu
      260           265           270

Met Pro Asn Gly Asp Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg
      275           280           285

Ala Ile Lys Cys Thr Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile
 290           295           300

Asp Glu Pro Ile Ser Asp Ala Ile Ser Leu Arg His Val Val Ile Asn
 305           310           315           320

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Asp Asp His Asp Gly Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp
 325 330 335

Gly Glu Gly Val Phe Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln
 340 345 350

Lys Ile Arg Thr Arg Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly
 355 360 365

Asp Glu Leu Val Phe Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly
 370 375 380

Val Thr Val Pro Tyr Asp Gly Arg Ser Leu Gly Glu Val Lys Gln Asp
 385 390 395 400

Phe Gly Val Gly Leu
 405

<210> 249

<211> 1213

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1213)

<223> RXN00343

<400> 249

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cacccaagct ctgtagaaa aaattgagga agcagtctaa atg aaa cac caa tat 115
 Met Lys His Gln Tyr
 1 5

gat gtc atc gtt gtc ggt tcc ggc gct ggc gga tta tca gct gca gtc 163
 Asp Val Ile Val Val Gly Ser Gly Ala Gly Gly Leu Ser Ala Ala Val
 10 15 20

agt gca gct tac ggc ggt aag aaa gtc gct gta att gaa aag gcc tca 211
 Ser Ala Ala Tyr Gly Gly Lys Lys Val Ala Val Ile Glu Lys Ala Ser
 25 30 35

gta ctc ggt gga gcc acc acc tgg tcc ggc ggt tgg gct tgg act cct 259
 Val Leu Gly Gly Ala Thr Thr Trp Ser Gly Gly Trp Ala Trp Thr Pro
 40 45 50

gga acc agc ctt gcg cgc aaa gac gga gta gtg gaa tcc aaa gaa gaa 307
 Gly Thr Ser Leu Ala Arg Lys Asp Gly Val Val Glu Ser Lys Glu Glu
 55 60 65

ttc caa acc tac ctg caa gcg gta gtg ggg gag tac tac caa gaa gac 355
 Phe Gln Thr Tyr Leu Gln Ala Val Val Gly Glu Tyr Tyr Gln Glu Asp
 70 75 80 85

aac atc tcc gcc ttc ttg gac gca gcc cct gaa atg gtc gat ttc ttt 403
 Asn Ile Ser Ala Phe Leu Asp Ala Ala Pro Glu Met Val Asp Phe Phe
 90 95 100

gaa aaa aac acc gac ctg cag tgg acc ccc ggc gcg aaa atc aac gac 451

Glu Lys Asn Thr Asp Leu Gln Trp Thr Pro Gly Ala Lys Ile Asn Asp	
105 110 115	
atc tac ggc aac ctc ccc ggt gct ggc act gga cac cgc tcc gtt ggg	499
Ile Tyr Gly Asn Leu Pro Gly Ala Gly Thr Gly His Arg Ser Val Gly	
120 125 130	
cca aaa cca ttc aac gga cgc aaa gta ccc aag agt gtt ctt cca aaa	547
Pro Lys Pro Phe Asn Gly Arg Lys Val Pro Lys Ser Val Leu Pro Lys	
135 140 145	
ctg cgc cac cag ctg tat gaa acc tcc ttc ctg gga atg ggc atc atg	595
Leu Arg His Gln Leu Tyr Glu Thr Ser Phe Leu Gly Met Gly Ile Met	
150 155 160 165	
gct ggg cct gac ctg acg aaa ttc ctc tct gct tca cag ttc gat cca	643
Ala Gly Pro Asp Leu Thr Lys Phe Leu Ser Ala Ser Gln Phe Asp Pro	
170 175 180	
cgt ggt tgg gta cat gcc gcc agg cgc gtc atc gtg cac atg tgg gac	691
Arg Gly Trp Val His Ala Ala Arg Arg Val Ile Val His Met Trp Asp	
185 190 195	
atg gtc gtg cac aaa cgc aat atg cag atg gtc aac ggt gca gca ctc	739
Met Val Val His Lys Arg Asn Met Gln Met Val Asn Gly Ala Ala Leu	
200 205 210	
acc gct cga ctg gct acc tct gca gac aag ctg ggc gtt gat ctc ctg	787
Thr Ala Arg Leu Ala Thr Ser Ala Asp Lys Leu Gly Val Asp Leu Leu	
215 220 225	
gtc aat cac tcc gca gtg tcg ttg aat tac aaa aac gac cgc gtt acc	835
Val Asn His Ser Ala Val Ser Leu Asn Tyr Lys Asn Asp Arg Val Thr	
230 235 240 245	
ggc gtg aaa gta caa acc cca cag ggc ttg gta gat ttc gaa gcc act	883
Gly Val Lys Val Gln Thr Pro Gln Gly Leu Val Asp Phe Glu Ala Thr	
250 255 260	
gcc ggc gtc gtg ctc gcc act ggt gga ttc ccc aac aac gtt gac ctg	931
Ala Gly Val Val Leu Ala Thr Gly Gly Phe Pro Asn Asn Val Asp Leu	
265 270 275	
cgc aag gaa ctc ttc cca cgc acc cca tca ggt caa gaa cac tgg acc	979
Arg Lys Glu Leu Phe Pro Arg Thr Pro Ser Gly Gln Glu His Trp Thr	
280 285 290	
ctc gcg cca gca gaa acc acc ggc gac gga cta tcc atg gct cgg gaa	1027
Leu Ala Pro Ala Glu Thr Thr Gly Asp Gly Leu Ser Met Ala Arg Glu	
295 300 305	
atc ggt gca ggt ttt gtc aac gac ctg aaa tcc cca gca gca tgg tgc	1075
Ile Gly Ala Gly Phe Val Asn Asp Leu Lys Ser Pro Ala Ala Trp Cys	
310 315 320 325	
cct gtt tca ttg gtc cca tac ttc aac gga aaa gtc ggc acc ttc ccc	1123
Pro Val Ser Leu Val Pro Tyr Phe Asn Gly Lys Val Gly Thr Phe Pro	
330 335 340	
cac atc atg gac cgc gca aaa cca ggc tcc atc ggt gtt gtc tcc acä	1171
His Ile Met Asp Arg Ala Lys Pro Gly Ser Ile Gly Val Val Ser Thr	

345 350 355
 ggt aag cga ttc gtc aat gaa gcc aac ggc tac tac gac tac 1213
 Gly Lys Arg Phe Val Asn Glu Ala Asn Gly Tyr Tyr Asp Tyr
 360 365 370

 <210> 250
 <211> 371
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 250
 Met Lys His Gln Tyr Asp Val Ile Val Val Gly Ser Gly Ala Gly Gly
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 Leu Ser Ala Ala Val Ser Ala Ala Tyr Gly Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Ala Ser Val Leu Gly Gly Ala Thr Thr Trp Ser Gly Gly
 35 40 45
 Trp Ala Trp Thr Pro Gly Thr Ser Leu Ala Arg Lys Asp Gly Val Val
 50 55 60
 Glu Ser Lys Glu Glu Phe Gln Thr Tyr Leu Gln Ala Val Val Gly Glu
 65 70 75 80
 Tyr Tyr Gln Glu Asp Asn Ile Ser Ala Phe Leu Asp Ala Ala Pro Glu
 85 90 95
 Met Val Asp Phe Phe Glu Lys Asn Thr Asp Leu Gln Trp Thr Pro Gly
 100 105 110
 Ala Lys Ile Asn Asp Ile Tyr Gly Asn Leu Pro Gly Ala Gly Thr Gly
 115 120 125
 His Arg Ser Val Gly Pro Lys Pro Phe Asn Gly Arg Lys Val Pro Lys
 130 135 140
 Ser Val Leu Pro Lys Leu Arg His Gln Leu Tyr Glu Thr Ser Phe Leu
 145 150 155 160
 Gly Met Gly Ile Met Ala Gly Pro Asp Leu Thr Lys Phe Leu Ser Ala
 165 170 175
 Ser Gln Phe Asp Pro Arg Gly Trp Val His Ala Ala Arg Arg Val Ile.
 180 185 190
 Val His Met Trp Asp Met Val Val His Lys Arg Asn Met Gln Met Val
 195 200 205
 Asn Gly Ala Ala Leu Thr Ala Arg Leu Ala Thr Ser Ala Asp Lys Leu
 210 215 220
 Gly Val Asp Leu Leu Val Asn His Ser Ala Val Ser Leu Asn Tyr Lys
 225 230 235 240
 Asn Asp Arg Val Thr Gly Val Lys Val Gln Thr Pro Gln Gly Leu Val
 245 250 255

Asp Phe Glu Ala Thr Ala Gly Val Val Leu Ala Thr Gly Gly Phe Pro
 260 265 270

Asn Asn Val Asp Leu Arg Lys Glu Leu Phe Pro Arg Thr Pro Ser Gly
 275 280 285

Gln Glu His Trp Thr Leu Ala Pro Ala Glu Thr Thr Gly Asp Gly Leu
 290 295 300

Ser Met Ala Arg Glu Ile Gly Ala Gly Phe Val Asn Asp Leu Lys Ser
 305 310 315 320

Pro Ala Ala Trp Cys Pro Val Ser Leu Val Pro Tyr Phe Asn Gly Lys
 325 330 335

Val Gly Thr Phe Pro His Ile Met Asp Arg Ala Lys Pro Gly Ser Ile
 340 345 350

Gly Val Val Ser Thr Gly Lys Arg Phe Val Asn Glu Ala Asn Gly Tyr
 355 360 365

Tyr Asp Tyr
 370

<210> 251

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXN01555

<400> 251

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cgcggtagtc aatcatgggg gagtatccca ccgtatccgc gtg aac aag ggc gtg 115
 Val Asn Lys Gly Val
 1 5

gtg ctg gta gca ggt gga ttc tcc cag aat cca gaa ctg cgc atg aag 163
 Val Leu Val Ala Gly Gly Phe Ser Gln Asn Pro Glu Leu Arg Met Lys
 10 15 20

tac atg cca gaa ccc acc cca cag ttc tcc cgc acc aac gaa agc gcc 211
 Tyr Met Pro Glu Pro Thr Pro Gln Phe Ser Arg Thr Asn Glu Ser Ala
 25 30 35

acc ggc gac acc atg gcc ctt gct gcg aaa gtg gga gca cgc cta ggc 259
 Thr Gly Asp Thr Met Ala Leu Ala Ala Lys Val Gly Ala Arg Leu Gly
 40 45 50

gac gac aac ggt gaa aac gca ctg tgg ttc cca tcg tcc atc ggc acc 307
 Asp Asp Asn Gly Glu Asn Ala Leu Trp Phe Pro Ser Ser Ile Gly Thr
 55 60 65

cgc gcc gac gga tcc acc gcg gtg tac cca cac att tgg gac cgt ggc 355
 Arg Ala Asp Gly Ser Thr Ala Val Tyr Pro His Ile Trp Asp Arg Gly
 70 75 80 85

cgc ctc gga gtc atc gca gtc aac gca gca ggc gag cgt ttc gtc gat	403
Arg Leu Gly Val Ile Ala Val Asn Ala Ala Gly Glu Arg Phe Val Asp	
90 95 100	
gaa tcc gtc tcc tac cac cgc ttc gtg cgc gcc atg tac gaa tcc aac	451
Glu Ser Val Ser Tyr His Arg Phe Val Arg Ala Met Tyr Glu Ser Asn	
105 110 115	
aaa acc acc ccg act gtt tca gcc tgg ctc att gtt gat tcc cac acc	499
Lys Thr Thr Pro Thr Val Ser Ala Trp Leu Ile Val Asp Ser His Thr	
120 125 130	
ctg gca aaa tac ggc ctc ggc atg atc acc atg cca cac ctg cct aaa	547
Leu Ala Lys Tyr Gly Leu Gly Met Ile Thr Met Pro His Leu Pro Lys	
135 140 145	
ctc gct ctg caa aaa tac atc gac tcc gga tac ctg cac gca gga tca	595
Leu Ala Leu Gln Lys Tyr Ile Asp Ser Gly Tyr Leu His Ala Gly Ser	
150 155 160 165	
tcc ttg gat gaa ttg gca cgc agc att ggt gtg gac gct cgc ggc ctg	643
Ser Leu Asp Glu Leu Ala Arg Ser Ile Gly Val Asp Ala Arg Gly Leu	
170 175 180	
gaa caa acc gtc aaa cgc tac aat acc ttc gct aaa acg ggt atc gac	691
Glu Gln Thr Val Lys Arg Tyr Asn Thr Phe Ala Lys Thr Gly Ile Asp	
185 190 195	
gaa gac ttc cac aag ggc gaa ctc ctc ttc ggt caa gcc gcc ggc gat	739
Glu Asp Phe His Lys Gly Glu Leu Leu Phe Gly Gln Ala Ala Gly Asp	
200 205 210	
cca gac aac aag cca aac ccc aac gtc gga cca atc aag aag gga ccg	787
Pro Asp Asn Lys Pro Asn Pro Asn Val Gly Pro Ile Lys Lys Gly Pro	
215 220 225	
ttc tac gca atc gct gta gtc cca acc cct ctg gcc act gcc ttt ggc	835
Phe Tyr Ala Ile Ala Val Val Pro Thr Pro Leu Ala Thr Ala Phe Gly	
230 235 240 245	
atc agc atc aac ccc aac gga cag gtt gtt agt gaa gat ggg gag ccc	883
Ile Ser Ile Asn Pro Asn Gly Gln Val Val Ser Glu Asp Gly Glu Pro	
250 255 260	
atc att gga ctg tac tcc gca gga aat gat gcc caa tct gtc atg gct	931
Ile Ile Gly Leu Tyr Ser Ala Gly Asn Asp Ala Gln Ser Val Met Ala	
265 270 275	
tct gaa tat cct ggt gct ggt tca cag gtt ggt tcc gga atg acc ttt	979
Ser Glu Tyr Pro Gly Ala Gly Ser Gln Val Gly Ser Gly Met Thr Phe	
280 285 290	
ggt tgg atc gca gca cag cac gcg gtg ggg aaa gcg gga aaa tcc gga	1027
Gly Trp Ile Ala Ala Gln His Ala Val Gly Lys Ala Gly Lys Ser Gly	
295 300 305	
gga gct aag gca gga tat gcc gcg tct tct aag taattgcttg gtgggttgct	1080
Gly Ala Lys Ala Gly Tyr Ala Ala Ser Ser Lys	
310 315 320	

tac

1083

<210> 252

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Asn Lys Gly Val Val Leu Val Ala Gly Gly Phe Ser Gln Asn Pro
 1 5 10 15

Glu Leu Arg Met Lys Tyr Met Pro Glu Pro Thr Pro Gln Phe Ser Arg
 20 25 30

Thr Asn Glu Ser Ala Thr Gly Asp Thr Met Ala Leu Ala Ala Lys Val
 35 40 45

Gly Ala Arg Leu Gly Asp Asp Asn Gly Glu Asn Ala Leu Trp Phe Pro
 50 55 60

Ser Ser Ile Gly Thr Arg Ala Asp Gly Ser Thr Ala Val Tyr Pro His
 65 70 75 80

Ile Trp Asp Arg Gly Arg Leu Gly Val Ile Ala Val Asn Ala Ala Gly
 85 90 95

Glu Arg Phe Val Asp Glu Ser Val Ser Tyr His Arg Phe Val Arg Ala
 100 105 110

Met Tyr Glu Ser Asn Lys Thr Thr Pro Thr Val Ser Ala Trp Leu Ile
 115 120 125

Val Asp Ser His Thr Leu Ala Lys Tyr Gly Leu Gly Met Ile Thr Met
 130 135 140

Pro His Leu Pro Lys Leu Ala Leu Gln Lys Tyr Ile Asp Ser Gly Tyr
 145 150 155 160

Leu His Ala Gly Ser Ser Leu Asp Glu Leu Ala Arg Ser Ile Gly Val
 165 170 175

Asp Ala Arg Gly Leu Glu Gln Thr Val Lys Arg Tyr Asn Thr Phe Ala
 180 185 190

Lys Thr Gly Ile Asp Glu Asp Phe His Lys Gly Glu Leu Leu Phe Gly
 195 200 205

Gln Ala Ala Gly Asp Pro Asp Asn Lys Pro Asn Pro Asn Val Gly Pro
 210 215 220

Ile Lys Lys Gly Pro Phe Tyr Ala Ile Ala Val Val Pro Thr Pro Leu
 225 230 235 240

Ala Thr Ala Phe Gly Ile Ser Ile Asn Pro Asn Gly Gln Val Val Ser
 245 250 255

Glu Asp Gly Glu Pro Ile Ile Gly Leu Tyr Ser Ala Gly Asn Asp Ala
 260 265 270

Gln Ser Val Met Ala Ser Glu Tyr Pro Gly Ala Gly Ser Gln Val Gly

275	280	285
Ser Gly Met Thr Phe Gly Trp Ile Ala Ala Gln His Ala Val Gly Lys		
290	295	300
Ala Gly Lys Ser Gly Gly Ala Lys Ala Gly Tyr Ala Ala Ser Ser Lys		
305	310	315
		320

<210> 253
 <211> 1428
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1405)
 <223> RXN01166

<400> 253
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 atgcgcgtaa tccaaacccg cgcacactaa tgtggccgat atg ggc tac acc aac 115
 Met Gly Tyr Thr Asn
 1 5
 ctc aac gac aca cgg gtc ttg cgc gcc ggg tca tgt gat gcc tgg tgg 163
 Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser Cys Asp Ala Trp Trp
 10 15 20
 cgc acg atg tct ccg cta gtg cag cag gga agt gag gca gtc ttt cgg 211
 Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser Glu Ala Val Phe Arg
 25 30 35
 cgc atc atg ggt ctc tcg cgg cgt cct gat cgg aaa cct ggc ttt gac 259
 Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg Lys Pro Gly Phe Asp
 40 45 50
 gat gtc cca cat ttc ggc gca gct gtt cga gtt ccc ggt cta aaa cac 307
 Asp Val Pro His Phe Gly Ala Ala Val Arg Val Pro Gly Leu Lys His
 55 60 65
 ggc acg ttg gtc aat gct gca ccc ttg aaa gtt ttg ggc gca cgg ggc 355
 Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val Leu Gly Ala Arg Gly
 70 75 80 85
 gag ccc aac ccc gcg agt tcg tac cgt ttt gaa tac atc acc ggt gat 403
 Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu Tyr Ile Thr Gly Asp
 90 95 100
 tcc gca ggt cga gcc atc act gcg acc ggc gct gtc ctc ttt tcc aca 451
 Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala Val Leu Phe Ser Thr
 105 110 115
 cgc ccc tgg aca acc ggc ccg cgt ccc gcg atc gcc atg gct cca tcc 499
 Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile Ala Met Ala Pro Ser
 120 125 130

acc caa ggc gtc gca cag cac tgc gat ccc tcc cac acc tgc gcc atc	547
Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser His Thr Cys Ala Ile	
135 140 145	
gga ctc aac gca ttc tat gac aaa ccc ttc gac gca atc att gct tac	595
Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp Ala Ile Ile Ala Tyr	
150 155 160 165	
gaa ctc ccc gtc atc ctc tgg ttt cta gct cac gga ctt gac gtt gtg	643
Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His Gly Leu Asp Val Val	
170 175 180	
ttc atc gat tac ccc cgc gac ccc gca acc ggc gtc caa tac tat tgc	691
Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly Val Gln Tyr Tyr Cys	
185 190 195	
gat tcc atc gct gca gct aaa tcg ctt ctc gac gcc gtc ctc gcc tcc	739
Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp Ala Val Leu Ala Ser	
200 205 210	
aga caa ctc ggc ctt tca ccg gaa gca ccg ctt ggc ctg tgg gga ttc	787
Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu Gly Leu Trp Gly Phe	
215 220 225	
tcc caa gga ggc ggc gcc act ggc tgg gct gca caa ttg cag gat tac	835
Ser Gln Gly Gly Gly Ala Thr Gly Trp Ala Ala Gln Leu Gln Asp Tyr	
230 235 240 245	
gca cct gat gtc cgc cca aag gca gcg gtc gtg ggc gct cca cca gtg	883
Ala Pro Asp Val Arg Pro Lys Ala Ala Val Val Gly Ala Pro Pro Val	
250 255 260	
gat ctc ttc cgc gtc ttg gac act gtc gac ggc gga ttg ctc acc gga	931
Asp Leu Phe Arg Val Leu Asp Thr Val Asp Gly Gly Leu Leu Thr Gly	
265 270 275	
gtg att gcc tac gcc atc gcg gga ctt gca gtg aac tct tca gag atg	979
Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser Ser Glu Met	
280 285 290	
ttt gag gaa atc atg tcg gtg tta aat gaa cgc gga gtc agt gat gtg	1027
Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val Ser Asp Val	
295 300 305	
ctg aaa aat atc acc agc tgc gcg gga ggt tcc ttg ttg gcc agt ggc	1075
Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu Ala Ser Gly	
310 315 320 325	
tac tcg tct tcc cgc ggg tgg aca cat cag ggc acg ccg ctg gca gac	1123
Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro Leu Ala Asp	
330 335 340	
att ctg gac gat ctg cca ctt gtt gtc gct gag ttt ggg aag caa aag	1171
Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly Lys Gln Lys	
345 350 355	
ctg ggt cgt gtg gcg cca gaa atc cca gtg ctg ttg tgg ggc tct aaa	1219
Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp Gly Ser Lys	
360 365 370	
aat gat gat gtc att ccc att gat ccc att agg gaa ttg cgt gat agc	1267

Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu Arg Asp Ser
 375 380 385
 tgg gcg gac aag ggt acg cca ttg acc tgg cat gaa tcc caa gcg ccg 1315
 Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser Gln Ala Pro
 390 395 400 405
 cgt gtg cca gga cgc aca ggt ctc aac cat ttc ggg ccc tat ttt aga 1363
 Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro Tyr Phe Arg
 410 415 420
 aac ctg gaa aag tac tcg gga tgg ctc ata gat cat ctt gtc 1405
 Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu Val
 425 430 435
 tgagtgccgt tttaaaggct cgg 1428

<210> 254
 <211> 435
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 254
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 Cys Asp Ala Trp Trp Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser
 20 25 30
 Glu Ala Val Phe Arg Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg
 35 40 45
 Lys Pro Gly Phe Asp Asp Val Pro His Phe Gly Ala Ala Val Arg Val
 50 55 60
 Pro Gly Leu Lys His Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val
 65 70 75 80
 Leu Gly Ala Arg Gly Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu
 85 90 95
 Tyr Ile Thr Gly Asp Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala
 100 105 110
 Val Leu Phe Ser Thr Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile
 115 120 125
 Ala Met Ala Pro Ser Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser
 130 135 140
 His Thr Cys Ala Ile Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp
 145 150 155 160
 Ala Ile Ile Ala Tyr Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His
 165 170 175
 Gly Leu Asp Val Val Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly
 180 185 190
 Val Gln Tyr Tyr Cys Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp

195	200	205
Ala Val Leu Ala Ser Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu 210 215 220		
Gly Leu Trp Gly Phe Ser Gln Gly Gly Gly Ala Thr Gly Trp Ala Ala 225 230 235 240		
Gln Leu Gln Asp Tyr Ala Pro Asp Val Arg Pro Lys Ala Ala Val Val 245 250 255		
Gly Ala Pro Pro Val Asp Leu Phe Arg Val Leu Asp Thr Val Asp Gly 260 265 270		
Gly Leu Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val 275 280 285		
Asn Ser Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg 290 295 300		
Gly Val Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser 305 310 315 320		
Leu Leu Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly 325 330 335		
Thr Pro Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu 340 345 350		
Phe Gly Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu 355 360 365		
Leu Trp Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg 370 375 380		
Glu Leu Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His 385 390 395 400		
Glu Ser Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe 405 410 415		
Gly Pro Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp 420 425 430		
His Leu Val 435		

<210> 255
 <211> 1281
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1258)
 <223> RXN02001

 <400> 255
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gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
Met Pro Val Ile Asn
1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
10 15 20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
25 30 35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
40 45 50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
55 60 65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
70 75 80 85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
90 95 100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
105 110 115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
120 125 130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
135 140 145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
150 155 160 165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
170 175 180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
185 190 195

ggt gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly
200 205 210

att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc 787
Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val
215 220 225

gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat 835

Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp
 230 235 240 245
 aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc 883
 Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe
 250 255 260
 aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc 931
 Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val
 265 270 275
 gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac 979
 Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn
 280 285 290
 cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027
 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala
 295 300 305
 gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075
 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser
 310 315 320 325
 cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123
 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro
 330 335 340
 ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171
 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn
 345 350 355
 ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc 1219
 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe
 360 365 370
 ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgateccatgg 1268
 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly
 375 380 385
 cgctcgaaga tgc 1281

 <210> 256
 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 256
 Met Pro Val Ile Asn Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg
 1 5 10 15
 Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
 20 25 30
 Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
 35 40 45
 Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
 50 55 60
 Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala

65	70	75	80
Leu Pro Leu Thr	Glu Ile Thr Gly Val	Asp Tyr Ala Ser Thr Thr Pro	
	85	90	95
Gly Lys Met His	Ala Cys Gly His	Asp Gly His Thr Thr Met Leu Leu	
	100	105	110
Gly Ala Ala Lys	Tyr Leu Ala Glu Thr Arg Asn Phe	Ala Gly Thr Val	
	115	120	125
Ala Leu Ile Phe	Gln Pro Ala Glu Glu Asn Gly Gly	Gly Ala Gly Val	
	130	135	140
Met Val Asp Glu	Gly Val Leu Asp Arg Phe	Ala Ile Ala Glu Val Tyr	
	145	150	155
Ala Leu His Asn	Gln Pro Gly Leu Pro Leu Gly His Phe	Met Thr Thr	
	165	170	175
Ala Gly Pro Ile	Met Ala Ala Val Asp Thr Phe Asp	Ile Asn Ile Thr	
	180	185	190
Gly Arg Gly Gly	His Gly Ala Lys Pro His Gln Thr Arg	Asp Pro Ile	
	195	200	205
Val Ala Ala Val	Gly Ile Val Gln Ala Phe Gln Thr	Ile Val Ser Arg	
	210	215	220
Asn His Asn Pro	Val Glu Asp Leu Val Val Ser Val Thr	Gln Ile His	
	225	230	235
Thr Gly Ser Ala	Asp Asn Ile Ile Pro Glu Thr Ala Tyr	Ile Asn Gly	
	245	250	255
Thr Val Arg Thr	Phe Asn Lys Asp Val Gln Ala Met Val	Ile Thr Arg	
	260	265	270
Met Glu Glu Ile	Val Ala Gly Gln Ala Ala Ala Tyr Gly	Val Glu Ala	
	275	280	285
Thr Leu Thr Tyr	Asn Arg Asn Tyr Pro Ala Thr Ile	Asn Asp Ala Ala	
	290	295	300
Lys Ala Ala Ile	Ala Ala Glu Val Ala Gly Glu Val Gly	Leu Gly Val	
	305	310	315
Asn Pro Asn Gly	Ser Arg Gly Met Gly Ala Glu Asp Phe	Ser Tyr Phe	
	325	330	335
Leu Glu Lys Arg	Pro Gly Ala Tyr Leu Phe Val Gly	Asn Gly Asp Ser	
	340	345	350
Ala Gly Leu His	Asn Pro Ala Tyr Asn Phe Asn Asp	Glu Ala Ala Pro	
	355	360	365
Tyr Gly Ala Ser	Phe Leu Ala Arg Met Ala Glu Arg	Pro Leu Pro Leu	
	370	375	380
Lys Gly			
385			

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<210> 257
<211> 570
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(547)  
<223> RXN03145
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<210> 258
<211> 149
<212> PRT
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<213> Corynebacterium glutamicum

<400> 258

Met Pro Thr Tyr Thr Cys Trp Ser Gln Arg Ile Arg Ile Ser Arg Glu
 1 5 10 15
 Ala Lys Gln Arg Ile Ala Glu Ala Ile Thr Asp Ala His His Glu Leu
 20 25 30
 Ala His Ala Pro Lys Tyr Leu Val Gln Val Ile Phe Asn Glu Val Glu
 35 40 45
 Pro Asp Ser Tyr Phe Ile Ala Ala Gln Ser Ala Ser Glu Asn His Ile
 50 55 60
 Trp Val Gln Ala Thr Ile Arg Ser Gly Arg Thr Glu Lys Gln Lys Glu
 65 70 75 80
 Glu Leu Leu Leu Arg Leu Thr Gln Glu Ile Ala Leu Ile Leu Gly Ile
 85 90 95
 Pro Asn Glu Glu Val Trp Val Tyr Ile Pro Glu Ile Pro Gly Ser Asn
 100 105 110
 Met Thr Glu Tyr Gly Arg Leu Leu Met Glu Pro Gly Glu Glu Glu Lys
 115 120 125
 Trp Phe Asn Ser Leu Pro Glu Gly Leu Arg Glu Arg Leu Thr Glu Leu
 130 135 140
 Glu Gly Ser Ser Glu
 145

<210> 259

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXN01466

<400> 259

aatccatgat cccaaactac ctcaaagcgc ttgtaggcta agacttatgg atacacaacg 60
 cggtcattg cggggaaaag ctcataaagc aaggctaaag atg acg cca aat ggt 115
 Met Thr Pro Asn Gly
 1 5
 cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt 163
 Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg
 10 15 20
 acc ccg ggt cta aaa cac gtc gac cgc cac acc atc gtg gac tcc gac 211
 Thr Pro Gly Leu Lys His Val Asp Arg His Thr Ile Val Asp Ser Asp
 25 30 35
 ggc ctc agc atc cac acg tac atg gtt ggc cat gcc gaa aat gcc acg 259
 Gly Leu Ser Ile His Thr Tyr Met Val Gly His Ala Glu Asn Ala Thr

40	45	50	
gca acg gtc gtg ttc atc cac ggc ttc acc ctc gcc gcc gaa gtg tat			307
Ala Thr Val Val Phe Ile His Gly Phe Thr Leu Ala Ala Glu Val Tyr			
55	60	65	
tac atg cag gtc gac tac cta caa acc ttt tac cca aat att aaa agc			355
Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr Pro Asn Ile Lys Ser			
70	75	80	85
gtg ctt atc gac gcc cgc ggc cac ggc gcc acc ggc cag atc cgc cca			403
Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr Gly Gln Ile Arg Pro			
90	95	100	
gag ctc tgc acc atc gaa gga aca gcg aac gat gtt ctc gca gcc atc			451
Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp Val Leu Ala Ala Ile			
105	110	115	
cac gaa cac gca ccg acc ggc ccg ctc att ttg gtt ggg cat tcc ctc			499
His Glu His Ala Pro Thr Gly Pro Leu Ile Leu Val Gly His Ser Leu			
120	125	130	
ggc gga ctc acg gca ctt aac ctg gtt aaa cgg gca gat cac tca ctt			547
Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg Ala Asp His Ser Leu			
135	140	145	
cgg aag agg atc gtc ggc atg gtt cta gtc gcc aca tcg atc gaa tca			595
Arg Lys Arg Ile Val Gly Met Val Leu Val Ala Thr Ser Ile Glu Ser			
150	155	160	165
tta tcc acc caa ggt cta cca caa gtc ctg gca tca ccc ctt gcc gac			643
Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala Ser Pro Leu Ala Asp			
170	175	180	
aac atc aaa aac gcc gtc gaa gca gcc ccc aac gat gcc caa aaa ttc			691
Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn Asp Ala Gln Lys Phe			
185	190	195	
cgc caa tac gcc acc aca ttt cta gcc ccc acc ctg gcc acc gca gtc			739
Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr Leu Ala Thr Ala Val			
200	205	210	
ttc caa cga gac aca aac gat gaa gtc atc gat ttc cac gcc gcc atg			787
Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp Phe His Ala Ala Met			
215	220	225	
atc cac gaa acc ccc ttg gat acc ttc gtc ggt ttc ttc gac gac ctc			835
Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly Phe Phe Asp Asp Leu			
230	235	240	245
caa gaa cac gac gaa ctc gat gcc gca cca gca ttg gaa ggc ctc aaa			883
Gln Glu His Asp Glu Leu Asp Ala Ala Pro Ala Leu Glu Gly Leu Lys			
250	255	260	
ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca att agc caa			931
Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro Ile Ser Gln			
265	270	275	
gcc gac cgc atc tgc gaa gtc tgg ccc ggc gca cgc ctt caa atc gca			979
Ala Asp Arg Ile Cys Glu Val Trp Pro Gly Ala Arg Leu Gln Ile Ala			
280	285	290	

gaa gga gca ggt cat atg ctt ccg ctt gaa gcg cca gga atc ctc aat 1027
 Glu Gly Ala Gly His Met Leu Pro Leu Glu Ala Pro Gly Ile Leu Asn
 295 300 305

aat gcg atc ggc aac att ttg gac ggg ctg ggc tgaggaacct gggtcgggcg 1080
 Asn Ala Ile Gly Asn Ile Leu Asp Gly Leu Gly
 310 315 320

tgg 1083

<210> 260

<211> 320

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 260

Met Thr Pro Asn Gly Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala
 1 5 10 15

Phe Ser Lys Asn Arg Thr Pro Gly Leu Lys His Val Asp Arg His Thr
 20 25 30

Ile Val Asp Ser Asp Gly Leu Ser Ile His Thr Tyr Met Val Gly His
 35 40 45

Ala Glu Asn Ala Thr Ala Thr Val Val Phe Ile His Gly Phe Thr Leu
 50 55 60

Ala Ala Glu Val Tyr Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr
 65 70 75 80

Pro Asn Ile Lys Ser Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr
 85 90 95

Gly Gln Ile Arg Pro Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp
 100 105 110

Val Leu Ala Ala Ile His Glu His Ala Pro Thr Gly Pro Leu Ile Leu
 115 120 125

Val Gly His Ser Leu Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg
 130 135 140

Ala Asp His Ser Leu Arg Lys Arg Ile Val Gly Met Val Leu Val Ala
 145 150 155 160

Thr Ser Ile Glu Ser Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala
 165 170 175

Ser Pro Leu Ala Asp Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn
 180 185 190

Asp Ala Gln Lys Phe Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr
 195 200 205

Leu Ala Thr Ala Val Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp
 210 215 220

Phe His Ala Ala Met Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly

225	230	235	240
Phe Phe Asp Asp	Leu Gln Glu His Asp	Glu Leu Asp Ala Ala	Pro Ala
	245	250	255
Leu Glu Gly Leu	Lys Gly Tyr Val	Leu Ala Gly Glu Leu	Asp Asp Val
	260	265	270
Thr Pro Ile Ser	Gln Ala Asp Arg	Ile Cys Glu Val	Trp Pro Gly Ala
	275	280	285
Arg Leu Gln Ile	Ala Glu Gly Ala	Gly His Met	Leu Pro Leu Glu Ala
	290	295	300
Pro Gly Ile Leu	Asn Asn Ala Ile	Gly Asn Ile	Leu Asp Gly Leu Gly
305	310	315	320

<210> 261

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXN01145

<400> 261

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cttttcacca aaattttttac gaaaggcgag attttctccc	atg gct att gaa ctg	115
	Met Ala Ile Glu Leu	
	1 5	

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt	163
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val	
10 15 20	

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc	211
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu	
25 30 35	

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag	259
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys	
40 45 50	

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	451
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	499
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	547
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	595
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	643
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	691
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	739
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	787
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	835
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	883
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	931
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	979
280 285 290	
gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser	1027
295 300 305	
tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu	1075
310 315 320 325	
atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala	1124
330 335	

ccctttgacg gct

1137

<210> 262

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
 145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
 165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
 180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205

Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220

Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240

Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270

Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe

275

280

285

Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300

Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320

Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335

Thr Ala

<210> 263

<211> 487

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(487)

<223> RXN03088

<400> 263

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ccggcggcga tgaactctc gaattggagg caaagaacta atg ggt caa acc cgc 115
 Met Gly Gln Thr Arg
 1 5

atc att tcc ggc gac gca cgc ggc cgc aag atc gaa gta cca cca gca 163
 Ile Ile Ser Gly Asp Ala Arg Gly Arg Lys Ile Glu Val Pro Pro Ala
 10 15 20

ggt acc cgc ccc acc tct gac cgc gca cgc gaa ggt ctc ttc tcc tca 211
 Gly Thr Arg Pro Thr Ser Asp Arg Ala Arg Glu Gly Leu Phe Ser Ser
 25 30 35

ctg cag gtc cgt ttc gga ttt gag ggc cag cgc gtc ctc gac att ttt 259
 Leu Gln Val Arg Phe Gly Phe Glu Gly Gln Arg Val Leu Asp Ile Phe
 40 45 50

gcc ggc tcc ggc gca ctc gga ttg gaa gct gcc tcc agg ggt gcc gat 307
 Ala Gly Ser Gly Ala Leu Gly Leu Glu Ala Ala Ser Arg Gly Ala Asp
 55 60 65

gag gta gtt ctg gtc gag tcg aat cct aag gcc gta gag gta att cga 355
 Glu Val Val Leu Val Glu Ser Asn Pro Lys Ala Val Glu Val Ile Arg
 70 75 80 85

cgg aat gtg gac gtc gta aag cat cct cgc gta acc gtc gca gag atg 403
 Arg Asn Val Asp Val Val Lys His Pro Arg Val Thr Val Ala Glu Met
 90 95 100

aaa gca tcc acc tac ctt gcg tcc gca ccc gat aag ttt ttc acg atg 451
 Lys Ala Ser Thr Tyr Leu Ala Ser Ala Pro Asp Lys Phe Phe Thr Met
 105 110 115

gtg ctc gcc gac ccg ccc tat gag ctt gcg acg acg 487

Val Leu Ala Asp Pro Pro Tyr Glu Leu Ala Thr Thr
120 125

<210> 264

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Gly Gln Thr Arg Ile Ile Ser Gly Asp Ala Arg Gly Arg Lys Ile
1 5 10 15

Glu Val Pro Pro Ala Gly Thr Arg Pro Thr Ser Asp Arg Ala Arg Glu
20 25 30

Gly Leu Phe Ser Ser Leu Gln Val Arg Phe Gly Phe Glu Gly Gln Arg
35 40 45

Val Leu Asp Ile Phe Ala Gly Ser Gly Ala Leu Gly Leu Glu Ala Ala
50 55 60

Ser Arg Gly Ala Asp Glu Val Val Leu Val Glu Ser Asn Pro Lys Ala
65 70 75 80

Val Glu Val Ile Arg Arg Asn Val Asp Val Val Lys His Pro Arg Val
85 90 95

Thr Val Ala Glu Met Lys Ala Ser Thr Tyr Leu Ala Ser Ala Pro Asp
100 105 110

Lys Phe Phe Thr Met Val Leu Ala Asp Pro Pro Tyr Glu Leu Ala Thr
115 120 125

Thr

<210> 265

<211> 639

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(616)

<223> RXN02952

<400> 265

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cctgatcttt gatctcgcta cctcattcac aagcgccggc atg agc tcc cca gca 115
Met Ser Ser Pro Ala
1 5

ctt gac gct gca aaa cag cgc ctt gct gaa tcc gat ggc ctg atc gct 163
Leu Asp Ala Ala Lys Gln Arg Leu Ala Glu Ser Asp Gly Leu Ile Ala
10 15 20

gtt acc cca gta ttt acc gcg agc tac tcc ggc atc ttc aag atg ttc 211
Val Thr Pro Val Phe Thr Ala Ser Tyr Ser Gly Ile Phe Lys Met Phe

	25	30	35	
ttt gat gtc ctg gac ccc aag acc att gtg ggt ctg ccc acc atc att				259
Phe Asp Val Leu Asp Pro Lys Thr Ile Val Gly Leu Pro Thr Ile Ile				
	40	45	50	
gcg gca tct gct gga acg gca cgc cac tca ttg gtt ctc gac cac gcc				307
Ala Ala Ser Ala Gly Thr Ala Arg His Ser Leu Val Leu Asp His Ala				
	55	60	65	
atc cga cca ctg ttt acc tac ttg cga gca gtt gtc gta ccc acc ggc				355
Ile Arg Pro Leu Phe Thr Tyr Leu Arg Ala Val Val Val Pro Thr Gly				
	70	75	80	85
gtg ttc gca gcc acg gaa gat ttc ggc act gaa gct ggc gca gac att				403
Val Phe Ala Ala Thr Glu Asp Phe Gly Thr Glu Ala Gly Ala Asp Ile				
	90	95	100	
gaa cgt cgc gtg aac cgc gca gct ggc gaa tta gcg aca ctc atg ttg				451
Glu Arg Arg Val Asn Arg Ala Ala Gly Glu Leu Ala Thr Leu Met Leu				
	105	110	115	
cag gat tac tcc agt gtg caa ggc ctt ggg ggc gca acc gcg aac caa				499
Gln Asp Tyr Ser Ser Val Gln Gly Leu Gly Gly Ala Thr Ala Asn Gln				
	120	125	130	
gac gct gac ctt tcc ttc cgt cgc acc act ggc gtg acc ccg gga gag				547
Asp Ala Asp Leu Ser Phe Arg Arg Thr Thr Gly Val Thr Pro Gly Glu				
	135	140	145	
aac ttc agc agc ttt gcc gat ctt tct caa agg aca cga cgg aaa cgg				595
Asn Phe Ser Ser Phe Ala Asp Leu Ser Gln Arg Thr Arg Arg Lys Arg				
	150	155	160	165
cta aat tcg cgg atc tcc gtt taaggcattg aagcatttgg agg				639
Leu Asn Ser Arg Ile Ser Val				
	170			

<210> 266

<211> 172

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Met Ser Ser Pro Ala Leu Asp Ala Ala Lys Gln Arg Leu Ala Glu Ser				
1	5	10	15	
Asp Gly Leu Ile Ala Val Thr Pro Val Phe Thr Ala Ser Tyr Ser Gly				
	20	25	30	
Ile Phe Lys Met Phe Phe Asp Val Leu Asp Pro Lys Thr Ile Val Gly				
	35	40	45	
Leu Pro Thr Ile Ile Ala Ala Ser Ala Gly Thr Ala Arg His Ser Leu				
	50	55	60	
Val Leu Asp His Ala Ile Arg Pro Leu Phe Thr Tyr Leu Arg Ala Val				
	65	70	75	80
Val Val Pro Thr Gly Val Phe Ala Ala Thr Glu Asp Phe Gly Thr Glu				

	85	90	95
Ala Gly Ala Asp Ile Glu Arg Arg Val Asn Arg Ala Ala Gly Glu Leu	100	105	110
Ala Thr Leu Met Leu Gln Asp Tyr Ser Ser Val Gln Gly Leu Gly Gly	115	120	125
Ala Thr Ala Asn Gln Asp Ala Asp Leu Ser Phe Arg Arg Thr Thr Gly	130	135	140
Val Thr Pro Gly Glu Asn Phe Ser Ser Phe Ala Asp Leu Ser Gln Arg	145	150	155
Thr Arg Arg Lys Arg Leu Asn Ser Arg Ile Ser Val	165	170	
<210> 267			
<211> 1044			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1021)			
<223> RXN00513			
<400> 267			
cacagcggtac gcacgagctt gaggatcttt cagaactcaa cattgaattg gatgccgata 60			
ttttggccaa ggctcctgtg attccggaag gactgttctg atg gcg ggt ttg ttt			115
		Met Ala Gly Leu Phe	
		1 5	
tcc tct gct gtt gca cca acg gag cgt cga aaa gca tta cgc gcg gca			163
Ser Ser Ala Val Ala Pro Thr Glu Arg Arg Lys Ala Leu Arg Ala Ala	10	15	20
ctg gct gcg cct gaa att gcc cgc atg cct ggt gca ttc tcc ccg ctg			211
Leu Ala Ala Pro Glu Ile Ala Arg Met Pro Gly Ala Phe Ser Pro Leu	25	30	35
gcg gcg cgc gca atc cag gaa gcc gga ttt gaa ggc gtg tac gtc tcg			259
Ala Ala Arg Ala Ile Gln Glu Ala Gly Phe Glu Gly Val Tyr Val Ser	40	45	50
ggc gcc gtc gtg gcg gct gac ctt gca ttg ccg gat atc ggc ttg acc			307
Gly Ala Val Val Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr	55	60	65
aca ttg acc gaa gtg gcg cac cgc tcc cgg cag atc gca cgc gtg aca			355
Thr Leu Thr Glu Val Ala His Arg Ser Arg Gln Ile Ala Arg Val Thr	70	75	80
gac ttg ccc gtg ctg gtc gac gcc gac acc ggc ttc ggc gaa ccc atg			403
Asp Leu Pro Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met	90	95	100
tcc gca gcg cgc acc gtc tcc gaa ctc gaa gat gca ggt gtc gcg ggc			451
Ser Ala Ala Arg Thr Val Ser Glu Leu Glu Asp Ala Gly Val Ala Gly			

105	110	115	
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agg ctg tat gag ctg ctg cgc tac aac gag tac aac gct ttc gac cag Arg Leu Tyr Glu Leu Leu Arg Tyr Asn Glu Tyr Asn Ala Phe Asp Gln 280 285 290			979
caa gta ttc acc tat tcc gct gac agc tac aag ccc atc ttc Gln Val Phe Thr Tyr Ser Ala Asp Ser Tyr Lys Pro Ile Phe 295 300 305			1021
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<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30
 Ala Phe Ser Pro Leu Ala Ala Arg Ala Ile Gln Glu Ala Gly Phe Glu
 35 40 45
 Gly Val Tyr Val Ser Gly Ala Val Val Ala Ala Asp Leu Ala Leu Pro
 50 55 60
 Asp Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ser Arg Gln
 65 70 75 80
 Ile Ala Arg Val Thr Asp Leu Pro Val Leu Val Asp Ala Asp Thr Gly
 85 90 95
 Phe Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ser Glu Leu Glu Asp
 100 105 110
 Ala Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg
 115 120 125
 Cys Gly His Leu Asp Gly Lys Glu Val Val Gly Thr Asp Ile Met Val
 130 135 140
 Arg Arg Ile Ala Ala Ala Val Asn Glu Arg Arg Asp Glu Gln Phe Val
 145 150 155 160
 Ile Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ser Ala
 165 170 175
 Ile Glu Arg Ala Lys Ala Tyr Ala Asp Ala Gly Ala Asp Met Ile Phe
 180 185 190
 Thr Glu Ala Leu Tyr Ser Pro Ala Asp Phe Glu Lys Phe Arg Ala Ala
 195 200 205
 Val Asp Ile Pro Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Glu
 210 215 220
 Leu Leu Pro Ala Gln Leu Leu Glu Asp Ile Gly Tyr Asn Ala Val Ile
 225 230 235 240
 Tyr Pro Val Thr Leu Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala
 245 250 255
 Leu Gly Asp Ile Ala Asn Thr Gly Ile Gln Thr Asp Trp Val Asp Arg
 260 265 270
 Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Asn Glu Tyr
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Pro Phe Gln Ala Gly Asp Arg Val Gln Leu Thr Asp Ala Lys Arg Arg
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His Phe Thr Ile Ile Leu Glu Pro Gly Thr Thr Tyr His Thr His Arg
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Glu Arg Pro Ala Thr Trp Asp Pro Arg Leu Gly Asp Leu Lys Glu Val
          150          155          160          165
acc gtt gag gat ctc ggc gga cct gtt gac cgc atc atc ttg gat atg 643
Thr Val Glu Asp Leu Gly Gly Pro Val Asp Arg Ile Ile Leu Asp Met
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gtc atg gaa ggc atc cgc gag caa aaa tgc ttc acg gag cca cgc gcg				787
Val Met Glu Gly Ile Arg Glu Gln Lys Cys Phe Thr Glu Pro Arg Ala				
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tgg gaa tct ttg gtt cgt gat tgg aag gtg gag ggc ttg gca aca cgc				835
Trp Glu Ser Leu Val Arg Asp Trp Lys Val Glu Gly Leu Ala Thr Arg				
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cct gag cac cgc atg aat gcc cac acc gcg ttc ttg gtg ttg acc agg				883
Pro Glu His Arg Met Asn Ala His Thr Ala Phe Leu Val Leu Thr Arg				
	250	255	260	
cgt ttg gct gat ggc gtg gag cct cct cgt ccg cag cgt aag gca cgt				931
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<213> Corynebacterium glutamicum

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Ala Val Ile Tyr Pro Lys Asp Ser Ala Gln Ile Leu Val Glu Gly Asp			
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Ile Phe Pro Gly Ala Arg Val Leu Glu Ala Gly Ala Gly Ser Gly Ala			
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Leu Ser Met Ala Leu Leu Arg Ala Val Gly Glu Lys Gly Asn Val Ile			
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Val Ser Gln Pro Leu																
1 5																
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Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala Ser Ala Phe Ile Val																
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Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys Ala Gln Ala Asn Glu																
25 30 35																
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Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly Ser Met Thr Ala Gln																
40 45 50																
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Gln	Asp	Val	Thr	Ile	Leu	Gly	Gly	Pro	Ser	Arg	Gly	Asn	Ala	Asp	Thr	
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Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly	Ile	Asn	Leu	Val	Ile	
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Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala	Arg	Glu	Glu	Leu	Glu	
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Cys	Ile	Ala	Gly	Val	Gly	Gly	Gly	Thr	Tyr	Ala	Asp	Ala	Ser	Asp	Ala	
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cca	caa	gaa	tcc	cgc	ttt	tgg	aaa	atc	cct	gta	gag	cca	ggt	gaa	acc	931
Pro	Gln	Glu	Ser	Arg	Phe	Trp	Lys	Ile	Pro	Val	Glu	Pro	Gly	Glu	Thr	
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Ile	Ser	Val	Ser	Ala	Asn	Thr	Val	Thr	Asp	Pro	Thr	Val	Leu	Thr	Met	
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Gly	Gln	Gly	Gly	Ile	Lys	Leu	Glu	Ala	Gln	Leu	His	Thr	Glu	Glu	Ala	
		295				300					305					
cca	caa	tac	ggc	ctg	cgt	ggt	cgg	tgc	act	cgg	gtc	tca	ttt	gat	aat	1075
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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Ser Met Thr Ala Gln Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala
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Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
 65 70 75 80

Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
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Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
 100 105 110

Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg
 115 120 125

Gly Phe Thr Pro Ile Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu
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Pro Glu Gly Gly Asn Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys
 145 150 155 160

Thr Pro Pro Asp Val Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly
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Ile Asn Leu Val Ile Asn Thr Ile Gly Leu Asn Val Asp Pro Ala Ala
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 Phe Leu Thr Asp Leu Pro Gln Glu Ser Arg Phe Trp Lys Ile Pro Val
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 His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr Arg
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 Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn Gly
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 Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val Asp
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 Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp Tyr
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Ser	Phe	Leu	Arg	Lys	Gly	Thr	Val	Gly	Ser	Glu	Gly	Gln	Gln	Ile	Phe			
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 Arg Asn Arg Trp Ala Phe Asp Lys Val Val Arg Ser Thr His Gly Val
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 Asn Cys Thr Gly Ser Cys Ser Trp Lys Val Tyr Val Lys Asp Gly Val
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 Ile Thr Trp Glu Ser Gln Ala Val Asp Tyr Pro Thr Thr Gly Ala Asp
 85 90 95
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 100 105 110
 Trp Tyr Thr Tyr Ser Pro Thr Arg Ile Arg Tyr Pro Tyr Ile Gly Gly
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<221> CDS  
<222> (101)..(466)  
<223> FRXA01302
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<210> 276
<211> 122
<212> PRT
<213> Corynebacterium glutamicum
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<400> 276
Met Thr Thr Thr Thr Ser Ser Gly Lys Ser Ser Glu Lys Ile Asn Pro
  1             5             10             15
Leu Phe Lys Leu Gly Ser Phe Leu Arg Lys Gly Thr Val Gly Ser Glu
          20          25          30

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Gly Gln Gln Ile Phe Leu Gln Gly Gly Arg Gln Ala Asp Val Phe Tyr
35 40 45
Arg Asn Arg Trp Ala Phe Asp Lys Val Val Arg Ser Thr His Gly Val
50 55 60
Asn Cys Thr Gly Ser Cys Ser Trp Lys Val Tyr Val Lys Asp Gly Val
65 70 75 80
Ile Thr Trp Glu Ser Gln Ala Val Asp Tyr Pro Thr Thr Gly Ala Asp
85 90 95
Met Pro Asp Asn Glu Pro Arg Gly Cys Pro Arg Gly Ala Ser Phe Ser
100 105 110
Trp Tyr Thr Tyr Ser Pro Thr Gly Ile Arg
115 120

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<210> 277
<211> 2503
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(2503)  
<223> RXN01308
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t t g a t a t g t c c g c g a a g c c a a g g a a c g c c t g g g c g a t c c g g t g c t g g c g t g g c g c	115
	Val Leu Ala Trp Arg 1 5
g a c a t t g t a g a a a c c c c a g a a a a g c g c a a a g c a . t a t g t a t c c c a g c g g	163
A s p I l e V a l G l u T h r P r o G l u L y s A r g L y s A l a T y r V a l S e r G l n A r g	10 15 20
g g c a a a g g t g g c c t c a t c c g c g t t c a g t a t g a g g a a g c c a t g g a g a t t	211
G l y L y s G l y G l y L e u I l e A r g V a l G l n T y r G l u G l u A l a M e t G l u I l e	25 30 35
g c t g c g g c a g c c c a t g t g t a c a c c a t c c g c c a a t a c g g c c c c g a c c g c	259
A l a A l a A l a A l a H i s V a l T y r T h r I l e A r g G l n T y r G l y P r o A s p A r g	40 45 50
a t t c a t g g a t t c a c c g t t a t t c c c g c a a t g t c g c a g g t g t c t t a c g g t	307
I l e H i s G l y P h e T h r V a l I l e P r o A l a M e t S e r C l n V a l S e r T y r G l y	55 60 65
g c t g g t a c t c g c t t c t t g c a g a t g a t c g g c g g a g t g g c g c t g t c c t t c	355
A l a G l y T h r A r g P h e L e u G l n M e t I l e G l y G l y V a l A l a L e u S e r P h e	70 75 80 85
c a c g a t t g g t a c g c c g a c c t c c c a c c a g c a t c a c c a c a a a c t t t c g g c	403
T y r A s p T r p T y r A l a A s p L e u P r o P r o A l a S e r P r o G l n T h r P h e G l y	90 95 100

gat caa act gac gtt ccg gaa tct ggc gac tgg tac aac tcc agc tac	451
Asp Gln Thr Asp Val Pro Glu Ser Gly Asp Trp Tyr Asn Ser Ser Tyr	
105 110 115	
ctc atg atg tgg ggt tcc aac att ccg gtg acc cgc acg cct gac tcc	499
Leu Met Met Trp Gly Ser Asn Ile Pro Val Thr Arg Thr Pro Asp Ser	
120 125 130	
cac ttc atg gtg gaa gcc cgc tac aag ggc acc aag gtt gtt gtg gtt	547
His Phe Met Val Glu Ala Arg Tyr Lys Gly Thr Lys Val Val Val Val	
135 140 145	
tcc ccg gat ttc gct gac tcc acc aaa ttt gct gat gaa tgg gca cgc	595
Ser Pro Asp Phe Ala Asp Ser Thr Lys Phe Ala Asp Glu Trp Ala Arg	
150 155 160 165	
atc cac cct ggt act gac ggc gca ctc gcc ttt gcc atg ggc cat gtg	643
Ile His Pro Gly Thr Asp Gly Ala Leu Ala Phe Ala Met Gly His Val	
170 175 180	
atc ttg aag gaa ttc cat gtt gac aag aag acg ccg tac ttc atg gac	691
Ile Leu Lys Glu Phe His Val Asp Lys Lys Thr Pro Tyr Phe Met Asp	
185 190 195	
tac atg cgc aaa tac acg gac tct cct ttc ctc gtg gaa tta gat gag	739
Tyr Met Arg Lys Tyr Thr Asp Ser Pro Phe Leu Val Glu Leu Asp Glu	
200 205 210	
cac ggc gat ggc acc tac acc cca ggt aaa ttc ctc act gca gac cgc	787
His Gly Asp Gly Thr Tyr Thr Pro Gly Lys Phe Leu Thr Ala Asp Arg	
215 220 225	
gca gct gat atc tcc cca gcg ctt gcc gcc act cca aat gcc acc cac	835
Ala Ala Asp Ile Ser Pro Ala Leu Ala Ala Thr Pro Asn Ala Thr His	
230 235 240 245	
cgt ctc ctt gtg ctg caa aaa gat ggc tca gtt gta gat ccc ggt ggc	883
Arg Leu Leu Val Leu Gln Lys Asp Gly Ser Val Val Asp Pro Gly Gly	
250 255 260	
act gtc gcg gac cgt tgg ggt gaa gaa ggc atg ggt aag tgg aat ctg	931
Thr Val Ala Asp Arg Trp Gly Glu Gly Met Gly Lys Trp Asn Leu	
265 270 275	
cgc tta gac ggc gta gat cca gtg atg act att gca gat gta cag act	979
Arg Leu Asp Gly Val Asp Pro Val Met Thr Ile Ala Asp Val Gln Thr	
280 285 290	
gac acc gaa act gcg gaa gtc ctc ttc ccc cgc ttc gat ctc cca gca	1027
Asp Thr Glu Thr Ala Glu Val Leu Phe Pro Arg Phe Asp Leu Pro Ala	
295 300 305	
act gcc acc caa gaa ggc ccc att ggt gct ggc acc atc agc cgg ggc	1075
Thr Ala Thr Gln Glu Gly Pro Ile Gly Ala Gly Thr Ile Ser Arg Gly	
310 315 320 325	
gtt ccc acc atc acg ttg aat ggc cga aag tac acc act gtc ttt gat	1123
Val Pro Thr Ile Thr Leu Asn Gly Arg Lys Tyr Thr Thr Val Phe Asp	
330 335 340	
gtg ttg ctc gca cac tac ggt gtg aac cgc gaa gag ctc aac ctt cct	1171

Val Leu Leu Ala His Tyr Gly Val Asn Arg Glu Glu Leu Asn Leu Pro	
345 350 355	
ggt gag tgg cct aag gat ttc cag gat cca gtc atg ggt act cct gcg	1219
Gly Glu Trp Pro Lys Asp Phe Gln Asp Pro Val Met Gly Thr Pro Ala	
360 365 370	
tgg cag gaa gag ctc acg ggt gtt cct gct aat cag gcg att cgt ttg	1267
Trp Gln Glu Glu Leu Thr Gly Val Pro Ala Asn Gln Ala Ile Arg Leu	
375 380 385	
ggt cgg gaa ttt gct cag aat gct gat gat tcc aag ggc cgt tcc cag	1315
Gly Arg Glu Phe Ala Gln Asn Ala Asp Asp Ser Lys Gly Arg Ser Gln	
390 395 400 405	
atc atc atg ggt gct ggt gtg aac cac tac ttc cat gcg gat tct att	1363
Ile Ile Met Gly Ala Gly Val Asn His Tyr Phe His Ala Asp Ser Ile	
410 415 420	
tat cgc aca ttc ttg gcg ctg acc tct atg tgt ggc acc caa ggt gtt	1411
Tyr Arg Thr Phe Leu Ala Leu Thr Ser Met Cys Gly Thr Gln Gly Val	
425 430 435	
aac ggt ggc ggt tgg gct cac tac gtt ggt cag gag aaa ctc cgt cca	1459
Asn Gly Gly Gly Trp Ala His Tyr Val Gly Gln Glu Lys Leu Arg Pro	
440 445 450	
atg aat ggt tgg gca cag tat gcc ttt gct aca gac tgg cag cgt cca	1507
Met Asn Gly Trp Ala Gln Tyr Ala Phe Ala Thr Asp Trp Gln Arg Pro	
455 460 465	
cca cgt cag atg atc acc act ggt ttc tac tac ctc acc acg gat cag	1555
Pro Arg Gln Met Ile Thr Thr Gly Phe Tyr Tyr Leu Thr Thr Asp Gln	
470 475 480 485	
tgg agg tat gac aac act cgt gct aat cgt ctg gct tcc cca ctg gct	1603
Trp Arg Tyr Asp Asn Thr Arg Ala Asn Arg Leu Ala Ser Pro Leu Ala	
490 495 500	
aat cgt ggc acc gtg ggt gac aaa atg acg gcg gat acc ttg gtg gaa	1651
Asn Arg Gly Thr Val Gly Asp Lys Met Thr Ala Asp Thr Leu Val Glu	
505 510 515	
tcc atg aaa cgt gga tgg atg ccg tca ttc ccg caa ttc aac cgc aat	1699
Ser Met Lys Arg Gly Trp Met Pro Ser Phe Pro Gln Phe Asn Arg Asn	
520 525 530	
ccc ctc atc ttg agc cag gag gcg gaa gaa aag ggc gtg tct gtt tct	1747
Pro Leu Ile Leu Ser Gln Glu Ala Glu Glu Lys Gly Val Ser Val Ser	
535 540 545	
gac cat att gtt cag cag ctc acc gat ggt gac ttg cag ttc gcc tgc	1795
Asp His Ile Val Gln Gln Leu Thr Asp Gly Asp Leu Gln Phe Ala Cys	
550 555 560 565	
gag gat ccg gat gca ccg gaa aac tgg cca cgc att ctg ctt aac tgg	1843
Glu Asp Pro Asp Ala Pro Glu Asn Trp Pro Arg Ile Leu Leu Asn Trp	
570 575 580	
cgc aca aac cta atg ggc tct tca gct aag ggc acg gag ttt ttc ttg	1891
Arg Thr Asn Leu Met Gly Ser Ser Ala Lys Gly Thr Glu Phe Phe Leu	

585	590	595	
cgc cat atg ttg ggt gtg gat tct gat gca tct gct gaa gaa aac gcg Arg His Met Leu Gly Val Asp Ser Asp Ala Ser Ala Glu Glu Asn Ala 600 605 610			1939
ccg gag gat cgt cca agt tcc att gtg tgg agg gat gag gct ccg gaa Pro Glu Asp Arg Pro Ser Ser Ile Val Trp Arg Asp Glu Ala Pro Glu 615 620 625			1987
gga aag ctc gat ttg atg ctg acc acg gat ttc cgc aac act tcc acc Gly Lys Leu Asp Leu Met Leu Thr Thr Asp Phe Arg Asn Thr Ser Thr 630 635 640 645			2035
acc ttg gtc tcg gat atc gtg ctg ccg gca gcc acc tgg tat gag aag Thr Leu Val Ser Asp Ile Val Leu Pro Ala Ala Thr Trp Tyr Glu Lys 650 655 660			2083
cat gat ttg tcc acc acg gat atg cac ccc ttc atc cac tcg ttc aat His Asp Leu Ser Thr Thr Asp Met His Pro Phe Ile His Ser Phe Asn 665 670 675			2131
gct gcg atc aac cca ccg tgg gag acg cgt act gac tgg gag gtc ttc Ala Ala Ile Asn Pro Pro Trp Glu Thr Arg Thr Asp Trp Glu Val Phe 680 685 690			2179
cac gat ctc acc aaa gaa ttc tcc tca cag gca gca acc tgg ttg ggc His Asp Leu Thr Lys Glu Phe Ser Ser Gln Ala Ala Thr Trp Leu Gly 695 700 705			2227
acc caa acc gat gtg atc acc gca ccg att gcc cat gac tcc ccg gat Thr Gln Thr Asp Val Ile Thr Ala Pro Ile Ala His Asp Ser Pro Asp 710 715 720 725			2275
gag ctc aat atg cct ggc ggt atc gtg cca gat att gat gag gtc ggg Glu Leu Asn Met Pro Gly Gly Ile Val Pro Asp Ile Asp Glu Val Gly 730 735 740			2323
ctg atc cct ggc aag acg atg gcc aag atc atc ccg gtg gaa cgt gat Leu Ile Pro Gly Lys Thr Met Ala Lys Ile Ile Pro Val Glu Arg Asp 745 750 755			2371
tac tcc aag gtg tat gaa aag tgg aca cac ttg gga cca ctc acc gcc Tyr Ser Lys Val Tyr Glu Lys Trp Thr His Leu Gly Pro Leu Thr Ala 760 765 770			2419
aaa gcg ggt acc gga acc cac ggc act gcg ttt aac gtg acc aag caa Lys Ala Gly Thr Gly Thr His Gly Thr Ala Phe Asn Val Thr Lys Gln 775 780 785			2467
acc gag gag ctg gcg ctg atc aac ggc acc tcc atc Thr Glu Glu Leu Ala Leu Ile Asn Gly Thr Ser Ile 790 795 800			2503

<210> 278

<211> 801

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val Leu Ala Trp Arg Asp Ile Val Glu Thr Pro Glu Lys Arg Lys Ala
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 Tyr Val Ser Gln Arg Gly Lys Gly Gly Leu Ile Arg Val Gln Tyr Glu
 20 25 30
 Glu Ala Met Glu Ile Ala Ala Ala Ala His Val Tyr Thr Ile Arg Gln
 35 40 45
 Tyr Gly Pro Asp Arg Ile His Gly Phe Thr Val Ile Pro Ala Met Ser
 50 55 60
 Gln Val Ser Tyr Gly Ala Gly Thr Arg Phe Leu Gln Met Ile Gly Gly
 65 70 75 80
 Val Ala Leu Ser Phe Tyr Asp Trp Tyr Ala Asp Leu Pro Pro Ala Ser
 85 90 95
 Pro Gln Thr Phe Gly Asp Gln Thr Asp Val Pro Glu Ser Gly Asp Trp
 100 105 110
 Tyr Asn Ser Ser Tyr Leu Met Met Trp Gly Ser Asn Ile Pro Val Thr
 115 120 125
 Arg Thr Pro Asp Ser His Phe Met Val Glu Ala Arg Tyr Lys Gly Thr
 130 135 140
 Lys Val Val Val Val Ser Pro Asp Phe Ala Asp Ser Thr Lys Phe Ala
 145 150 155 160
 Asp Glu Trp Ala Arg Ile His Pro Gly Thr Asp Gly Ala Leu Ala Phe
 165 170 175
 Ala Met Gly His Val Ile Leu Lys Glu Phe His Val Asp Lys Lys Thr
 180 185 190
 Pro Tyr Phe Met Asp Tyr Met Arg Lys Tyr Thr Asp Ser Pro Phe Leu
 195 200 205
 Val Glu Leu Asp Glu His Gly Asp Gly Thr Tyr Thr Pro Gly Lys Phe
 210 215 220
 Leu Thr Ala Asp Arg Ala Ala Asp Ile Ser Pro Ala Leu Ala Ala Thr
 225 230 235 240
 Pro Asn Ala Thr His Arg Leu Leu Val Leu Gln Lys Asp Gly Ser Val
 245 250 255
 Val Asp Pro Gly Gly Thr Val Ala Asp Arg Trp Gly Glu Glu Gly Met
 260 265 270
 Gly Lys Trp Asn Leu Arg Leu Asp Gly Val Asp Pro Val Met Thr Ile
 275 280 285
 Ala Asp Val Gln Thr Asp Thr Glu Thr Ala Glu Val Leu Phe Pro Arg
 290 295 300
 Phe Asp Leu Pro Ala Thr Ala Thr Gln Glu Gly Pro Ile Gly Ala Gly
 305 310 315 320
 Thr Ile Ser Arg Gly Val Pro Thr Ile Thr Leu Asn Gly Arg Lys Tyr

325										330				335			
Thr	Thr	Val	Phe	Asp	Val	Leu	Leu	Ala	His	Tyr	Gly	Val	Asn	Arg	Glu		
			340					345					350				
Glu	Leu	Asn	Leu	Pro	Gly	Glu	Trp	Pro	Lys	Asp	Phe	Gln	Asp	Pro	Val		
		355					360					365					
Met	Gly	Thr	Pro	Ala	Trp	Gln	Glu	Glu	Leu	Thr	Gly	Val	Pro	Ala	Asn		
	370					375					380						
Gln	Ala	Ile	Arg	Leu	Gly	Arg	Glu	Phe	Ala	Gln	Asn	Ala	Asp	Asp	Ser		
385					390					395					400		
Lys	Gly	Arg	Ser	Gln	Ile	Ile	Met	Gly	Ala	Gly	Val	Asn	His	Tyr	Phe		
				405					410					415			
His	Ala	Asp	Ser	Ile	Tyr	Arg	Thr	Phe	Leu	Ala	Leu	Thr	Ser	Met	Cys		
			420					425					430				
Gly	Thr	Gln	Gly	Val	Asn	Gly	Gly	Gly	Trp	Ala	His	Tyr	Val	Gly	Gln		
		435					440					445					
Glu	Lys	Leu	Arg	Pro	Met	Asn	Gly	Trp	Ala	Gln	Tyr	Ala	Phe	Ala	Thr		
	450					455					460						
Asp	Trp	Gln	Arg	Pro	Pro	Arg	Gln	Met	Ile	Thr	Thr	Gly	Phe	Tyr	Tyr		
465					470					475					480		
Leu	Thr	Thr	Asp	Gln	Trp	Arg	Tyr	Asp	Asn	Thr	Arg	Ala	Asn	Arg	Leu		
				485					490					495			
Ala	Ser	Pro	Leu	Ala	Asn	Arg	Gly	Thr	Val	Gly	Asp	Lys	Met	Thr	Ala		
			500					505					510				
Asp	Thr	Leu	Val	Glu	Ser	Met	Lys	Arg	Gly	Trp	Met	Pro	Ser	Phe	Pro		
		515					520					525					
Gln	Phe	Asn	Arg	Asn	Pro	Leu	Ile	Leu	Ser	Gln	Glu	Ala	Glu	Glu	Lys		
	530					535					540						
Gly	Val	Ser	Val	Ser	Asp	His	Ile	Val	Gln	Gln	Leu	Thr	Asp	Gly	Asp		
545					550					555					560		
Leu	Gln	Phe	Ala	Cys	Glu	Asp	Pro	Asp	Ala	Pro	Glu	Asn	Trp	Pro	Arg		
				565					570					575			
Ile	Leu	Leu	Asn	Trp	Arg	Thr	Asn	Leu	Met	Gly	Ser	Ser	Ala	Lys	Gly		
			580					585					590				
Thr	Glu	Phe	Phe	Leu	Arg	His	Met	Leu	Gly	Val	Asp	Ser	Asp	Ala	Ser		
		595					600					605					
Ala	Glu	Glu	Asn	Ala	Pro	Glu	Asp	Arg	Pro	Ser	Ser	Ile	Val	Trp	Arg		
	610					615					620						
Asp	Glu	Ala	Pro	Glu	Gly	Lys	Leu	Asp	Leu	Met	Leu	Thr	Thr	Asp	Phe		
625					630					635					640		
Arg	Asn	Thr	Ser	Thr	Thr	Leu	Val	Ser	Asp	Ile	Val	Leu	Pro	Ala	Ala		
				645					650					655			

Thr Trp Tyr Glu Lys His Asp Leu Ser Thr Thr Asp Met His Pro Phe
 660 665 670
 Ile His Ser Phe Asn Ala Ala Ile Asn Pro Pro Trp Glu Thr Arg Thr
 675 680 685
 Asp Trp Glu Val Phe His Asp Leu Thr Lys Glu Phe Ser Ser Gln Ala
 690 695 700
 Ala Thr Trp Leu Gly Thr Gln Thr Asp Val Ile Thr Ala Pro Ile Ala
 705 710 715 720
 His Asp Ser Pro Asp Glu Leu Asn Met Pro Gly Gly Ile Val Pro Asp
 725 730 735
 Ile Asp Glu Val Gly Leu Ile Pro Gly Lys Thr Met Ala Lys Ile Ile
 740 745 750
 Pro Val Glu Arg Asp Tyr Ser Lys Val Tyr Glu Lys Trp Thr His Leu
 755 760 765
 Gly Pro Leu Thr Ala Lys Ala Gly Thr Gly Thr His Gly Thr Ala Phe
 770 775 780
 Asn Val Thr Lys Gln Thr Glu Glu Leu Ala Leu Ile Asn Gly Thr Ser
 785 790 795 800
 Ile

<210> 279
 <211> 765
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (85)..(765)
 <223> FRXA01307

<400> 279
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 gccaaaggaac gcctggggcga tccggtg ctg gcg tgg cgc gac att gta gaa acc 114
 Val Leu Ala Trp Arg Asp Ile Val Glu Thr
 1 5 10
 cca gaa aag cgc aaa gca tat gta tcc cag cgg ggc aaa ggt ggc ctc 162
 Pro Glu Lys Arg Lys Ala Tyr Val Ser Gln Arg Gly Lys Gly Gly Leu
 15 20 25
 atc cgc gtt cag tat gag gaa gcc atg gag att gct gcg gca gcc cat 210
 Ile Arg Val Gln Tyr Glu Glu Ala Met Glu Ile Ala Ala Ala Ala His
 30 35 40
 gtg tac acc atc cgc caa tac ggc ccc gac cgc att cat gga ttc acc 258
 Val Tyr Thr Ile Arg Gln Tyr Gly Pro Asp Arg Ile His Gly Phe Thr
 45 50 55

gtt att ccc gca atg tcg cag gtg tct tac ggt gct ggt act cgc ttc 306
 Val Ile Pro Ala Met Ser Gln Val Ser Tyr Gly Ala Gly Thr Arg Phe
 60 65 70
 ttg cag atg atc ggc gga gtg gcg ctg tcc ttc tac gat tgg tac gcc 354
 Leu Gln Met Ile Gly Val Ala Leu Ser Phe Tyr Asp Trp Tyr Ala
 75 80 85 90
 gac ctc cca cca gca tca cca caa act ttc ggc gat caa act gac gtt 402
 Asp Leu Pro Pro Ala Ser Pro Gln Thr Phe Gly Asp Gln Thr Asp Val
 95 100 105
 ccg gaa tct ggc gac tgg tac aac tcc agc tac ctc atg atg tgg ggt 450
 Pro Glu Ser Gly Asp Trp Tyr Asn Ser Ser Tyr Leu Met Met Trp Gly
 110 115 120
 tcc aac att ccg gtg acc cgc acg cct gac tcc cac ttc atg gtg gaa 498
 Ser Asn Ile Pro Val Thr Arg Thr Pro Asp Ser His Phe Met Val Glu
 125 130 135
 gcc cgc tac aag ggc acc aag gtt gtt gtg gtt tcc ccg gat ttc gct 546
 Ala Arg Tyr Lys Gly Thr Lys Val Val Val Val Ser Pro Asp Phe Ala
 140 145 150
 gac tcc acc aaa ttt gct gat gaa tgg gca cgc atc cac cct ggt act 594
 Asp Ser Thr Lys Phe Ala Asp Glu Trp Ala Arg Ile His Pro Gly Thr
 155 160 165 170
 gac ggc gca ctc gcc ttt gcc atg ggc cat gtg atc ttg aag gaa ttc 642
 Asp Gly Ala Leu Ala Phe Ala Met Gly His Val Ile Leu Lys Glu Phe
 175 180 185
 cat gtt gac aag aag acg ccg tac ttc atg gac tac atg cgc aaa tac 690
 His Val Asp Lys Lys Thr Pro Tyr Phe Met Asp Tyr Met Arg Lys Tyr
 190 195 200
 acg gac tct cct ttc ctc gtg gaa tta gat gag cac ggc gat ggc acc 738
 Thr Asp Ser Pro Phe Leu Val Glu Leu Asp Glu His Gly Asp Gly Thr
 205 210 215
 tac acc cca ggt aaa ttc ctc act gca 765
 Tyr Thr Pro Gly Lys Phe Leu Thr Ala
 220 225

<210> 280

<211> 227

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 280

Val Leu Ala Trp Arg Asp Ile Val Glu Thr Pro Glu Lys Arg Lys Ala
 1 5 10 15
 Tyr Val Ser Gln Arg Gly Lys Gly Gly Leu Ile Arg Val Gln Tyr Glu
 20 25 30
 Glu Ala Met Glu Ile Ala Ala Ala Ala His Val Tyr Thr Ile Arg Gln
 35 40 45
 Tyr Gly Pro Asp Arg Ile His Gly Phe Thr Val Ile Pro Ala Met Ser

50 55 60
 Gln Val Ser Tyr Gly Ala Gly Thr Arg Phe Leu Gln Met Ile Gly Gly
 65 70 75 80
 Val Ala Leu Ser Phe Tyr Asp Trp Tyr Ala Asp Leu Pro Pro Ala Ser
 85 90 95
 Pro Gln Thr Phe Gly Asp Gln Thr Asp Val Pro Glu Ser Gly Asp Trp
 100 105 110
 Tyr Asn Ser Ser Tyr Leu Met Met Trp Gly Ser Asn Ile Pro Val Thr
 115 120 125
 Arg Thr Pro Asp Ser His Phe Met Val Glu Ala Arg Tyr Lys Gly Thr
 130 135 140
 Lys Val Val Val Val Ser Pro Asp Phe Ala Asp Ser Thr Lys Phe Ala
 145 150 155 160
 Asp Glu Trp Ala Arg Ile His Pro Gly Thr Asp Gly Ala Leu Ala Phe
 165 170 175
 Ala Met Gly His Val Ile Leu Lys Glu Phe His Val Asp Lys Lys Thr
 180 185 190
 Pro Tyr Phe Met Asp Tyr Met Arg Lys Tyr Thr Asp Ser Pro Phe Leu
 195 200 205
 Val Glu Leu Asp Glu His Gly Asp Gly Thr Tyr Thr Pro Gly Lys Phe
 210 215 220
 Leu Thr Ala
 225

 <210> 281
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (1)..(1206)
 <223> FRXA01308

 <400> 281
 gcc gcc act cca aat gcc acc cac cgt ctc ctt gtg ctg caa aaa gat 48
 Ala Ala Thr Pro Asn Ala Thr His Arg Leu Leu Val Leu Gln Lys Asp
 1 5 10 15
 ggc tca gtt gta gat ccc ggt ggc act gtc gcg gac cgt tgg ggt gaa 96
 Gly Ser Val Val Asp Pro Gly Gly Thr Val Ala Asp Arg Trp Gly Glu
 20 25 30
 gaa ggc atg ggt aag tgg aat ctg cgc tta gac ggc gta gat cca gtg 144
 Glu Gly Met Gly Lys Trp Asn Leu Arg Leu Asp Gly Val Asp Pro Val
 35 40 45
 atg act att gca gat gta cag act gac acc gaa act gcg gaa gtc ctc 192
 Met Thr Ile Ala Asp Val Gln Thr Asp Thr Glu Thr Ala Glu Val Leu

50	55	60	
ttc ccc cgc ttc gat ctc cca gca act gcc acc caa gaa ggc ccc att			240
Phe Pro Arg Phe Asp Leu Pro Ala Thr Ala Thr Gln Glu Gly Pro Ile			
65	70	75	80
ggt gct ggc acc atc agc cgg ggc gtt ccc acc atc acg ttg aat ggc			288
Gly Ala Gly Thr Ile Ser Arg Gly Val Pro Thr Ile Thr Leu Asn Gly			
	85	90	95
cga aag tac acc act gtc ttt gat gtg ttg ctc gca cac tac ggt gtg			336
Arg Lys Tyr Thr Thr Val Phe Asp Val Leu Leu Ala His Tyr Gly Val			
	100	105	110
aac cgc gaa gag ctc aac ctt cct ggt gag tgg cct aag gat ttc cag			384
Asn Arg Glu Glu Leu Asn Leu Pro Gly Glu Trp Pro Lys Asp Phe Gln			
	115	120	125
gat cca gtc atg ggt act cct gcg tgg cag gaa gag ctc acg ggt gtt			432
Asp Pro Val Met Gly Thr Pro Ala Trp Gln Glu Glu Leu Thr Gly Val			
	130	135	140
cct gct aat cag gcg att cgt ttg ggt cgg gaa ttt gct cag aat gct			480
Pro Ala Asn Gln Ala Ile Arg Leu Gly Arg Glu Phe Ala Gln Asn Ala			
145	150	155	160
gat gat tcc aag ggc cgt tcc cag atc atc atg ggt gct ggt gtg aac			528
Asp Asp Ser Lys Gly Arg Ser Gln Ile Ile Met Gly Ala Gly Val Asn			
	165	170	175
cac tac ttc cat gcg gat tct att tat cgc aca ttc ttg gcg ctg acc			576
His Tyr Phe His Ala Asp Ser Ile Tyr Arg Thr Phe Leu Ala Leu Thr			
	180	185	190
tct atg tgt ggc acc caa ggt gtt aac ggt ggc ggt tgg gct cac tac			624
Ser Met Cys Gly Thr Gln Gly Val Asn Gly Gly Gly Trp Ala His Tyr			
	195	200	205
gtt ggt cag gag aaa ctc cgt cca atg aat ggt tgg gca cag tat gcc			672
Val Gly Gln Glu Lys Leu Arg Pro Met Asn Gly Trp Ala Gln Tyr Ala			
	210	215	220
ttt gct aca gac tgg cag cgt cca cca cgt cag atg atc acc act ggt			720
Phe Ala Thr Asp Trp Gln Arg Pro Pro Arg Gln Met Ile Thr Thr Gly			
225	230	235	240
ttc tac tac ctc acc acg gat cag tgg agg tat gac aac act cgt gct			768
Phe Tyr Tyr Leu Thr Thr Asp Gln Trp Arg Tyr Asp Asn Thr Arg Ala			
	245	250	255
aat cgt ctg gct tcc cca ctg gct aat cgt ggc acc gtg ggt gac aaa			816
Asn Arg Leu Ala Ser Pro Leu Ala Asn Arg Gly Thr Val Gly Asp Lys			
	260	265	270
atg acg gcg gat acc ttg gtg gaa tcc atg aaa cgt gga tgg atg ccg			864
Met Thr Ala Asp Thr Leu Val Glu Ser Met Lys Arg Gly Trp Met Pro			
	275	280	285
tca ttc ccg caa ttc aac cgc aat ccc ctc atc ttg agc cag gag gcg			912
Ser Phe Pro Gln Phe Asn Arg Asn Pro Leu Ile Leu Ser Gln Glu Ala			
	290	295	300

gaa gaa aag ggc gtg tct gtt tct gac cat att gtt cag cag ctc acc 960
 Glu Glu Lys Gly Val Ser Val Ser Asp His Ile Val Gln Gln Leu Thr
 305 310 315 320
 gat ggt gac ttg cag ttc gcc tgc gag gat ccg gat gca ccg gaa aac 1008
 Asp Gly Asp Leu Gln Phe Ala Cys Glu Asp Pro Asp Ala Pro Glu Asn
 325 330 335
 tgg cca cgc att ctg ctt aac tgg cgc aca aac cta atg ggc tct tca 1056
 Trp Pro Arg Ile Leu Leu Asn Trp Arg Thr Asn Leu Met Gly Ser Ser
 340 345 350
 gct aag ggc acg gag ttt ttc ttg cgc cat atg ttg ggt gtg gat tct 1104
 Ala Lys Gly Thr Glu Phe Phe Leu Arg His Met Leu Gly Val Asp Ser
 355 360 365
 gat gca tct gct gaa aaa aac gcg ccg gag gat cgt cca agt tcc att 1152
 Asp Ala Ser Ala Glu Lys Asn Ala Pro Glu Asp Arg Pro Ser Ser Ile
 370 375 380
 gtg tgg agg gat gaa gct tcc gaa ggg aag ctc gat ttg atg ctg acc 1200
 Val Trp Arg Asp Glu Ala Ser Glu Gly Lys Leu Asp Leu Met Leu Thr
 385 390 395 400
 acg gat
 Thr Asp 1206

<210> 282

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Ala Ala Thr Pro Asn Ala Thr His Arg Leu Leu Val Leu Gln Lys Asp
 1 5 10 15
 Gly Ser Val Val Asp Pro Gly Gly Thr Val Ala Asp Arg Trp Gly Glu
 20 25 30
 Glu Gly Met Gly Lys Trp Asn Leu Arg Leu Asp Gly Val Asp Pro Val
 35 40 45
 Met Thr Ile Ala Asp Val Gln Thr Asp Thr Glu Thr Ala Glu Val Leu
 50 55 60
 Phe Pro Arg Phe Asp Leu Pro Ala Thr Ala Thr Gln Glu Gly Pro Ile
 65 70 75 80
 Gly Ala Gly Thr Ile Ser Arg Gly Val Pro Thr Ile Thr Leu Asn Gly
 85 90 95
 Arg Lys Tyr Thr Thr Val Phe Asp Val Leu Leu Ala His Tyr Gly Val
 100 105 110
 Asn Arg Glu Glu Leu Asn Leu Pro Gly Glu Trp Pro Lys Asp Phe Gln
 115 120 125
 Asp Pro Val Met Gly Thr Pro Ala Trp Gln Glu Glu Leu Thr Gly Val

130 135 140
 Pro Ala Asn Gln Ala Ile Arg Leu Gly Arg Glu Phe Ala Gln Asn Ala
 145 150 155 160
 Asp Asp Ser Lys Gly Arg Ser Gln Ile Ile Met Gly Ala Gly Val Asn
 165 170 175
 His Tyr Phe His Ala Asp Ser Ile Tyr Arg Thr Phe Leu Ala Leu Thr
 180 185 190
 Ser Met Cys Gly Thr Gln Gly Val Asn Gly Gly Gly Trp Ala His Tyr
 195 200 205
 Val Gly Gln Glu Lys Leu Arg Pro Met Asn Gly Trp Ala Gln Tyr Ala
 210 215 220
 Phe Ala Thr Asp Trp Gln Arg Pro Pro Arg Gln Met Ile Thr Thr Gly
 225 230 235 240
 Phe Tyr Tyr Leu Thr Thr Asp Gln Trp Arg Tyr Asp Asn Thr Arg Ala
 245 250 255
 Asn Arg Leu Ala Ser Pro Leu Ala Asn Arg Gly Thr Val Gly Asp Lys
 260 265 270
 Met Thr Ala Asp Thr Leu Val Glu Ser Met Lys Arg Gly Trp Met Pro
 275 280 285
 Ser Phe Pro Gln Phe Asn Arg Asn Pro Leu Ile Leu Ser Gln Glu Ala
 290 295 300
 Glu Glu Lys Gly Val Ser Val Ser Asp His Ile Val Gln Gln Leu Thr
 305 310 315 320
 Asp Gly Asp Leu Gln Phe Ala Cys Glu Asp Pro Asp Ala Pro Glu Asn
 325 330 335
 Trp Pro Arg Ile Leu Leu Asn Trp Arg Thr Asn Leu Met Gly Ser Ser
 340 345 350
 Ala Lys Gly Thr Glu Phe Phe Leu Arg His Met Leu Gly Val Asp Ser
 355 360 365
 Asp Ala Ser Ala Glu Lys Asn Ala Pro Glu Asp Arg Pro Ser Ser Ile
 370 375 380
 Val Trp Arg Asp Glu Ala Ser Glu Gly Lys Leu Asp Leu Met Leu Thr
 385 390 395 400
 Thr Asp

<210> 283

<211> 824

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(801)

<223> RXN01309

<400> 283

att gca gac cac gaa ggt acc cac atc aat tgg gac atg gtc aaa gaa	48
Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu	
1 5 10 15	
cgt tcc gcc gag gtg atc acc tca ccg gag tgg act ggt tcc aag aag	96
Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys	
20 25 30	
gac gga cgt cgc tac acc gcg ttt tcc atc aac att gaa tac gac aag	144
Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys	
35 40 45	
ccg tgg cac acc ctg tct ggt cgc atg cac tac tac ctc gac cac gat	192
Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp	
50 55 60	
tgg ttt att gat tac ggc gag cag ttg cca atc ttt agg cca ccg ttg	240
Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu	
65 70 75 80	
gac aag atc cac atc aat ggt gag gtc ggc cct ggc cag tcg gtc aca	288
Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr	
85 90 95	
ggc acc gac ggc gaa cca gaa gta acc gtg cgt tat ctg acc acc cac	336
Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His	
100 105 110	
aac aag tgg tcg att cac tcg cag tac tac gac aat ctg cat gtg ctt	384
Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu	
115 120 125	
tct att tct cgt ggc ggc cag gtg atc tgg atg tcc aac aag gat gca	432
Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala	
130 135 140	
gag aaa ctc ggt atc gct gac aac gat tgg atc gag gct tat aac cgc	480
Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg	
145 150 155 160	
aac ggc gtt gtt tct gct cgt gcg att gtc tcc cac cgc att cct gaa	528
Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu	
165 170 175	
ggc acc gtg ttt atg aac cac gcg cag gaa cgc acc gct ggc acc ccg	576
Gly Thr Val Phe Met Asn His Ala Gln Glu Arg Thr Ala Gly Thr Pro	
180 185 190	
ctg aac gag aag tct ggc agg cgc ggc gga act cac aac tct ctt act	624
Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr	
195 200 205	
cga atc atg att aag ccg gtc cat gtt gcc ggt ggc tac ggc cac tta	672
Arg Ile Met Ile Lys Pro Val His Val Ala Gly Gly Tyr Gly His Leu	
210 215 220	
acc tat ggc ttc aac tac atc ggc caa ccg gaa ata acc gcg atg agg	720

Thr Tyr Gly Phe Asn Tyr Ile Gly Gln Pro Glu Ile Thr Ala Met Arg
 225 230 235 240

tca cca gaa ttc gtc gcc gct ccc agg agg tgc agt act aat gaa ggt 768
 Ser Pro Glu Phe Val Ala Ala Pro Arg Arg Cys Ser Thr Asn Glu Gly
 245 250 255

cat ggc tca gat cgc aat gat cat gaa ctt gga taagtgcatt ggctgccaca 821
 His Gly Ser Asp Arg Asn Asp His Glu Leu Gly
 260 265

cgt 824

<210> 284
 <211> 267
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 284
 Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu
 1 5 10 15

Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys
 20 25 30

Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys
 35 40 45

Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp
 50 55 60

Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu
 65 70 75 80

Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr
 85 90 95

Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His
 100 105 110

Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu
 115 120 125

Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala
 130 135 140

Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg
 145 150 155 160

Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu
 165 170 175

Gly Thr Val Phe Met Asn His Ala Gln Glu Arg Thr Ala Gly Thr Pro
 180 185 190

Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr
 195 200 205

Arg Ile Met Ile Lys Pro Val His Val Ala Gly Gly Tyr Gly His Leu
 210 215 220

Thr Tyr Gly Phe Asn Tyr Ile Gly Gln Pro Glu Ile Thr Ala Met Arg
 225 230 235 240

Ser Pro Glu Phe Val Ala Ala Pro Arg Arg Cys Ser Thr Asn Glu Gly
 245 250 255

His Gly Ser Asp Arg Asn Asp His Glu Leu Gly
 260 265

<210> 285

<211> 692

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(669)

<223> FRXA01309

<400> 285

att gca gac cac gaa ggt acc cac atc aat tgg gac atg gtc aaa gaa 48
 Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu
 1 5 10 15

cgt tcc gcc gag gtg atc acc tca ccg gag tgg act ggt tcc aag aag 96
 Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys
 20 25 30

gac gga cgt cgc tac acc gcg ttt tcc atc aac att gaa tac gac aag 144
 Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys
 35 40 45

ccg tgg cac acc ctg tct ggt cgc atg cac tac tac ctc gac cac gat 192
 Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp
 50 55 60

tgg ttt att gat tac ggc gag cag ttg cca atc ttt agg cca ccg ttg 240
 Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu
 65 70 75 80

gac aag atc cac atc aat ggt gag gtc ggc cct ggc cag tcg gtc aca 288
 Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr
 85 90 95

ggc acc gac ggc gaa cca gaa gta acc gtg cgt tat ctg acc acc cac 336
 Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His
 100 105 110

aac aag tgg tcg att cac tcg cag tac tac gac aat ctg cat gtg ctt 384
 Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu
 115 120 125

tct att tct cgt ggc ggc cag gtg atc tgg atg tcc aac aag gat gca 432
 Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala
 130 135 140

gag aaa ctc ggt atc gct gac aac gat tgg atc gag gct tat aac cgc 480
 Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg
 145 150 155 160

aac ggc gtt gtt tct gct cgt gcg att gtc tcc cac cgc att cct gaa 528
 Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu
 165 170 175

 ggc acc gtg ttt atg aac cac gcg cag gaa ccc acc gct ggc acc ccg 576
 Gly Thr Val Phe Met Asn His Ala Gln Glu Pro Thr Ala Gly Thr Pro
 180 185 190

 ctg aac gag aag tct ggc agg cgc ggc gga act cac aac tct ctt act 624
 Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr
 195 200 205

 cga atc atg att aaa acg gtc cat gtt gcc ggt ggc tac ggc act 669
 Arg Ile Met Ile Lys Thr Val His Val Ala Gly Gly Tyr Gly Thr
 210 215 220

 taacctatgg cttaactaca tcg 692

<210> 286
 <211> 223
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 286
 Ile Ala Asp His Glu Gly Thr His Ile Asn Trp Asp Met Val Lys Glu
 1 5 10 15

 Arg Ser Ala Glu Val Ile Thr Ser Pro Glu Trp Thr Gly Ser Lys Lys
 20 25 30

 Asp Gly Arg Arg Tyr Thr Ala Phe Ser Ile Asn Ile Glu Tyr Asp Lys
 35 40 45

 Pro Trp His Thr Leu Ser Gly Arg Met His Tyr Tyr Leu Asp His Asp
 50 55 60

 Trp Phe Ile Asp Tyr Gly Glu Gln Leu Pro Ile Phe Arg Pro Pro Leu
 65 70 75 80

 Asp Lys Ile His Ile Asn Gly Glu Val Gly Pro Gly Gln Ser Val Thr
 85 90 95

 Gly Thr Asp Gly Glu Pro Glu Val Thr Val Arg Tyr Leu Thr Thr His
 100 105 110

 Asn Lys Trp Ser Ile His Ser Gln Tyr Tyr Asp Asn Leu His Val Leu
 115 120 125

 Ser Ile Ser Arg Gly Gly Gln Val Ile Trp Met Ser Asn Lys Asp Ala
 130 135 140

 Glu Lys Leu Gly Ile Ala Asp Asn Asp Trp Ile Glu Ala Tyr Asn Arg
 145 150 155 160

 Asn Gly Val Val Ser Ala Arg Ala Ile Val Ser His Arg Ile Pro Glu
 165 170 175

 Gly Thr Val Phe Met Asn His Ala Gln Glu Pro Thr Ala Gly Thr Pro
 180 185 190

Leu Asn Glu Lys Ser Gly Arg Arg Gly Gly Thr His Asn Ser Leu Thr
 195 200 205

Arg Ile Met Ile Lys Thr Val His Val Ala Gly Gly Tyr Gly Thr
 210 215 220

<210> 287

<211> 807

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(784)

<223> RXA02017

<400> 287

gcctgtggca cgggagctcc cagcggcaag gtgagttctga cctcgtggaa cgttggcgaa 60

cgccccgctg cgatgttccc accaaggaag gactaggcgg atg cgc acc cat act 115
 Met Arg Thr His Thr
 1 5

ggc aaa att ccg gat cac ttt gtg cct cgc atc tcc atg acg gag gag 163
 Gly Lys Ile Pro Asp His Phe Val Pro Arg Ile Ser Met Thr Glu Glu
 10 15 20

cag cgg cgc gtg gtg ttc atg ctg aat agt ttg ctg ttg gat tat cca 211
 Gln Arg Arg Val Val Phe Met Leu Asn Ser Leu Leu Leu Asp Tyr Pro
 25 30 35

gag gag gga ttc gtc gac aag cta aat gcc gtc gag gcg cag ctt gat 259
 Glu Glu Gly Phe Val Asp Lys Leu Asn Ala Val Glu Ala Gln Leu Asp
 40 45 50

gtc ctt ccg ctc ccc gtc gcg gcg cac gtg gtc gag ttc ctt gac gcg 307
 Val Leu Pro Leu Pro Val Ala Ala His Val Val Glu Phe Leu Asp Ala
 55 60 65

gca cgc gtc gct ggg cta cgc gcc atg cag gaa gcc tac gtt gag acc 355
 Ala Arg Val Ala Gly Leu Arg Ala Met Gln Glu Ala Tyr Val Glu Thr
 70 75 80 85

ttt gac cag cgc cga cgc tgc tca ctg ttt ctc acc tac tac gct gtg 403
 Phe Asp Gln Arg Arg Arg Cys Ser Leu Phe Leu Thr Tyr Tyr Ala Val
 90 95 100

ggc gac acc cgg cag cgc ggc acg gcg atc ctc acc ttc cgt caa acg 451
 Gly Asp Thr Arg Gln Arg Gly Thr Ala Ile Leu Thr Phe Arg Gln Thr
 105 110 115

ctg caa cag ctc gga ttt gaa tcc gag cgc gac gaa ttg ccc gac cac 499
 Leu Gln Gln Leu Gly Phe Glu Ser Glu Arg Asp Glu Leu Pro Asp His
 120 125 130

ctc tgc gtc gtg ctt gag gcc gca gcg ctt gct gat tct tcg ctt ttc 547
 Leu Cys Val Val Leu Glu Ala Ala Ala Leu Ala Asp Ser Ser Leu Phe
 135 140 145

gac gcc gcc acc cag gtg tta tca gct cac cgc gac ggc atc gaa gtg 595
 Asp Ala Ala Thr Gln Val Leu Ser Ala His Arg Asp Gly Ile Glu Val
 150 155 160 165

ttg cgc gca gcc ctc gac aac ctc gac tcg ccc tac aga tac ctg atc 643
 Leu Arg Ala Ala Leu Asp Asn Leu Asp Ser Pro Tyr Arg Tyr Leu Ile
 170 175 180

atg tct ttg tgc cag gca ttg cca gaa atc gat gaa gaa acc gcc aac 691
 Met Ser Leu Cys Gln Ala Leu Pro Glu Ile Asp Glu Glu Thr Ala Asn
 185 190 195

agc tac atg gag ctc atc cgc agc ggt cca cca gca gaa atg gtg ggc 739
 Ser Tyr Met Glu Leu Ile Arg Ser Gly Pro Pro Ala Glu Met Val Gly
 200 205 210

atc ggc acg cct cta ccg ttc ccc acc tca caa ccg gac att cac 784
 Ile Gly Thr Pro Leu Pro Phe Pro Thr Ser Gln Pro Asp Ile His
 215 220 225

taggacacac tatgtcaaac ttt 807

<210> 288
 <211> 228
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 288
 Met Arg Thr His Thr Gly Lys Ile Pro Asp His Phe Val Pro Arg Ile
 1 5 10 15

Ser Met Thr Glu Glu Gln Arg Arg Val Val Phe Met Leu Asn Ser Leu
 20 25 30

Leu Leu Asp Tyr Pro Glu Glu Gly Phe Val Asp Lys Leu Asn Ala Val
 35 40 45

Glu Ala Gln Leu Asp Val Leu Pro Leu Pro Val Ala Ala His Val Val
 50 55 60

Glu Phe Leu Asp Ala Ala Arg Val Ala Gly Leu Arg Ala Met Gln Glu
 65 70 75 80

Ala Tyr Val Glu Thr Phe Asp Gln Arg Arg Arg Cys Ser Leu Phe Leu
 85 90 95

Thr Tyr Tyr Ala Val Gly Asp Thr Arg Gln Arg Gly Thr Ala Ile Leu
 100 105 110

Thr Phe Arg Gln Thr Leu Gln Gln Leu Gly Phe Glu Ser Glu Arg Asp
 115 120 125

Glu Leu Pro Asp His Leu Cys Val Val Leu Glu Ala Ala Ala Leu Ala
 130 135 140

Asp Ser Ser Leu Phe Asp Ala Ala Thr Gln Val Leu Ser Ala His Arg
 145 150 155 160

Asp Gly Ile Glu Val Leu Arg Ala Ala Leu Asp Asn Leu Asp Ser Pro
 165 170 175

Tyr Arg Tyr Leu Ile Met Ser Leu Cys Gln Ala Leu Pro Glu Ile Asp
 180 185 190

Glu Glu Thr Ala Asn Ser Tyr Met Glu Leu Ile Arg Ser Gly Pro Pro
 195 200 205

Ala Glu Met Val Gly Ile Gly Thr Pro Leu Pro Phe Pro Thr Ser Gln
 210 215 220

Pro Asp Ile His
 225

<210> 289

<211> 1073

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1050)

<223> RXA02018

<400> 289

cgc atc tgc gag cac tgc ctc aac ccc acc tgt gtg tcc tcc tgc cca 48
 Arg Ile Cys Glu His Cys Leu Asn Pro Thr Cys Val Ser Ser Cys Pro
 1 5 10 15

tcc ggt gct atg tac aaa cgc gcc gaa gac ggc atc gtg ctg gtt gac 96
 Ser Gly Ala Met Tyr Lys Arg Ala Glu Asp Gly Ile Val Leu Val Asp
 20 25 30

cag gat caa tgc cgt ggc tgg cgc atg tgt gtt tcc ggc tgc ccc tac 144
 Gln Asp Gln Cys Arg Gly Trp Arg Met Cys Val Ser Gly Cys Pro Tyr
 35 40 45

aaa aag gtc tac ttc aat cac aaa tcg ggc aag gcc gaa aag tgt acg 192
 Lys Lys Val Tyr Phe Asn His Lys Ser Gly Lys Ala Glu Lys Cys Thr
 50 55 60

ctg tgc tat ccg cgc ctc gag gtc ggc cag ccg acc gtg tgc tcc gag 240
 Leu Cys Tyr Pro Arg Leu Glu Val Gly Gln Pro Thr Val Cys Ser Glu
 65 70 75 80

acg tgc gtg ggt cgc ttg cgc tac ttg ggc gtt ttg ctt tac gac gcc 288
 Thr Cys Val Gly Arg Leu Arg Tyr Leu Gly Val Leu Leu Tyr Asp Ala
 85 90 95

gac cgt gtc gct gaa gtc gcc gcc acg cca gac gaa aag gat ctt ttc 336
 Asp Arg Val Ala Glu Val Ala Ala Thr Pro Asp Glu Lys Asp Leu Phe
 100 105 110

gaa gcc caa aag acc ctc ttc cta gat ccc cac gac cca cag gtg atc 384
 Glu Ala Gln Lys Thr Leu Phe Leu Asp Pro His Asp Pro Gln Val Ile
 115 120 125

gcc gac gcc caa cgc aac ggc atc ccg cac tcc tgg ctc gaa gct gcg 432
 Ala Asp Ala Gln Arg Asn Gly Ile Pro His Ser Trp Leu Glu Ala Ala
 130 135 140

cag aac tct cca att tac gat ctc atc ttc aaa tac gag gtt gcc ctc 480
 Gln Asn Ser Pro Ile Tyr Asp Leu Ile Phe Lys Tyr Glu Val Ala Leu
 145 150 155 160
 ccg ctt cac cct gaa tac cgc acc ttg ccg atg gtt tgg tac att ccg 528
 Pro Leu His Pro Glu Tyr Arg Thr Leu Pro Met Val Trp Tyr Ile Pro
 165 170 175
 cca cta agc ccc atc gtt gat gag gtg acc gcg tcc ggc aac gac ggc 576
 Pro Leu Ser Pro Ile Val Asp Glu Val Thr Ala Ser Gly Asn Asp Gly
 180 185 190
 gaa gac cac aag atc ctg ctc acc gcg ctg tcc acc atg cgc atc ccg 624
 Glu Asp His Lys Ile Leu Leu Thr Ala Leu Ser Thr Met Arg Ile Pro
 195 200 205
 ctg gaa tac ctg gct gga ttg ttc act gcc ggt gat acc agg ccg gtg 672
 Leu Glu Tyr Leu Ala Gly Leu Phe Thr Ala Gly Asp Thr Arg Pro Val
 210 215 220
 gaa aaa tcc ctc cga cgc cta gcc gcc atg cga tca tat atg cgc gat 720
 Glu Lys Ser Leu Arg Arg Leu Ala Ala Met Arg Ser Tyr Met Arg Asp
 225 230 235 240
 atc agt ttg ggc cgc gaa cct cag gaa gaa atc gca gag gct gtc gga 768
 Ile Ser Leu Gly Arg Glu Pro Gln Glu Glu Ile Ala Glu Ala Val Gly
 245 250 255
 atg acc ggc aag gtg gtg cag gaa atg tat cgc atc ctg gcc att gcc 816
 Met Thr Gly Lys Val Val Gln Glu Met Tyr Arg Ile Leu Ala Ile Ala
 260 265 270
 aag tat gac gat cgc tat gtc atc ccc acc gcc tcc cct gag acc ccg 864
 Lys Tyr Asp Asp Arg Tyr Val Ile Pro Thr Ala Ser Pro Glu Thr Pro
 275 280 285
 cgc gga att tct tcc ctg gat cct ttc ggc gat gtc gat cca gcc cga 912
 Arg Gly Ile Ser Ser Leu Asp Pro Phe Gly Asp Val Asp Pro Ala Arg
 290 295 300
 gcc acc gag cag ctc aac atc ggt ttg ggc gaa ggc gct cca gag gcc 960
 Ala Thr Glu Gln Leu Asn Ile Gly Leu Gly Glu Gly Ala Pro Glu Ala
 305 310 315 320
 tgt ggc acg gga gct ccc agc ggc aag gtg agt ctg acc tcg tgg aac 1008
 Cys Gly Thr Gly Ala Pro Ser Gly Lys Val Ser Leu Thr Ser Trp Asn
 325 330 335
 gtt ggc gaa cgc ccc gct gcg atg ttc cca cca agg aag gac 1050
 Val Gly Glu Arg Pro Ala Ala Met Phe Pro Pro Arg Lys Asp
 340 345 350
 taggcggatg cgacccata ctg 1073

<210> 290

<211> 350

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Arg Ile Cys Glu His Cys Leu Asn Pro Thr Cys Val Ser Ser Cys Pro
 1 5 10 15
 Ser Gly Ala Met Tyr Lys Arg Ala Glu Asp Gly Ile Val Leu Val Asp
 20 25 30
 Gln Asp Gln Cys Arg Gly Trp Arg Met Cys Val Ser Gly Cys Pro Tyr
 35 40 45
 Lys Lys Val Tyr Phe Asn His Lys Ser Gly Lys Ala Glu Lys Cys Thr
 50 55 60
 Leu Cys Tyr Pro Arg Leu Glu Val Gly Gln Pro Thr Val Cys Ser Glu
 65 70 75 80
 Thr Cys Val Gly Arg Leu Arg Tyr Leu Gly Val Leu Leu Tyr Asp Ala
 85 90 95
 Asp Arg Val Ala Glu Val Ala Ala Thr Pro Asp Glu Lys Asp Leu Phe
 100 105 110
 Glu Ala Gln Lys Thr Leu Phe Leu Asp Pro His Asp Pro Gln Val Ile
 115 120 125
 Ala Asp Ala Gln Arg Asn Gly Ile Pro His Ser Trp Leu Glu Ala Ala
 130 135 140
 Gln Asn Ser Pro Ile Tyr Asp Leu Ile Phe Lys Tyr Glu Val Ala Leu
 145 150 155 160
 Pro Leu His Pro Glu Tyr Arg Thr Leu Pro Met Val Trp Tyr Ile Pro
 165 170 175
 Pro Leu Ser Pro Ile Val Asp Glu Val Thr Ala Ser Gly Asn Asp Gly
 180 185 190
 Glu Asp His Lys Ile Leu Leu Thr Ala Leu Ser Thr Met Arg Ile Pro
 195 200 205
 Leu Glu Tyr Leu Ala Gly Leu Phe Thr Ala Gly Asp Thr Arg Pro Val
 210 215 220
 Glu Lys Ser Leu Arg Arg Leu Ala Ala Met Arg Ser Tyr Met Arg Asp
 225 230 235 240
 Ile Ser Leu Gly Arg Glu Pro Gln Glu Glu Ile Ala Glu Ala Val Gly
 245 250 255
 Met Thr Gly Lys Val Val Gln Glu Met Tyr Arg Ile Leu Ala Ile Ala
 260 265 270
 Lys Tyr Asp Asp Arg Tyr Val Ile Pro Thr Ala Ser Pro Glu Thr Pro
 275 280 285
 Arg Gly Ile Ser Ser Leu Asp Pro Phe Gly Asp Val Asp Pro Ala Arg
 290 295 300
 Ala Thr Glu Gln Leu Asn Ile Gly Leu Gly Glu Gly Ala Pro Glu Ala
 305 310 315 320
 Cys Gly Thr Gly Ala Pro Ser Gly Lys Val Ser Leu Thr Ser Trp Asn

325

330

335

Val Gly Glu Arg Pro Ala Ala Met Phe Pro Pro Arg Lys Asp
 340 345 350

<210> 291
 <211> 900
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(877)
 <223> RXA02016

<400> 291
 acatggagct catccgcagc ggtccaccag cagaaatggt gggcatcggc acgcctctac 60
 cgttccccac ctcacaaccg gacattcact aggacacact atg tca aac ttt gaa 115
 Met Ser Asn Phe Glu
 1 5
 acg ttc ctc tgg gtt gcc tac ccc tgg ctg tgt atc gcc gcc tac atc 163
 Thr Phe Leu Trp Val Ala Tyr Pro Trp Leu Cys Ile Ala Ala Tyr Ile
 10 15 20
 atc ggc att tct tgg cgc tgg cgc gcc gac caa ttc ggt tgg acc acc 211
 Ile Gly Ile Ser Trp Arg Trp Arg Ala Asp Gln Phe Gly Trp Thr Thr
 25 30 35
 cac tcc tcc caa atc tac gaa tcc aaa ctc ctc cgc atc gcc tcc cca 259
 His Ser Ser Gln Ile Tyr Glu Ser Lys Leu Leu Arg Ile Ala Ser Pro
 40 45 50
 ctc ttc cac tgg ggc atg gtg ttc gtg gtg atc ggc cac ctc atg gga 307
 Leu Phe His Trp Gly Met Val Phe Val Val Ile Gly His Leu Met Gly
 55 60 65
 ctt gcc atc ccc aag agc tgg acc caa gct gta gga att tct gac gcc 355
 Leu Ala Ile Pro Lys Ser Trp Thr Gln Ala Val Gly Ile Ser Asp Ala
 70 75 80 85
 gct tac cac ctc atc gcc acc atc cca ggc acc att gcc ggc atc gct 403
 Ala Tyr His Leu Ile Ala Thr Ile Pro Gly Thr Ile Ala Gly Ile Ala
 90 95 100
 gca gtc ctt gga ctc atc ggc ttg att atc cgt cgc gtg atc aac aaa 451
 Ala Val Leu Gly Leu Ile Gly Leu Ile Ile Arg Arg Val Ile Asn Lys
 105 110 115
 acc gtc ttc ctg tcc acc tca cgc tcc gac aaa gtg atg tat gtg cta 499
 Thr Val Phe Leu Ser Thr Ser Arg Ser Asp Lys Val Met Tyr Val Leu
 120 125 130
 ctc ggc gct gca att ttg tcc ggt ttc atc gcc acc gtc tcc acc cag 547
 Leu Gly Ala Ala Ile Leu Ser Gly Phe Ile Ala Thr Val Ser Thr Gln
 135 140 145
 gtc ttc ggc ggc gca cac ggc tac gac tac cgc gaa acc atc tcc cca 595
 Val Phe Gly Gly Ala His Gly Tyr Asp Tyr Arg Glu Thr Ile Ser Pro

150	155	160	165	
tgg gtg cgc caa ctg ctc atc ttc aac gct	caa cca gag ctc atg gct	643		
Trp Val Arg Gln Leu Leu Ile Phe Asn Ala Gln Pro Glu Leu Met Ala				
170	175	180		
gat gtc cct tgg gaa ttc aag gtc cac atc gtc gct gga ttc acc ctc	691			
Asp Val Pro Trp Glu Phe Lys Val His Ile Val Ala Gly Phe Thr Leu				
185	190	195		
atc gca ctg tgg cca ttc acc cgc cta gtc cac gcg ttc tcc gca cca	739			
Ile Ala Leu Trp Pro Phe Thr Arg Leu Val His Ala Phe Ser Ala Pro				
200	205	210		
gtt gga tac gtc acc cgc ccc tac gtg gtc tat cgc acc cgc gac acc	787			
Val Gly Tyr Val Thr Arg Pro Tyr Val Val Tyr Arg Thr Arg Asp Thr				
215	220	225		
acc tct gaa ccg gca cgc caa aac gtc gcc tgg gaa ccg atc cgc tcg	835			
Thr Ser Glu Pro Ala Arg Gln Asn Val Ala Trp Glu Pro Ile Arg Ser				
230	235	240	245	
gtc aaa aat cag ctc gac aat gac tcg aaa tgg cac ggc gcc	877			
Val Lys Asn Gln Leu Asp Asn Asp Ser Lys Trp His Gly Ala				
250	255			
taaattcctc acaagccccc tag	900			
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<211> 259				
<212> PRT				
<213> Corynebacterium glutamicum				
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Ile Ala Ala Tyr Ile Ile Gly Ile Ser Trp Arg Trp Arg Ala Asp Gln				
20	25	30		
Phe Gly Trp Thr Thr His Ser Ser Gln Ile Tyr Glu Ser Lys Leu Leu				
35	40	45		
Arg Ile Ala Ser Pro Leu Phe His Trp Gly Met Val Phe Val Val Ile				
50	55	60		
Gly His Leu Met Gly Leu Ala Ile Pro Lys Ser Trp Thr Gln Ala Val				
65	70	75	80	
Gly Ile Ser Asp Ala Ala Tyr His Leu Ile Ala Thr Ile Pro Gly Thr				
85	90	95		
Ile Ala Gly Ile Ala Ala Val Leu Gly Leu Ile Gly Leu Ile Ile Arg				
100	105	110		
Arg Val Ile Asn Lys Thr Val Phe Leu Ser Thr Ser Arg Ser Asp Lys				
115	120	125		
Val Met Tyr Val Leu Leu Gly Ala Ala Ile Leu Ser Gly Phe Ile Ala				
130	135	140		

Thr Val Ser Thr Gln Val Phe Gly Gly Ala His Gly Tyr Asp Tyr Arg
 145 150 155 160
 Glu Thr Ile Ser Pro Trp Val Arg Gln Leu Leu Ile Phe Asn Ala Gln
 165 170 175
 Pro Glu Leu Met Ala Asp Val Pro Trp Glu Phe Lys Val His Ile Val
 180 185 190
 Ala Gly Phe Thr Leu Ile Ala Leu Trp Pro Phe Thr Arg Leu Val His
 195 200 205
 Ala Phe Ser Ala Pro Val Gly Tyr Val Thr Arg Pro Tyr Val Val Tyr
 210 215 220
 Arg Thr Arg Asp Thr Thr Ser Glu Pro Ala Arg Gln Asn Val Ala Trp
 225 230 235 240
 Glu Pro Ile Arg Ser Val Lys Asn Gln Leu Asp Asn Asp Ser Lys Trp
 245 250 255
 His Gly Ala

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 <212> DNA
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 <223> RXA00471

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 Met Val Asp Val Phe
 1 5
 ttg gtc gat gac cac tcc gtg ttt cgc tcc ggc gtc aaa gca gaa cta 163
 Leu Val Asp Asp His Ser Val Phe Arg Ser Gly Val Lys Ala Glu Leu
 10 15 20
 ggc aac gcc gtc aca gta gtc ggc gaa gca ggg acg gtg gcc gac gcc 211
 Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly Thr Val Ala Asp Ala
 25 30 35
 gta gcc ggc atc aag gca agc aaa cca gag gta gtg ctt ctc gac gtc 259
 Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val Val Leu Leu Asp Val
 40 45 50
 cac atg ccc gac ggc ggc ggc ctc gca gtg ctc cag cag atc aac gac 307
 His Met Pro Asp Gly Gly Glu Leu Ala Val Leu Gln Gln Ile Asn Asp
 55 60 65
 tcc gat gtg gac acc att ttc ttg gca ctc agt gtc tct gat gct gcg 355
 Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser Val Ser Asp Ala Ala

70	75	80	85	
gaa gat gtc atc gcc atc atc cgt ggc ggt gcc agg gga tac gtg acc				403
Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala Arg Gly Tyr Val Thr				
	90	95	100	
aaa tca atc tcc ggt gaa gaa ctc atc gaa gcc atc aac cgc gtg aaa				451
Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala Ile Asn Arg Val Lys				
	105	110	115	
tcc ggc gac gca ttc ttc tca cca cgc ctg gca ggc ttt gtc ctc gac				499
Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala Gly Phe Val Leu Asp				
	120	125	130	
gcc ttc gcc gcc ccc gat tcc gca gct ggc gca ggc att gtc gac gca				547
Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala Gly Ile Val Asp Ala				
	135	140	145	
ccc gaa aaa gac gcc gcc gta gaa tcc gga aaa atc ctc gac gac cca				595
Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys Ile Leu Asp Asp Pro				
	150	155	160	165
gtt gtc gac gcc ctc acc cgc cgc gaa ctc gaa gtc ctc cgc cta cta				643
Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu Val Leu Arg Leu Leu				
	170	175	180	
gcc cgc ggc tac acc tac aaa gaa atc ggc aaa gaa ctg ttc att tcc				691
Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys Glu Leu Phe Ile Ser				
	185	190	195	
gtc aaa acc gtg gaa acc cac gcc tca aac att ctg cgg aaa acc caa				739
Val Lys Thr Val Glu Thr His Ala Ser Asn Ile Leu Arg Lys Thr Gln				
	200	205	210	
caa tcc aac cgc cac gcg ttg acc cgg tgg gct cac tcg agg gat ctt				787
Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala His Ser Arg Asp Leu				
	215	220	225	
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Asp				
230				
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<400> 294				
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	20	25	30	
Thr Val Ala Asp Ala Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val				
	35	40	45	
Val Leu Leu Asp Val His Met Pro Asp Gly Gly Gly Leu Ala Val Leu				
	50	55	60	

Gln Gln Ile Asn Asp Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser
 65 70 75 80
 Val Ser Asp Ala Ala Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala
 85 90 95
 Arg Gly Tyr Val Thr Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala
 100 105 110
 Ile Asn Arg Val Lys Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala
 115 120 125
 Gly Phe Val Leu Asp Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala
 130 135 140
 Gly Ile Val Asp Ala Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys
 145 150 155 160
 Ile Leu Asp Asp Pro Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu
 165 170 175
 Val Leu Arg Leu Leu Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys
 180 185 190
 Glu Leu Phe Ile Ser Val Lys Thr Val Glu Thr His Ala Ser Asn Ile
 195 200 205
 Leu Arg Lys Thr Gln Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala
 210 215 220
 His Ser Arg Asp Leu Asp
 225 230

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 <223> RXA00133

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 aatttgaagg tggataccca gcggattaaa gatgatgaag atg cta ttc gtt cgg 115
 Met Leu Phe Val Arg
 1 5
 cgg ctg aca tcg ctg aaa acc gca aca ggc atc cca gtc acc atg ttc 163
 Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile Pro Val Thr Met Phe
 10 15 20
 gcc act gtg ttg cag gac aat cgc ctg caa att act cag tgg gtt ggg 211
 Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile Thr Gln Trp Val Gly
 25 30 35
 ttg cgt acc ccg gct ctg cag aat ctg gtc att gaa cca ggt gtg ggc 259
 Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile Glu Pro Gly Val Gly

40	45	50	
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tac acc agg gca aat gtc att tca cat gag aag gat tcc gcg att cag Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys Asp Ser Ala Ile Gln 70 75 80 85			355
gat gag ggc ctt cat tcc att gtc gca gtt ccc gtg atc gtg cac cgc Asp. Glu Gly Leu His Ser Ile Val Ala Val Pro Val Ile Val His Arg 90 95 100			403
gaa att cgt ggc gtt ttg tat gtt ggc gtt cac tct gcg gtg cgt ctc Glu Ile Arg Gly Val Leu Tyr Val Gly Val His Ser Ala Val Arg Leu 105 110 115			451
ggc gac act gtt att gaa gaa gtc acc atg act gcg cgc acg ttg gaa Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr Ala Arg Thr Leu Glu 120 125 130			499
caa aac ctg gcg atc aac tcc gcg ctt cgc cgc aat ggc gtt cct gat Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg Asn Gly Val Pro Asp 135 140 145			547
ggt cgc ggt tcc ctc aaa gct aac cgc gtg atg aat ggg gcg gag tgg Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met Asn Gly Ala Glu Trp 150 155 160 165			595
gag cag gtt cgt tcc act cat tcc aag ctg cgc atg ctg gca aat cgt Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg Met Leu Ala Asn Arg 170 175 180			643
gtg acc gat gag gat ctg cgc cgc gat ttg gaa gag ctt tgc gat cag Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu Glu Leu Cys Asp Gln 185 190 195			691
atg gtc acc cca gtc cgc atc aag cag acc acc aag ctg tcc gcg cgt Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr Lys Leu Ser Ala Arg 200 205 210			739
gag ttg gac gtg ctg gct tgt gtc gcg ctc ggt cac acc aac gtc gaa Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly His Thr Asn Val Glu 215 220 225			787
gct gct gaa gag atg ggc atc ggc gcg gaa acc gtc aag agc tac ctg Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr Val Lys Ser Tyr Leu 230 235 240 245			835
cgc tcg gtc atg cgc aag ctc ggc gcc cac acg cgc tac gag gca gtc Arg Ser Val Met Arg Lys Leu Gly Ala His Thr Arg Tyr Glu Ala Val 250 255 260			883
aac gca gca cgc cgg atc ggc gca ctg cct taaaaagatt ttgctttacg Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro 265 270			933
acg			936

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Thr Gln Trp Val Gly Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile
 35 40 45
 Glu Pro Gly Val Gly Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro
 50 55 60
 Val Gly Val Ser Asp Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys
 65 70 75 80
 Asp Ser Ala Ile Gln Asp Glu Gly Leu His Ser Ile Val Ala Val Pro
 85 90 95
 Val Ile Val His Arg Glu Ile Arg Gly Val Leu Tyr Val Gly Val His
 100 105 110
 Ser Ala Val Arg Leu Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr
 115 120 125
 Ala Arg Thr Leu Glu Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg
 130 135 140
 Asn Gly Val Pro Asp Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met
 145 150 155 160
 Asn Gly Ala Glu Trp Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg
 165 170 175
 Met Leu Ala Asn Arg Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu
 180 185 190
 Glu Leu Cys Asp Gln Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr
 195 200 205
 Lys Leu Ser Ala Arg Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly
 210 215 220
 His Thr Asn Val Glu Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr
 225 230 235 240
 Val Lys Ser Tyr Leu Arg Ser Val Met Arg Lys Leu Gly Ala His Thr
 245 250 255
 Arg Tyr Glu Ala Val Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro
 260 265 270

<210> 297
 <211> 759
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXA00650

<400> 297

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cgaaacgaag tgcgccattg ggaaggacct agttcaaaca atg att cgc gtg ctg 115
                                   Met Ile Arg Val Leu
                                   1       5

ctt gct gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg 163
Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu
              10              15              20

gaa agc gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa 211
Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu
              25              30              35

ggt gcg gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg 259
Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met
              40              45              50

gac ctc cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc 307
Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly
              55              60              65

gca gac gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa 355
Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys
              70              75              80              85

gtc ctg gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca 403
Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala
              90              95              100

atc gaa gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc 451
Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser
              105              110              115

gaa ctc ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg 499
Glu Leu Leu Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu
              120              125              130

tca ccc atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa 547
Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys
              135              140              145

acc tca ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt 595
Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly
              150              155              160              165

gga tcc tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc 643
Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala
              170              175              180

acg gtg aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg 691
Thr Val Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg
              185              190              195

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tca cgt acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg 736
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tagcgggggt tgctgcaagg ctt 759

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 <213> Corynebacterium glutamicum

<400> 298
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 20 25 30
 Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile
 35 40 45
 Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr
 50 55 60
 Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile
 65 70 75 80
 Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr
 85 90 95
 Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys
 100 105 110
 Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu
 115 120 125
 Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg
 130 135 140
 Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu
 145 150 155 160
 Lys Leu Val Ala Gly Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu
 165 170 175
 Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp
 180 185 190
 Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu
 195 200 205
 Gln Gly Leu Leu
 210

<210> 299
 <211> 655
 <212> DNA
 <213> Corynebacterium glutamicum

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<221> CDS

<222> (24)..(632)

<223> RXA01189

<400> 299

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gcc ctg atc gca agc tcc ctg gca acc ttg ctc agc ttg gaa ccc gat 101
Ala Leu Ile Ala Ser Ser Leu Ala Thr Leu Leu Ser Leu Glu Pro Asp
                  15                      20                      25

tta gac gtc cga cct acc gca gga tcc ggt gaa gaa ctc att gaa acg 149
Leu Asp Val Arg Pro Thr Ala Gly Ser Gly Glu Glu Leu Ile Glu Thr
                  30                      35                      40

tgg gcg gat cca agc aac cga acc gat gta tgc gtc ctt gac ctt caa 197
Trp Ala Asp Pro Ser Asn Arg Thr Asp Val Cys Val Leu Asp Leu Gln
                  45                      50                      55

ctc gga ggc atc gac ggc atc gac acc gcc acc cgg ctc atg gaa acc 245
Leu Gly Gly Ile Asp Gly Ile Asp Thr Ala Thr Arg Leu Met Glu Thr
                  60                      65                      70

acc cca gat ttg gcc gtg ctc atc gtg acc agc cac gcc agg ccc cga 293
Thr Pro Asp Leu Ala Val Leu Ile Val Thr Ser His Ala Arg Pro Arg
                  75                      80                      85                      90

caa ctc aaa cgc gcg ctt gca gca ggt gtt tta gga ttc ttg ccc aaa 341
Gln Leu Lys Arg Ala Leu Ala Ala Gly Val Leu Gly Phe Leu Pro Lys
                  95                      100                      105

aca tcc acc gca gat gaa ttc gcc acc gca atc cgc acc gtt cac gct 389
Thr Ser Thr Ala Asp Glu Phe Ala Thr Ala Ile Arg Thr Val His Ala
                  110                      115                      120

gga cga cgc tac atc gac ccc gaa cta gcc gcc atg acg atc agc gcc 437
Gly Arg Arg Tyr Ile Asp Pro Glu Leu Ala Ala Met Thr Ile Ser Ala
                  125                      130                      135

ggt gaa tcc cca tta acc aac cgt gaa gaa gaa gtc ctc gaa cta gca 485
Gly Glu Ser Pro Leu Thr Asn Arg Glu Glu Glu Val Leu Glu Leu Ala
                  140                      145                      150

ggc caa gga cta agc gcc gaa gaa att gcg gtg gca gcg cac ctc gcg 533
Gly Gln Gly Leu Ser Ala Glu Glu Ile Ala Val Ala Ala His Leu Ala
                  155                      160                      165                      170

ccg gga acc acc cgc aac tat tta tcc caa gct atg aca aaa gta ggc 581
Pro Gly Thr Thr Arg Asn Tyr Leu Ser Gln Ala Met Thr Lys Val Gly
                  175                      180                      185

gcg cag aat cgc ttt gaa gcg ttc acg cgc gcc agg gaa ttg ggc tgg 629
Ala Gln Asn Arg Phe Glu Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp
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Leu

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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Arg Thr Asp Val Cys Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly
 50 55 60
 Ile Asp Thr Ala Thr Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val
 65 70 75 80
 Leu Ile Val Thr Ser His Ala Arg Pro Arg Gln Leu Lys Arg Ala Leu
 85 90 95
 Ala Ala Gly Val Leu Gly Phe Leu Pro Lys Thr Ser Thr Ala Asp Glu
 100 105 110
 Phe Ala Thr Ala Ile Arg Thr Val His Ala Gly Arg Arg Tyr Ile Asp
 115 120 125
 Pro Glu Leu Ala Ala Met Thr Ile Ser Ala Gly Glu Ser Pro Leu Thr
 130 135 140
 Asn Arg Glu Glu Glu Val Leu Glu Leu Ala Gly Gln Gly Leu Ser Ala
 145 150 155 160
 Glu Glu Ile Ala Val Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn
 165 170 175
 Tyr Leu Ser Gln Ala Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu
 180 185 190
 Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp Leu
 195 200

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 <211> 753
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(730)
 <223> RXA01607

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                                   Val Ile Arg Ile Leu
                                   1 5

ttg gct gat gat cat ccc gtt gtt cgc gca ggc ctt gcc tcc ttg ctg 163
Leu Ala Asp Asp His Pro Val Val Arg Ala Gly Leu Ala Ser Leu Leu
                                   10 15 20

gtg agt gaa gat gat ttt gag ata gtg gac atg gtg ggc acc cca gat 211
Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met Val Gly Thr Pro Asp
                                   25 30 35

gat gcc gtt gcg cgc gcc gcg gaa ggc ggg gtg gat gtg gtg ttg atg 259
Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val Asp Val Val Leu Met
                                   40 45 50

gat ctg cgt ttt ggt gat caa cca ggc atc gag gtc gcc ggc ggg gta 307
Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu Val Ala Gly Gly Val
                                   55 60 65

gag gca acg cgt cgc atc cgt gcg ctg gac aac ccg cca cag gta ctg 355
Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn Pro Pro Gln Val Leu
                                   70 75 80 85

gtg gtg acc aac tac tcc aca gac ggc gat gtg gtg ggc gca gta tct 403
Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val Val Gly Ala Val Ser
                                   90 95 100

gct ggt gcc gtg ggg tat ttg ctc aaa gat agc tcc cca gaa gat ctc 451
Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser Ser Pro Glu Asp Leu
                                   105 110 115

att gcc ggt gtt cgc gat gcc gcg cgg gga gaa tca gtg ctt tca aag 499
Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu Ser Val Leu Ser Lys
                                   120 125 130

cag gtc gcc agc aag atc atg ggg cgg atg aac aac ccc atg act gct 547
Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn Asn Pro Met Thr Ala
                                   135 140 145

ctc agt gcc aga gaa att gaa gtg ctg tcc ttg gtg gcg caa ggg caa 595
Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu Val Ala Gln Gly Gln
                                   150 155 160 165

agc aat aga gaa atc ggc aag aaa ctt ttc ctc act gag gcc acg gtg 643
Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu Thr Glu Ala Thr Val
                                   170 175 180

aaa agt cac atg ggg cat gtg ttc aac aag ctg gat gtc acc tct aga 691
Lys Ser His Met Gly His Val Phe Asn Lys Leu Asp Val Thr Ser Arg
                                   185 190 195

aca gct gcg gta gct gaa gcc aga cag cgc gga att atc tagacgcaca 740
Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly Ile Ile
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cgtgttggtgta acc 753

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<210> 302

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 302

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 20 25 30

Val Gly Thr Pro Asp Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val
 35 40 45

Asp Val Val Leu Met Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu
 50 55 60

Val Ala Gly Gly Val Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn
 65 70 75 80

Pro Pro Gln Val Leu Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val
 85 90 95

Val Gly Ala Val Ser Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser
 100 105 110

Ser Pro Glu Asp Leu Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu
 115 120 125

Ser Val Leu Ser Lys Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn
 130 135 140

Asn Pro Met Thr Ala Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu
 145 150 155 160

Val Ala Gln Gly Gln Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu
 165 170 175

Thr Glu Ala Thr Val Lys Ser His Met Gly His Val Phe Asn Lys Leu
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Asp Val Thr Ser Arg Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly
 195 200 205

Ile Ile
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<210> 303

<211> 1392

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1369)

<223> RXN00470

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	Met Gly Glu Ser Pro	
	1 5	
gaa aag gtg gcg ttc agg gtc ttc cct gat ggt ttg gtg tcg cag ggg	163	
Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly Leu Val Ser Gln Gly		
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cat gac atg atc gaa gat atg agt aac aca cct gcg cct tat acc ccg	211	
His Asp Met Ile Glu Asp Met Ser Asn Thr Pro Ala Pro Tyr Thr Pro		
25 30 35		
cag cct gcg ggg caa gcg gtg cct tta tat ccc acg ttt acc cgg tca	259	
Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro Thr Phe Thr Arg Ser		
40 45 50		
aga gat ggt cgg gtt gtt gcg ggt gtc gca tcg ggg ctg gca aag cat	307	
Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser Gly Leu Ala Lys His		
55 60 65		
ctt aat gtg tcg gtg ttt tgg gtt cgt gcg ctg ctg att ttt gcg gcg	355	
Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu Leu Ile Phe Ala Ala		
70 75 80 85		
ttg ctg agc ggt gcg ggt ctt ttt gcg tat gcc ttg att tgg att ttt	403	
Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala Leu Ile Trp Ile Phe		
90 95 100		
acg cgc att gag aaa aag ggg agt ggg gag gcg tcg aca agc aag cgc	451	
Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala Ser Thr Ser Lys Arg		
105 110 115		
tgg gtg tcg tgg tgc ctg gtg ctg ctc gct atc ggt ggt gct gcg gcg	499	
Trp Val Ser Trp Cys Leu Val Leu Leu Ala Ile Gly Gly Ala Ala Ala		
120 125 130		
tcg gtg atg ctg agc acc ggc ttc gcg gtg ggc acg ttg gtg ccc atc	547	
Ser Val Met Leu Ser Thr Gly Phe Ala Val Gly Thr Leu Val Pro Ile		
135 140 145		
ggc gtg gtc ggt gtg ggc ctg ttg atg gtg tgg ctg gcg tat gac cgc	595	
Gly Val Val Gly Val Gly Leu Leu Met Val Trp Leu Ala Tyr Asp Arg		
150 155 160 165		
ggg gtg gaa tcc ggc ccg aat ctg ctg att att gcc acc ggc ggt gtg	643	
Gly Val Glu Ser Gly Pro Asn Leu Leu Ile Ile Ala Thr Gly Gly Val		
170 175 180		
ttg atg ctg gtg gcg atc gtg ctg atc gtg atg aat tgg aac acc cag	691	
Leu Met Leu Val Ala Ile Val Leu Ile Val Met Asn Trp Asn Thr Gln		
185 190 195		
gac ggc ttc gtc atg gcg ctg gtg gcc gtg gtg ctc acg ctg gtg ggt	739	
Asp Gly Phe Val Met Ala Leu Val Ala Val Val Leu Thr Leu Val Gly		
200 205 210		
gtg gct gcg ctg ggc gtt ccg ctg tgg gtg cgg atg tgg gat cag ctg	787	
Val Ala Ala Leu Gly Val Pro Leu Trp Val Arg Met Trp Asp Gln Leu		
215 220 225		
ggc gag gag cgc gcg gaa aaa gcc gca gct gct gag cgc gca gat att	835	

Gly Glu Glu Arg Ala Glu Lys Ala Ala Ala Ala Glu Arg Ala Asp Ile
 230 235 240 245
 gct tcc cgc ctg cat gat tcg gta ctg cag acc ttg gcg ctg att caa 883
 Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr Leu Ala Leu Ile Gln
 250 255 260
 aag cgt gcc gac gac ccc gcc gaa gtc gcc cgc ctg gcc cgc ggg cag 931
 Lys Arg Ala Asp Asp Pro Ala Glu Val Ala Arg Leu Ala Arg Gly Gln
 265 270 275
 gaa cgc gag ctg cgt caa tgg ctg ttt gat tcc caa gat aaa aca cct 979
 Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser Gln Asp Lys Thr Pro
 280 285 290
 caa aca acc ggc act gtc ttt act gcg ttg gag cgc gcc tgc ggt gaa 1027
 Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu Arg Ala Cys Gly Glu
 295 300 305
 gtc gag gat att tac gct ctg cgt atc gtg cct gtg acc gtg gga acc 1075
 Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro Val Thr Val Gly Thr
 310 315 320 325
 gat gaa gcg ctg act gag aaa acg cag gca gcg gtg atg gca gtc cgc 1123
 Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Ala Val Met Ala Val Arg
 330 335 340
 gaa gca ctc gtg aac gtg gcc aag cat gcc ggc gtg gaa acc gcc gat 1171
 Glu Ala Leu Val Asn Val Ala Lys His Ala Gly Val Glu Thr Ala Asp
 345 350 355
 gtg tac gcc gaa att atg ctc ggc gaa ctg aac att ttc gtc cgc gac 1219
 Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn Ile Phe Val Arg Asp
 360 365 370
 cgc ggt gca gga ttc gac ccc gac aac atc ccc gac ggg cac cac ggg 1267
 Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro Asp Gly His His Gly
 375 380 385
 ctc gcc gaa tcc gtc caa ggc cgc gtc gaa cga gcc ggc gga aaa gta 1315
 Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg Ala Gly Gly Lys Val
 390 395 400 405
 cgc atc aaa tct gaa atc ggc gaa ggc acc gaa gtg gca atc acc atg 1363
 Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu Val Ala Ile Thr Met
 410 415 420
 gat gtg tagttggtcg tacgcgcgtg tct 1392
 Asp Val

<210> 304

<211> 423

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 304

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 Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro
 35 40 45
 Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser
 50 55 60
 Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu
 65 70 75 80
 Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala
 85 90 95
 Leu Ile Trp Ile Phe Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala
 100 105 110
 Ser Thr Ser Lys Arg Trp Val Ser Trp Cys Leu Val Leu Leu Ala Ile
 115 120 125
 Gly Gly Ala Ala Ala Ser Val Met Leu Ser Thr Gly Phe Ala Val Gly
 130 135 140
 Thr Leu Val Pro Ile Gly Val Val Gly Val Gly Leu Leu Met Val Trp
 145 150 155 160
 Leu Ala Tyr Asp Arg Gly Val Glu Ser Gly Pro Asn Leu Leu Ile Ile
 165 170 175
 Ala Thr Gly Gly Val Leu Met Leu Val Ala Ile Val Leu Ile Val Met
 180 185 190
 Asn Trp Asn Thr Gln Asp Gly Phe Val Met Ala Leu Val Ala Val Val
 195 200 205
 Leu Thr Leu Val Gly Val Ala Ala Leu Gly Val Pro Leu Trp Val Arg
 210 215 220
 Met Trp Asp Gln Leu Gly Glu Glu Arg Ala Glu Lys Ala Ala Ala Ala
 225 230 235 240
 Glu Arg Ala Asp Ile Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr
 245 250 255
 Leu Ala Leu Ile Gln Lys Arg Ala Asp Asp Pro Ala Glu Val Ala Arg
 260 265 270
 Leu Ala Arg Gly Gln Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser
 275 280 285
 Gln Asp Lys Thr Pro Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu
 290 295 300
 Arg Ala Cys Gly Glu Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro
 305 310 315 320
 Val Thr Val Gly Thr Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Ala
 325 330 335
 Val Met Ala Val Arg Glu Ala Leu Val Asn Val Ala Lys His Ala Gly

340 345 350
 Val Glu Thr Ala Asp Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn
 355 360 365
 Ile Phe Val Arg Asp Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro
 370 375 380
 Asp Gly His His Gly Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg
 385 390 395 400
 Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu
 405 410 415
 Val Ala Ile Thr Met Asp Val
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 <210> 305
 <211> 1323
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(1300)
 <223> FRXA00470

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 caggggtcttc cctgatggtt tgggtgcgca ggggcatgac atg atc gaa gat atg 115
 Met Ile Glu Asp Met
 1 5
 agt aac aca cct gcg cct tat acc ccg cag cct gcg ggg caa gcg gtg 163
 Ser Asn Thr Pro Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val
 10 15 20
 cct tta tat ccc acg ttt acc cgg tca aga gat ggt cgg gtt gtt gcg 211
 Pro Leu Tyr Pro Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala
 25 30 35
 ggt gtc gca tcg ggg ctg gca aag cat ctt aat gtg tcg gtg ttt tgg 259
 Gly Val Ala Ser Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp
 40 45 50
 gtt cgt gcg ctg ctg att ttt gcg gcg ttg ctg agc ggt gcg ggt ctt 307
 Val Arg Ala Leu Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu
 55 60 65
 ttt gcg tat gcc ttg att tgg att ttt acg cgc att gag aaa aag ggg 355
 Phe Ala Tyr Ala Leu Ile Trp Ile Phe Thr Arg Ile Glu Lys Lys Gly
 70 75 80 85
 agt ggg gag gcg tcg aca agc aag cgc tgg gtg tcg tgg tgc ctg gtg 403
 Ser Gly Glu Ala Ser Thr Ser Lys Arg Trp Val Ser Trp Cys Leu Val
 90 95 100
 ctg ctc gct atc ggt ggt gct gcg gcg tcg gtg atg ctg agc acc ggc 451
 Leu Leu Ala Ile Gly Gly Ala Ala Ala Ser Val Met Leu Ser Thr Gly

105	110	115	
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ctg ctg att att gcc acc ggc ggt gtg ttg atg ctg gtg gcg atc gtg Leu Leu Ile Ile Ala Thr Gly Gly Val Leu Met Leu Val Ala Ile Val 150 155 160 165			595
ctg atc gtg atg aat tgg aac acc cag gac ggc ttc gtc atg gcg ctg Leu Ile Val Met Asn Trp Asn Thr Gln Asp Gly Phe Val Met Ala Leu 170 175 180			643
gtg gcc gtg gtg ctc acg ctg gtg ggt gtg gct gcg ctg ggc gtt ccg Val Ala Val Val Leu Thr Leu Val Gly Val Ala Ala Leu Gly Val Pro 185 190 195			691
ctg tgg gtg cgg atg tgg gat cag ctg ggc gag gag cgc gcg gaa aaa Leu Trp Val Arg Met Trp Asp Gln Leu Gly Glu Glu Arg Ala Glu Lys 200 205 210			739
gcc gca gct gct gag cgc gca gat att gct tcc cgc ctg cat gat tcg Ala Ala Ala Ala Glu Arg Ala Asp Ile Ala Ser Arg Leu His Asp Ser 215 220 225			787
gta ctg cag acc ttg gcg ctg att caa aag cgt gcc gac gac ccc gcc Val Leu Gln Thr Leu Ala Leu Ile Gln Lys Arg Ala Asp Asp Pro Ala 230 235 240 245			835
gaa gtc gcc cgc ctg gcc cgc ggg cag gaa cgc gag ctg cgt caa tgg Glu Val Ala Arg Leu Ala Arg Gly Gln Glu Arg Glu Leu Arg Gln Trp 250 255 260			883
ctg ttt gat tcc caa gat aaa aca cct caa aca acc ggc act gtc ttt Leu Phe Asp Ser Gln Asp Lys Thr Pro Gln Thr Thr Gly Thr Val Phe 265 270 275			931
act gcg ttg gag cgc gcc tgc ggt gaa gtc gag gat att tac gct ctg Thr Ala Leu Glu Arg Ala Cys Gly Glu Val Glu Asp Ile Tyr Ala Leu 280 285 290			979
cgt atc gtg cct gtg acc gtg gga acc gat gaa gcg ctg act gag aaa Arg Ile Val Pro Val Thr Val Gly Thr Asp Glu Ala Leu Thr Glu Lys 295 300 305			1027
acg cag gca gcg gtg atg gca gtc cgc gaa gca ctc gtg aac gtg gcc Thr Gln Ala Ala Val Met Ala Val Arg Glu Ala Leu Val Asn Val Ala 310 315 320 325			1075
aag cat gcc ggc gtg gaa acc gcc gat gtg tac gcc gaa att atg ctc Lys His Ala Gly Val Glu Thr Ala Asp Val Tyr Ala Glu Ile Met Leu 330 335 340			1123
ggc gaa ctg aac att ttc gtc cgc gac cgc ggt gca gga ttc gac ccc Gly Glu Leu Asn Ile Phe Val Arg Asp Arg Gly Ala Gly Phe Asp Pro 345 350 355			1171

gac aac atc ccc gac ggg cac cac ggg ctc gcc gaa tcc gtc caa ggc 1219
 Asp Asn Ile Pro Asp Gly His His Gly Leu Ala Glu Ser Val Gln Gly
 360 365 370

cgc gtc gaa cga gcc ggc gga aaa gta cgc atc aaa tct gaa atc ggc 1267
 Arg Val Glu Arg Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly
 375 380 385

gaa ggc acc gaa gtg gca atc acc atg gat gtg tagttggtcg tacgcgcgtg 1320
 Glu Gly Thr Glu Val Ala Ile Thr Met Asp Val
 390 395 400

tct 1323

<210> 306
 <211> 400
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 306
 Met Ile Glu Asp Met Ser Asn Thr Pro Ala Pro Tyr Thr Pro Gln Pro
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 20 25 30
 Gly Arg Val Val Ala Gly Val Ala Ser Gly Leu Ala Lys His Leu Asn
 35 40 45
 Val Ser Val Phe Trp Val Arg Ala Leu Leu Ile Phe Ala Ala Leu Leu
 50 55 60
 Ser Gly Ala Gly Leu Phe Ala Tyr Ala Leu Ile Trp Ile Phe Thr Arg
 65 70 75 80
 Ile Glu Lys Lys Gly Ser Gly Glu Ala Ser Thr Ser Lys Arg Trp Val
 85 90 95
 Ser Trp Cys Leu Val Leu Leu Ala Ile Gly Gly Ala Ala Ala Ser Val
 100 105 110
 Met Leu Ser Thr Gly Phe Ala Val Gly Thr Leu Val Pro Ile Gly Val
 115 120 125
 Val Gly Val Gly Leu Leu Met Val Trp Leu Ala Tyr Asp Arg Gly Val
 130 135 140
 Glu Ser Gly Pro Asn Leu Leu Ile Ile Ala Thr Gly Gly Val Leu Met
 145 150 155 160
 Leu Val Ala Ile Val Leu Ile Val Met Asn Trp Asn Thr Gln Asp Gly
 165 170 175
 Phe Val Met Ala Leu Val Ala Val Val Leu Thr Leu Val Gly Val Ala
 180 185 190
 Ala Leu Gly Val Pro Leu Trp Val Arg Met Trp Asp Gln Leu Gly Glu
 195 200 205

Glu Arg Ala Glu Lys Ala Ala Ala Glu Arg Ala Asp Ile Ala Ser
 210 215 220
 Arg Leu His Asp Ser Val Leu Gln Thr Leu Ala Leu Ile Gln Lys Arg
 225 230 235 240
 Ala Asp Asp Pro Ala Glu Val Ala Arg Leu Ala Arg Gly Gln Glu Arg
 245 250 255
 Glu Leu Arg Gln Trp Leu Phe Asp Ser Gln Asp Lys Thr Pro Gln Thr
 260 265 270
 Thr Gly Thr Val Phe Thr Ala Leu Glu Arg Ala Cys Gly Glu Val Glu
 275 280 285
 Asp Ile Tyr Ala Leu Arg Ile Val Pro Val Thr Val Gly Thr Asp Glu
 290 295 300
 Ala Leu Thr Glu Lys Thr Gln Ala Ala Val Met Ala Val Arg Glu Ala
 305 310 315 320
 Leu Val Asn Val Ala Lys His Ala Gly Val Glu Thr Ala Asp Val Tyr
 325 330 335
 Ala Glu Ile Met Leu Gly Glu Leu Asn Ile Phe Val Arg Asp Arg Gly
 340 345 350
 Ala Gly Phe Asp Pro Asp Asn Ile Pro Asp Gly His His Gly Leu Ala
 355 360 365
 Glu Ser Val Gln Gly Arg Val Glu Arg Ala Gly Gly Lys Val Arg Ile
 370 375 380
 Lys Ser Glu Ile Gly Glu Gly Thr Glu Val Ala Ile Thr Met Asp Val
 385 390 395 400

<210> 307

<211> 1119

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1096)

<223> RXA00756

<400> 307

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 Val Asn Ile Asp Val
 1 5

 cag gct tta aaa gcc atc gag tct gaa aaa gga atc cca gtt cca gac 163
 Gln Ala Leu Lys Ala Ile Glu Ser Glu Lys Gly Ile Pro Val Pro Asp
 10 15 20

ttg ctg cgc acc atc gcc tct gca ctt ttg cat tcg tac atg gat aat	211
Leu Leu Arg Thr Ile Ala Ser Ala Leu Leu His Ser Tyr Met Asp Asn	
25 30 35	
cgc gaa act gtt gcg tct gcg aac ctg aaa cca cgc gtg gac atc gat	259
Arg Glu Thr Val Ala Ser Ala Asn Leu Lys Pro Arg Val Asp Ile Asp	
40 45 50	
tcc aca act ggc acg gtc aac gtc atc gtc tca gaa ttc gac gaa aac	307
Ser Thr Thr Gly Thr Val Asn Val Ile Val Ser Glu Phe Asp Glu Asn	
55 60 65	
gga gag ctc gct tcc gaa tac gac gac acc cca tcc aac ttc gga cga	355
Gly Glu Leu Ala Ser Glu Tyr Asp Asp Thr Pro Ser Asn Phe Gly Arg	
70 75 80 85	
gtc agc gcc cgc gct gtt cgc gac gcg atc gtt aag tcc ctg cgc gaa	403
Val Ser Ala Arg Ala Val Arg Asp Ala Ile Val Lys Ser Leu Arg Glu	
90 95 100	
gca gaa gca agc cga gca ttc gat gcg tac gca gat tat gaa ggc acc	451
Ala Glu Ala Ser Arg Ala Phe Asp Ala Tyr Ala Asp Tyr Glu Gly Thr	
105 110 115	
gtt gtg tcc ggc atc gtt caa gca gat gcc cgc gca gct gaa cgc gga	499
Val Val Ser Gly Ile Val Gln Ala Asp Ala Arg Ala Ala Glu Arg Gly	
120 125 130	
atc atc atc gtg cag ctg ggt acc gaa gcg gac aac caa gac ggc gtt	547
Ile Ile Ile Val Gln Leu Gly Thr Glu Ala Asp Asn Gln Asp Gly Val	
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ttg ctc cca gcc gag cag atc cct ggc gaa aag ctc aag cac ggc gac	595
Leu Leu Pro Ala Glu Gln Ile Pro Gly Glu Lys Leu Lys His Gly Asp	
150 155 160 165	
cgc gtc aag tgc ttc gtc gtt ggc gtg ggc aag ggc aac act gac atc	643
Arg Val Lys Cys Phe Val Val Gly Val Gly Lys Gly Asn Thr Asp Ile	
170 175 180	
cag atc aac ctg tct cgt act cac cct gag ctg gtg cgc cga ctg ttt	691
Gln Ile Asn Leu Ser Arg Thr His Pro Glu Leu Val Arg Arg Leu Phe	
185 190 195	
gaa ctg gaa atc cca gaa gtt gct gac gga tcc gtg gaa att gtt gct	739
Glu Leu Glu Ile Pro Glu Val Ala Asp Gly Ser Val Glu Ile Val Ala	
200 205 210	
atc tcc cgc gaa gcc gga cac cgc tcc aag gtt gct gtt caa gcc aag	787
Ile Ser Arg Glu Ala Gly His Arg Ser Lys Val Ala Val Gln Ala Lys	
215 220 225	
gtg aag aac ctc aac gcc aag ggc gct tgc att ggc cca cgt gga cag	835
Val Lys Asn Leu Asn Ala Lys Gly Ala Cys Ile Gly Pro Arg Gly Gln	
230 235 240 245	
cgt gtg tcc aac atc atg cgt gaa ctc ggt gga gaa aaa atc gac atc	883
Arg Val Ser Asn Ile Met Arg Glu Leu Gly Gly Glu Lys Ile Asp Ile	
250 255 260	
atc gat tac tcc gaa gat cca gca acc ttc gtt gga aat gca ctg gca	931

Ile Asp Tyr Ser Glu Asp Pro Ala Thr Phe Val Gly Asn Ala Leu Ala
 265 270 275

cca tcc aag gtt gtc aac gta gag gtc acc gat ctt gaa gct caa acc 979
 Pro Ser Lys Val Val Asn Val Glu Val Thr Asp Leu Glu Ala Gln Thr
 280 285 290

gcg cgc gta act gtc cct gac tac cag ctt tca cta gca atc ggt aaa 1027
 Ala Arg Val Thr Val Pro Asp Tyr Gln Leu Ser Leu Ala Ile Gly Lys
 295 300 305

gaa ggt caa aac gcc cgc ttg gct gcc cgc ctg acc ggc tgg aag atc 1075
 Glu Gly Gln Asn Ala Arg Leu Ala Ala Arg Leu Thr Gly Trp Lys Ile
 310 315 320 325

gac atc cac tct gac atc gat taaaagtcgc ttgaaccggc atg 1119
 Asp Ile His Ser Asp Ile Asp
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<210> 308

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

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 20 25 30

Ser Tyr Met Asp Asn Arg Glu Thr Val Ala Ser Ala Asn Leu Lys Pro
 35 40 45

Arg Val Asp Ile Asp Ser Thr Thr Gly Thr Val Asn Val Ile Val Ser
 50 55 60

Glu Phe Asp Glu Asn Gly Glu Leu Ala Ser Glu Tyr Asp Asp Thr Pro
 65 70 75 80

Ser Asn Phe Gly Arg Val Ser Ala Arg Ala Val Arg Asp Ala Ile Val
 85 90 95

Lys Ser Leu Arg Glu Ala Glu Ala Ser Arg Ala Phe Asp Ala Tyr Ala
 100 105 110

Asp Tyr Glu Gly Thr Val Val Ser Gly Ile Val Gln Ala Asp Ala Arg
 115 120 125

Ala Ala Glu Arg Gly Ile Ile Ile Val Gln Leu Gly Thr Glu Ala Asp
 130 135 140

Asn Gln Asp Gly Val Leu Leu Pro Ala Glu Gln Ile Pro Gly Glu Lys
 145 150 155 160

Leu Lys His Gly Asp Arg Val Lys Cys Phe Val Val Gly Val Gly Lys
 165 170 175

Gly Asn Thr Asp Ile Gln Ile Asn Leu Ser Arg Thr His Pro Glu Leu
 180 185 190

Val Arg Arg Leu Phe Glu Leu Glu Ile Pro Glu Val Ala Asp Gly Ser
 195 200 205

Val Glu Ile Val Ala Ile Ser Arg Glu Ala Gly His Arg Ser Lys Val
 210 215 220

Ala Val Gln Ala Lys Val Lys Asn Leu Asn Ala Lys Gly Ala Cys Ile
 225 230 235 240

Gly Pro Arg Gly Gln Arg Val Ser Asn Ile Met Arg Glu Leu Gly Gly
 245 250 255

Glu Lys Ile Asp Ile Ile Asp Tyr Ser Glu Asp Pro Ala Thr Phe Val
 260 265 270

Gly Asn Ala Leu Ala Pro Ser Lys Val Val Asn Val Glu Val Thr Asp
 275 280 285

Leu Glu Ala Gln Thr Ala Arg Val Thr Val Pro Asp Tyr Gln Leu Ser
 290 295 300

Leu Ala Ile Gly Lys Glu Gly Gln Asn Ala Arg Leu Ala Ala Arg Leu
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Thr Gly Trp Lys Ile Asp Ile His Ser Asp Ile Asp
 325 330

<210> 309
 <211> 834
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(811)
 <223> RXA00139

<400> 309
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 Leu Ile Glu Gln Glu
 1 5

caa aga gaa caa aac gtg agc gag cgt cga caa gat tac aag cga cac 163
 Gln Arg Glu Gln Asn Val Ser Glu Arg Arg Gln Asp Tyr Lys Arg His
 10 15 20

gga tcc cgc tac aag gcg cgc atg cgt gcc gta gac atc cta ttt gaa 211
 Gly Ser Arg Tyr Lys Ala Arg Met Arg Ala Val Asp Ile Leu Phe Glu
 25 30 35

gcg gaa tcc cgc gat gtt gat ccc gtg gcc atc atc gat gac cgc cac 259
 Ala Glu Ser Arg Asp Val Asp Pro Val Ala Ile Ile Asp Asp Arg His
 40 45 50

aag ttg gcg cgc gat acc aac ccc atc gtt gca ccg gta gcg gaa tac 307
 Lys Leu Ala Arg Asp Thr Asn Pro Ile Val Ala Pro Val Ala Glu Tyr
 55 60 65

acc gaa acc atc atc aat ggc gtt gcc gtt gaa ctc gat acc ctc gat 355
 Thr Glu Thr Ile Ile Asn Gly Val Ala Val Glu Leu Asp Thr Leu Asp
 70 75 80 85

gtc ttc ctc gcg gaa cac atc gca gaa acc tgg act ctc gga cga ctc 403
 Val Phe Leu Ala Glu His Ile Ala Glu Thr Trp Thr Leu Gly Arg Leu
 90 95 100

cca tcc gtc gac cgc gca atc ctg cgc gtc gct tcc tgg gaa atg atc 451
 Pro Ser Val Asp Arg Ala Ile Leu Arg Val Ala Ser Trp Glu Met Ile
 105 110 115

tac aac gcc gac gtt cct gtc acc acc gca atc gtt gaa gcc gtg gaa 499
 Tyr Asn Ala Asp Val Pro Val Thr Thr Ala Ile Val Glu Ala Val Glu
 120 125 130

att gcc tcc gaa tac tcc gga gac aaa tcc agt gcc tac atc aac gcg 547
 Ile Ala Ser Glu Tyr Ser Gly Asp Lys Ser Ser Ala Tyr Ile Asn Ala
 135 140 145

aca ctt gac gcc atg gca tca aag gtg gag acc ctc cgc gag cgc gcc 595
 Thr Leu Asp Ala Met Ala Ser Lys Val Glu Thr Leu Arg Glu Arg Ala
 150 155 160 165

gcc aac cca gaa gca gtt ctg gcg gaa gct tcc gaa tct ctc gat gat 643
 Ala Asn Pro Glu Ala Val Leu Ala Glu Ala Ser Glu Ser Leu Asp Asp
 170 175 180

gct ccg gtc gcg ccg tgg gat gac tcg gat gct ttg gat gac tcg gat 691
 Ala Pro Val Ala Pro Trp Asp Asp Ser Asp Ala Leu Asp Asp Ser Asp
 185 190 195

gaa gat ttt gag gct gta gat gct gct gag gtt ttt gag gct gaa gag 739
 Glu Asp Phe Glu Ala Val Asp Ala Ala Glu Val Phe Glu Ala Glu Glu
 200 205 210

act gta gag gtt tcc gaa gtc gca gaa gac tct gaa gtt tca aag gtt 787
 Thr Val Glu Val Ser Glu Val Ala Glu Asp Ser Glu Val Ser Lys Val
 215 220 225

tca gaa gaa aag gct gac gag agc taaatctttt ctggctaaca cca 834
 Ser Glu Glu Lys Ala Asp Glu Ser
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<210> 310

<211> 237

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 310

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Asp Tyr Lys Arg His Gly Ser Arg Tyr Lys Ala Arg Met Arg Ala Val
 20 25 30

Asp Ile Leu Phe Glu Ala Glu Ser Arg Asp Val Asp Pro Val Ala Ile
 35 40 45

Ile Asp Asp Arg His Lys Leu Ala Arg Asp Thr Asn Pro Ile Val Ala
 50 55 60

Pro Val Ala Glu Tyr Thr Glu Thr Ile Ile Asn Gly Val Ala Val Glu
 65 70 75 80

Leu Asp Thr Leu Asp Val Phe Leu Ala Glu His Ile Ala Glu Thr Trp
 85 90 95

Thr Leu Gly Arg Leu Pro Ser Val Asp Arg Ala Ile Leu Arg Val Ala
 100 105 110

Ser Trp Glu Met Ile Tyr Asn Ala Asp Val Pro Val Thr Thr Ala Ile
 115 120 125

Val Glu Ala Val Glu Ile Ala Ser Glu Tyr Ser Gly Asp Lys Ser Ser
 130 135 140

Ala Tyr Ile Asn Ala Thr Leu Asp Ala Met Ala Ser Lys Val Glu Thr
 145 150 155 160

Leu Arg Glu Arg Ala Ala Asn Pro Glu Ala Val Leu Ala Glu Ala Ser
 165 170 175

Glu Ser Leu Asp Asp Ala Pro Val Ala Pro Trp Asp Asp Ser Asp Ala
 180 185 190

Leu Asp Asp Ser Asp Glu Asp Phe Glu Ala Val Asp Ala Ala Glu Val
 195 200 205

Phe Glu Ala Glu Glu Thr Val Glu Val Ser Glu Val Ala Glu Asp Ser
 210 215 220

Glu Val Ser Lys Val Ser Glu Glu Lys Ala Asp Glu Ser
 225 230 235

<210> 311
 <211> 1458
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1435)
 <223> RXA01303

<400> 311
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tgacggaaag cctttccgcg taaccatgaa gaggcatacac gtg aca caa ctc aac 115
 Val Thr Gln Leu Asn
 1 5

acc aaa ggc gtt gtt ctg caa ggg tgg gat cca gaa gat cct gaa cat 163
 Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro Glu Asp Pro Glu His
 10 15 20

tgg gac tcg aaa att gca tgg cga acc ctg tgg att acc acc ttc tcc 211
 Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp Ile Thr Thr Phe Ser
 25 30 35

atg att att ggg ttc tgc gtg tgg tat ttg gtt tct gcc atc gct ccc	259
Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val Ser Ala Ile Ala Pro	
40 45 50	
cta ctc aat cga att gga ttt gat ctc tca gca ggt cag ctt tat tgg	307
Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala Gly Gln Leu Tyr Trp	
55 60 65	
ctc gca tct atc ccc ggt ttg gcc ggc gga tta atc cga ttg att tac	355
Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu Ile Arg Leu Ile Tyr	
70 75 80 85	
atg ttc ctt cca ccg att ctt gga acc cgc aaa ttg gtc gga att tcc	403
Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys Leu Val Gly Ile Ser	
90 95 100	
tcc ggt cta ttt ttg atc ccc atg ttt ggg tgg ttc ctg gct gtc caa	451
Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp Phe Leu Ala Val Gln	
105 110 115	
gat tca agc act ccc tac tgg tgg ctt ctc aca ctc gct gca ctc act	499
Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr Leu Ala Ala Leu Thr	
120 125 130	
ggc att ggt ggt ggc gtg ttc tct gga tat atg ccg tcc acg gga tac	547
Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met Pro Ser Thr Gly Tyr	
135 140 145	
ttc ttc ccc aag gca aaa tcg ggc act gcg ctg ggc att cag gca ggt	595
Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu Gly Ile Gln Ala Gly	
150 155 160 165	
atc ggc aac ctc ggc gtc tcg ata att cag ttc atg ggc cca tgg gtc	643
Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe Met Gly Pro Trp Val	
170 175 180	
atg ggt ttc ggt ctg ctg ggc att ggt ttc ctc acc ccg cag cgc acc	691
Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu Thr Pro Gln Arg Thr	
185 190 195	
att gaa ggc acc acg gtg ttt gtg cac aat gct gcg att gtg ttg gtc	739
Ile Glu Gly Thr Thr Val Phe Val His Asn Ala Ala Ile Val Leu Val	
200 205 210	
ccg tgg act att ctc gcg gcc gtt tta tcc ttc ctg ttt ctt aaa gat	787
Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe Leu Phe Leu Lys Asp	
215 220 225	
gtc cca gtc acc gca aat ttc cgg caa cag atc gat atc ttt ggc aac	835
Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile Asp Ile Phe Gly Asn	
230 235 240 245	
aag aac aca tgg att ttg tcc att atc tac ttg atg aca ttc ggt gcc	883
Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu Met Thr Phe Gly Ala	
250 255 260	
ttc gcc ggt ttc gcc gcg cag ttc ggt ctg atc atc aac aac aac ttc	931
Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile Ile Asn Asn Asn Phe	
265 270 275	

ggc atc gct tcc ccg atg gca gag act tat cca gct gag atg ctt cac 979
 Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro Ala Glu Met Leu His
 280 285 290

gcc ggt gct acg ttc gcg ttt ctt gga cct ttg att ggt gct ttg gtg 1027
 Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu Ile Gly Ala Leu Val
 295 300 305

cgt gct gca tgg ggt cca ctg tgt gac aga ttc ggt gga gct atc tgg. 1075
 Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe Gly Gly Ala Ile Trp
 310 315 320 325

acc ttt gtc ggt ggc atc gga atg act atc gcc act gca gct gcc gca 1123
 Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala Thr Ala Ala Ala Ala
 330 335 340

atc ttc cta agc aga gcg gag aca cct gat gat ttc tgg cca ttc ctg 1171
 Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp Phe Trp Pro Phe Leu
 345 350 355

tgg tcc atg ctt gcc ctg ttc ttc ttc acc ggt ctg ggc aat gct ggc 1219
 Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly Leu Gly Asn Ala Gly
 360 365 370

acc ttc aaa caa atg ccc atg att ttg cct aaa cgc caa gca ggt ggc 1267
 Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys Arg Gln Ala Gly Gly
 375 380 385

gtg atc ggc tgg acc ggt gcc att ggt gcc ttc ggc ccc ttc att gtc 1315
 Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe Gly Pro Phe Ile Val
 390 395 400 405

ggt gtc ttg ctc tcc ttc act cca act gtc gcg ttc ttc tgg ggc tgc 1363
 Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala Phe Phe Trp Gly Cys
 410 415 420

gtg gtg ttc ttc atc atc gcc acc gct ttg acc tgg atc tac tac gcc 1411
 Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr Trp Ile Tyr Tyr Ala
 425 430 435

cgc ccg aac gct cca ttc ccg gga taaaccgaaa ggccaatcca tga 1458
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 440 445

<210> 312

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

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Glu Asp Pro Glu His Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp
 20 25 30

Ile Thr Thr Phe Ser Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val
 35 40 45

Ser Ala Ile Ala Pro Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala

50					55					60					
Gly	Gln	Leu	Tyr	Trp	Leu	Ala	Ser	Ile	Pro	Gly	Leu	Ala	Gly	Gly	Leu
65					70					75					80
Ile	Arg	Leu	Ile	Tyr	Met	Phe	Leu	Pro	Pro	Ile	Leu	Gly	Thr	Arg	Lys
				85					90					95	
Leu	Val	Gly	Ile	Ser	Ser	Gly	Leu	Phe	Leu	Ile	Pro	Met	Phe	Gly	Trp
		100						105					110		
Phe	Leu	Ala	Val	Gln	Asp	Ser	Ser	Thr	Pro	Tyr	Trp	Trp	Leu	Leu	Thr
	115						120					125			
Leu	Ala	Ala	Leu	Thr	Gly	Ile	Gly	Gly	Gly	Val	Phe	Ser	Gly	Tyr	Met
	130					135					140				
Pro	Ser	Thr	Gly	Tyr	Phe	Phe	Pro	Lys	Ala	Lys	Ser	Gly	Thr	Ala	Leu
145					150					155					160
Gly	Ile	Gln	Ala	Gly	Ile	Gly	Asn	Leu	Gly	Val	Ser	Ile	Ile	Gln	Phe
				165					170					175	
Met	Gly	Pro	Trp	Val	Met	Gly	Phe	Gly	Leu	Leu	Gly	Ile	Gly	Phe	Leu
			180					185					190		
Thr	Pro	Gln	Arg	Thr	Ile	Glu	Gly	Thr	Thr	Val	Phe	Val	His	Asn	Ala
		195					200					205			
Ala	Ile	Val	Leu	Val	Pro	Trp	Thr	Ile	Leu	Ala	Ala	Val	Leu	Ser	Phe
	210					215					220				
Leu	Phe	Leu	Lys	Asp	Val	Pro	Val	Thr	Ala	Asn	Phe	Arg	Gln	Gln	Ile
225					230					235					240
Asp	Ile	Phe	Gly	Asn	Lys	Asn	Thr	Trp	Ile	Leu	Ser	Ile	Ile	Tyr	Leu
				245					250					255	
Met	Thr	Phe	Gly	Ala	Phe	Ala	Gly	Phe	Ala	Ala	Gln	Phe	Gly	Leu	Ile
			260					265					270		
Ile	Asn	Asn	Asn	Phe	Gly	Ile	Ala	Ser	Pro	Met	Ala	Glu	Thr	Tyr	Pro
	275						280					285			
Ala	Glu	Met	Leu	His	Ala	Gly	Ala	Thr	Phe	Ala	Phe	Leu	Gly	Pro	Leu
	290					295					300				
Ile	Gly	Ala	Leu	Val	Arg	Ala	Ala	Trp	Gly	Pro	Leu	Cys	Asp	Arg	Phe
305					310					315					320
Gly	Gly	Ala	Ile	Trp	Thr	Phe	Val	Gly	Gly	Ile	Gly	Met	Thr	Ile	Ala
				325					330					335	
Thr	Ala	Ala	Ala	Ala	Ile	Phe	Leu	Ser	Arg	Ala	Glu	Thr	Pro	Asp	Asp
			340					345					350		
Phe	Trp	Pro	Phe	Leu	Trp	Ser	Met	Leu	Ala	Leu	Phe	Phe	Phe	Thr	Gly
		355					360					365			
Leu	Gly	Asn	Ala	Gly	Thr	Phe	Lys	Gln	Met	Pro	Met	Ile	Leu	Pro	Lys
	370					375					380				

Arg Gln Ala Gly Gly Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe
385 390 395 400

Gly Pro Phe Ile Val Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala
405 410 415

Phe Phe Trp Gly Cys Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr
420 425 430

Trp Ile Tyr Tyr Ala Arg Pro Asn Ala Pro Phe Pro Gly
435 440 445

<210> 313

<211> 327

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(304)

<223> RXA01412

<400> 313

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cttgagggag agagtacttc acctgaaagg ggccagtgac atg gca tta aag aac 115
Met Ala Leu Lys Asn
1 5

tac acc gtt gag ggc atg acc tgc gca cac tgc gtg gca tcg gta act 163
Tyr Thr Val Glu Gly Met Thr Cys Ala His Cys Val Ala Ser Val Thr
10 15 20

gaa gag gta agc gaa gtt aat ggc gtt agc gct gtt gac gtc act cta 211
Glu Glu Val Ser Glu Val Asn Gly Val Ser Ala Val Asp Val Thr Leu
25 30 35

gaa tca gga aac gtc gct gtc agt ggc gaa ggt ttc agc gat gca gag 259
Glu Ser Gly Asn Val Ala Val Ser Gly Glu Gly Phe Ser Asp Ala Glu
40 45 50

atc cag gct gct gta gag gaa gcc ggc tac aag atc gtt gcc tcc 304
Ile Gln Ala Ala Val Glu Glu Ala Gly Tyr Lys Ile Val Ala Ser
55 60 65

taaagcacc aagaacattt aaa 327

<210> 314

<211> 68

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Ala Leu Lys Asn Tyr Thr Val Glu Gly Met Thr Cys Ala His Cys
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Val Ala Ser Val Thr Glu Glu Val Ser Glu Val Asn Gly Val Ser Ala
20 25 30

Val Asp Val Thr Leu Glu Ser Gly Asn Val Ala Val Ser Gly Glu Gly
 35 40 45

Phe Ser Asp Ala Glu Ile Gln Ala Ala Val Glu Glu Ala Gly Tyr Lys
 50 55 60

Ile Val Ala Ser
 65

<210> 315

<211> 1266

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1243)

<223> RXA00773

<400> 315

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aatattttgc ccaacctgat tcacggggga caatagtttag gtg act tta aaa atc 115
                                     Val Thr Leu Lys Ile
                                     1 5

ggc ccc ttt gac ctt gcc tcc cct gtg gtt cta gcc ccc atg gct ggt 163
Gly Pro Phe Asp Leu Ala Ser Pro Val Val Leu Ala Pro Met Ala Gly
                                     10 15 20

gta acc aac gtt gct ttc cgc acg ctg tgc cgt gaa cag gaa atg caa 211
Val Thr Asn Val Ala Phe Arg Thr Leu Cys Arg Glu Gln Glu Met Gln
                                     25 30 35

cgc acg gga aca atc tcg ggg ctg tac gtc tgt gaa atg gtg act gcg 259
Arg Thr Gly Thr Ile Ser Gly Leu Tyr Val Cys Glu Met Val Thr Ala
                                     40 45 50

cgt gct ctt gtt gag cgc aat gag aaa acc atg cac atg acc acc ttc 307
Arg Ala Leu Val Glu Arg Asn Glu Lys Thr Met His Met Thr Thr Phe
                                     55 60 65

gcg ccg gat gaa aat ccc cga agc ttg cag ctg tac acg gtt gac ccg 355
Ala Pro Asp Glu Asn Pro Arg Ser Leu Gln Leu Tyr Thr Val Asp Pro
70 75 80 85

aag tac acc tac gaa gcg gcg aag atg atc gtt gat gaa aac ttg gcg 403
Lys Tyr Thr Tyr Glu Ala Ala Lys Met Ile Val Asp Glu Asn Leu Ala
90 95 100

gat cat att gat atg aac ttt ggc tgc ccg gtt cca aag gtc acg cgc 451
Asp His Ile Asp Met Asn Phe Gly Cys Pro Val Pro Lys Val Thr Arg
105 110 115

cgg ggt ggc ggt tct gcg att cct tac aag cgc cgt ttg ttt gaa aac 499
Arg Gly Gly Gly Ser Ala Ile Pro Tyr Lys Arg Arg Leu Phe Glu Asn
120 125 130

atc gtt tcc gcg gct gtg aag gct acg gaa ggc acg gac att ccg gtg 547

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Ile Val Ser Ala Ala Val Lys Ala Thr Glu Gly Thr Asp Ile Pro Val	
135 140 145	
acg gtg aag ttc cgc gtt ggt att gat gat gag cac cat act cac ttg	595
Thr Val Lys Phe Arg Val Gly Ile Asp Asp Glu His His Thr His Leu	
150 155 160 165	
gat gct gga cgc att gct gtc gac gcc ggc gcg aag tcc gta gcg ctt	643
Asp Ala Gly Arg Ile Ala Val Asp Ala Gly Ala Lys Ser Val Ala Leu	
170 175 180	
cac gcc cgc act gcg gcg cag cgc tat tcc ggt gag gct gat tgg aac	691
His Ala Arg Thr Ala Ala Gln Arg Tyr Ser Gly Glu Ala Asp Trp Asn	
185 190 195	
gag atc gcg cgc ctg aag gag cat ttg gca gat acc ggc atc cca gtt	739
Glu Ile Ala Arg Leu Lys Glu His Leu Ala Asp Thr Gly Ile Pro Val	
200 205 210	
ttg ggc aat ggc gat att ttc gcg gca tcc gat gca acg cgc atg atg	787
Leu Gly Asn Gly Asp Ile Phe Ala Ala Ser Asp Ala Thr Arg Met Met	
215 220 225	
gag caa act ggc tgc gat ggc gtc gtg gtt ggg cgt ggt tgc ctg ggc	835
Glu Gln Thr Gly Cys Asp Gly Val Val Val Gly Arg Gly Cys Leu Gly	
230 235 240 245	
agg cct tgg ctc ttt gct gag ctg tct gct gct gtt cgt gga gaa gaa	883
Arg Pro Trp Leu Phe Ala Glu Leu Ser Ala Ala Val Arg Gly Glu Glu	
250 255 260	
atc cca gag gag cct acc ttc ggc gaa gtt acc caa atc atc ctg cgc	931
Ile Pro Glu Glu Pro Thr Phe Gly Glu Val Thr Gln Ile Ile Leu Arg	
265 270 275	
cac gca gaa ctc ctc atg cag cat gat ggc gaa acc aag ggg ctg cgc	979
His Ala Glu Leu Leu Met Gln His Asp Gly Glu Thr Lys Gly Leu Arg	
280 285 290	
gat ctg cgt aag cac atg ggt tgg tac ctg cgc ggt ttc cct gtt ggc	1027
Asp Leu Arg Lys His Met Gly Trp Tyr Leu Arg Gly Phe Pro Val Gly	
295 300 305	
ggc gaa ttc cgc tcc aat ctg gcc aag gtt tcc acc tat gtg gag ctt	1075
Gly Glu Phe Arg Ser Asn Leu Ala Lys Val Ser Thr Tyr Val Glu Leu	
310 315 320 325	
gag gat ctc cta gca cca tgg gct gac tcc acc gcc aag gca gag gac	1123
Glu Asp Leu Leu Ala Pro Trp Ala Asp Ser Thr Ala Lys Ala Glu Asp	
330 335 340	
gcg gaa ggt gca cga ggt cga cag ggc gct cct gca aag gtg gca ctt	1171
Ala Glu Gly Ala Arg Gly Arg Gln Gly Ala Pro Ala Lys Val Ala Leu	
345 350 355	
cca gat ggc tgg ttg gac gat cct gag gat gcc act gtt cct aaa ggc	1219
Pro Asp Gly Trp Leu Asp Asp Pro Glu Asp Ala Thr Val Pro Lys Gly	
360 365 370	
gca gaa atg gaa aac tcc gga ggg tagttaattt aatacttacc ccc	1266
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375

380

<210> 316

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

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 20 25 30
 Glu Gln Glu Met Gln Arg Thr Gly Thr Ile Ser Gly Leu Tyr Val Cys
 35 40 45
 Glu Met Val Thr Ala Arg Ala Leu Val Glu Arg Asn Glu Lys Thr Met
 50 55 60
 His Met Thr Thr Phe Ala Pro Asp Glu Asn Pro Arg Ser Leu Gln Leu
 65 70 75 80
 Tyr Thr Val Asp Pro Lys Tyr Thr Tyr Glu Ala Ala Lys Met Ile Val
 85 90 95
 Asp Glu Asn Leu Ala Asp His Ile Asp Met Asn Phe Gly Cys Pro Val
 100 105 110
 Pro Lys Val Thr Arg Arg Gly Gly Gly Ser Ala Ile Pro Tyr Lys Arg
 115 120 125
 Arg Leu Phe Glu Asn Ile Val Ser Ala Ala Val Lys Ala Thr Glu Gly
 130 135 140
 Thr Asp Ile Pro Val Thr Val Lys Phe Arg Val Gly Ile Asp Asp Glu
 145 150 155 160
 His His Thr His Leu Asp Ala Gly Arg Ile Ala Val Asp Ala Gly Ala
 165 170 175
 Lys Ser Val Ala Leu His Ala Arg Thr Ala Ala Gln Arg Tyr Ser Gly
 180 185 190
 Glu Ala Asp Trp Asn Glu Ile Ala Arg Leu Lys Glu His Leu Ala Asp
 195 200 205
 Thr Gly Ile Pro Val Leu Gly Asn Gly Asp Ile Phe Ala Ala Ser Asp
 210 215 220
 Ala Thr Arg Met Met Glu Gln Thr Gly Cys Asp Gly Val Val Val Gly
 225 230 235 240
 Arg Gly Cys Leu Gly Arg Pro Trp Leu Phe Ala Glu Leu Ser Ala Ala
 245 250 255
 Val Arg Gly Glu Glu Ile Pro Glu Glu Pro Thr Phe Gly Glu Val Thr
 260 265 270
 Gln Ile Ile Leu Arg His Ala Glu Leu Leu Met Gln His Asp Gly Glu

<210> 318
<211> 89

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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 Lys Gly His Thr Glu Val Tyr Arg Gly Ala Glu Tyr Ala Val Asp Phe
 20 25 30
 Val Pro Lys Val Lys Ile Glu Val Ile Ile Ser Asp Ala Gln Ala Glu
 35 40 45
 Glu Val Ile Asn Ile Ile Val Glu Thr Ala Arg Thr Gly Lys Val Gly
 50 55 60
 Asp Gly Lys Val Trp Met Thr Asn Ile Glu Glu Leu Val Arg Val Arg
 65 70 75 80
 Thr Gly Glu Arg Gly Glu Ala Ala Leu
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<210> 319

<211> 902

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(879)

<223> RXA02745

<400> 319

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 1 5 10 15
 gga cct aat ggc gca ggc aaa acc acc acc att gaa atg tgc gaa ggt 96
 Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Ile Glu Met Cys Glu Gly
 20 25 30
 ttt acc gcc ccc acc tct ggc agc atc cga gtc ttg ggc atc gat cca 144
 Phe Thr Ala Pro Thr Ser Gly Ser Ile Arg Val Leu Gly Ile Asp Pro
 35 40 45
 gcc aca gaa cca gac cag gtg cgc cga cgc atc ggc atc atg ctt caa 192
 Ala Thr Glu Pro Asp Gln Val Arg Arg Arg Ile Gly Ile Met Leu Gln
 50 55 60
 ggt ggc ggt tcc tac agc gga atc cgc gtg ttt gaa atg ctc aag ctt 240
 Gly Gly Gly Ser Tyr Ser Gly Ile Arg Val Phe Glu Met Leu Lys Leu
 65 70 75 80
 gcg gcg tcc tac aac gac aac cca cac gat cct gaa tgg ctg ctf gat 288
 Ala Ala Ser Tyr Asn Asp Asn Pro His Asp Pro Glu Trp Leu Leu Asp
 85 90 95
 ctt gta gga ctg cgt gaa caa cgc aaa acc acc tac cga cgt ctg tca 336
 Leu Val Gly Leu Arg Glu Gln Arg Lys Thr Thr Tyr Arg Arg Leu Ser
 100 105 110

ggt ggc caa cag caa cgc ctt tct ttg gcc tta gca tta att ggt cgc 384
 Gly Gly Gln Gln Gln Arg Leu Ser Leu Ala Leu Ala Leu Ile Gly Arg
 115 120 125
 cct gag att atc ttc ctc gac gaa ccc acc gct ggc atg gat gcg caa 432
 Pro Glu Ile Ile Phe Leu Asp Glu Pro Thr Ala Gly Met Asp Ala Gln
 130 135 140
 tca cgc aac atg gtg tgg gag ctt gtc aac gat ctc cgc cgc gac ggc 480
 Ser Arg Asn Met Val Trp Glu Leu Val Asn Asp Leu Arg Arg Asp Gly
 145 150 155 160
 gtc acc atc gtg ctc acc acc cac ctg atg gat gag gcc gaa gca cta 528
 Val Thr Ile Val Leu Thr Thr His Leu Met Asp Glu Ala Glu Ala Leu
 165 170 175
 gct gac cac gtg atc atc gtt gcc aac ggt caa atc ctt gcc agt ggc 576
 Ala Asp His Val Ile Ile Val Ala Asn Gly Gln Ile Leu Ala Ser Gly
 180 185 190
 aca cct gat gaa ctc act gcg caa cgc gat cat ctt gaa att aat gtc 624
 Thr Pro Asp Glu Leu Thr Ala Gln Arg Asp His Leu Glu Ile Asn Val
 195 200 205
 tcc gta gag acc acg agc ccg ctt gat ctt gat cgc ttg gtg gat gat 672
 Ser Val Glu Thr Thr Ser Pro Leu Asp Leu Asp Arg Leu Val Asp Asp
 210 215 220
 ctc agc agc tta aac atc ggt gat gtg aaa gca cga gcc aac cgg cca 720
 Leu Ser Ser Leu Asn Ile Gly Asp Val Lys Ala Arg Ala Asn Arg Pro
 225 230 235 240
 ctg cat tat tca ctt cgg acg caa caa gcc acc ccg gat tcc ttg gcg 768
 Leu His Tyr Ser Leu Arg Thr Gln Gln Ala Thr Pro Asp Ser Leu Ala
 245 250 255
 cac atc gtc cag gct gtc gcc cgc caa aac gtc atg att cgc tct ttg 816
 His Ile Val Gln Ala Val Ala Arg Gln Asn Val Met Ile Arg Ser Leu
 260 265 270
 gat acg gga cac cgc tca ttg gaa gat gtc ttc ctg gac atc acc gga 864
 Asp Thr Gly His Arg Ser Leu Glu Asp Val Phe Leu Asp Ile Thr Gly
 275 280 285
 aaa gaa ctg agg agt taacgcacac catgtctaaa cct 902
 Lys Glu Leu Arg Ser
 290

<210> 320

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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 Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Ile Glu Met Cys Glu Gly
 20 25 30

Phe Thr Ala Pro Thr Ser Gly Ser Ile Arg Val Leu Gly Ile Asp Pro
 35 40 45
 Ala Thr Glu Pro Asp Gln Val Arg Arg Arg Ile Gly Ile Met Leu Gln
 50 55 60
 Gly Gly Gly Ser Tyr Ser Gly Ile Arg Val Phe Glu Met Leu Lys Leu
 65 70 75 80
 Ala Ala Ser Tyr Asn Asp Asn Pro His Asp Pro Glu Trp Leu Leu Asp
 85 90 95
 Leu Val Gly Leu Arg Glu Gln Arg Lys Thr Thr Tyr Arg Arg Leu Ser
 100 105 110
 Gly Gly Gln Gln Gln Arg Leu Ser Leu Ala Leu Ala Leu Ile Gly Arg
 115 120 125
 Pro Glu Ile Ile Phe Leu Asp Glu Pro Thr Ala Gly Met Asp Ala Gln
 130 135 140
 Ser Arg Asn Met Val Trp Glu Leu Val Asn Asp Leu Arg Arg Asp Gly
 145 150 155 160
 Val Thr Ile Val Leu Thr Thr His Leu Met Asp Glu Ala Glu Ala Leu
 165 170 175
 Ala Asp His Val Ile Ile Val Ala Asn Gly Gln Ile Leu Ala Ser Gly
 180 185 190
 Thr Pro Asp Glu Leu Thr Ala Gln Arg Asp His Leu Glu Ile Asn Val
 195 200 205
 Ser Val Glu Thr Thr Ser Pro Leu Asp Leu Asp Arg Leu Val Asp Asp
 210 215 220
 Leu Ser Ser Leu Asn Ile Gly Asp Val Lys Ala Arg Ala Asn Arg Pro
 225 230 235 240
 Leu His Tyr Ser Leu Arg Thr Gln Gln Ala Thr Pro Asp Ser Leu Ala
 245 250 255
 His Ile Val Gln Ala Val Ala Arg Gln Asn Val Met Ile Arg Ser Leu
 260 265 270
 Asp Thr Gly His Arg Ser Leu Glu Asp Val Phe Leu Asp Ile Thr Gly
 275 280 285
 Lys Glu Leu Arg Ser
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<210> 321
 <211> 486
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(463)

<223> RXN00820

<400> 321

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cctgggcttt tcgcagtggc gcactgtcac ccaggagatg gtg aac acc ttg gcg 115
 Val Asn Thr Leu Ala
 1 5

gac gca act gat gat cag cag tgg att cac act gat cct gag cgc gcc 163
 Asp Ala Thr Asp Asp Gln Gln Trp Ile His Thr Asp Pro Glu Arg Ala
 10 15 20

aag gac ggt cct ttt ggt ggc gca att gcc cac ggt ttc ctc acc ttg 211
 Lys Asp Gly Pro Phe Gly Gly Ala Ile Ala His Gly Phe Leu Thr Leu
 25 30 35

tcc atg atc att ccg ttc tgg ggc gag ctt ctc gat gtc acc ggc gtg 259
 Ser Met Ile Ile Pro Phe Trp Gly Glu Leu Leu Asp Val Thr Gly Val
 40 45 50

acc acc aag gtg aac tat ggc ctg gat aag gtg cgt ttc acc tct ccc 307
 Thr Thr Lys Val Asn Tyr Gly Leu Asp Lys Val Arg Phe Thr Ser Pro
 55 60 65

gtc aag gtc ggt tcc cgc atc cgc atg ggc gct gtg gtc cgt gag atc 355
 Val Lys Val Gly Ser Arg Ile Arg Met Gly Ala Val Val Arg Glu Ile
 70 75 80 85

tct gag gtg aag ggc aat ggc ctg cac ctg gtc gcc gat ggc act att 403
 Ser Glu Val Lys Gly Asn Gly Leu His Leu Val Ala Asp Gly Thr Ile
 90 95 100

gag atc gaa ggg cag gag cgc ccg gcc gtc gta gct acc ttc ctc acc 451
 Glu Ile Glu Gly Gln Glu Arg Pro Ala Val Val Ala Thr Phe Leu Thr
 105 110 115

cgc ttc tac gct taaaagcttg cttctcgacg caa 486
 Arg Phe Tyr Ala
 120

<210> 322

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Val Asn Thr Leu Ala Asp Ala Thr Asp Asp Gln Gln Trp Ile His Thr
 1 5 10 15

Asp Pro Glu Arg Ala Lys Asp Gly Pro Phe Gly Gly Ala Ile Ala His
 20 25 30

Gly Phe Leu Thr Leu Ser Met Ile Ile Pro Phe Trp Gly Glu Leu Leu
 35 40 45

Asp Val Thr Gly Val Thr Thr Lys Val Asn Tyr Gly Leu Asp Lys Val
 50 55 60

Arg Phe Thr Ser Pro Val Lys Val Gly Ser Arg Ile Arg Met Gly Ala

435

<210> 324
 <211> 121
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 324
 Val Asn Thr Phe Ala Asp Ala Thr Asp Asp Gln Gln Trp Ile His Thr
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 Asp Pro Glu Arg Ala Lys Asp Gly Pro Phe Gly Gly Ala Ile Ala His
 20 25 30
 Gly Phe Leu Thr Leu Ser Met Ile Ile Pro Phe Trp Gly Glu Leu Leu
 35 40 45
 Asp Val Thr Gly Val Thr Thr Lys Val Asn Tyr Gly Leu Asp Lys Val
 50 55 60
 Arg Phe Thr Ser Pro Val Lys Val Gly Ser Arg Ile Arg Met Gly Ala
 65 70 75 80
 Val Val Arg Glu Ile Ser Glu Val Lys Gly Asn Gly Leu His Leu Val
 85 90 95
 Ala Asp Gly Thr Ile Glu Ile Glu Gly Gln Glu Arg Pro Ala Val Val
 100 105 110
 Ala Thr Phe Leu Thr Arg Phe Tyr Ala
 115 120

<210> 325
 <211> 732
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(709)
 <223> RXA01059

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 atgcgggaac aaatttgaag gtttttcagt tgctataggt atg act aca gtt act 115
 Met Thr Thr Val Thr
 1 5
 caa gac ctt cta gca ctt gac gaa gac gca cag aac ctc ctt ttc cgt 163
 Gln Asp Leu Leu Ala Leu Asp Glu Asp Ala Gln Asn Leu Leu Phe Arg
 10 15 20
 gag gct cgc acc gca aat gct ttc act gat gaa cca atc tct gac gag 211
 Glu Ala Arg Thr Ala Asn Ala Phe Thr Asp Glu Pro Ile Ser Asp Glu
 25 30 35
 cag atc gaa gca atc ttc gac cta gtt aag tgg gca cca acc gca atg 259
 Gln Ile Glu Ala Ile Phe Asp Leu Val Lys Trp Ala Pro Thr Ala Met
 40 45 50

aac tcc cag cct ctg cgc gtg gta att gtt cgt tcc gaa gaa gcc aaa 307
 Asn Ser Gln Pro Leu Arg Val Val Ile Val Arg Ser Glu Glu Ala Lys
 55 60 65

gct cgc ctc gtg cca ttg atg gca gaa ggc aac cag gcc aag gtt gct 355
 Ala Arg Leu Val Pro Leu Met Ala Glu Gly Asn Gln Ala Lys Val Ala
 70 75 80 85

gca gct cct gcg gtc gca ctt ctt gca gcc gac atc gac ttc cac gaa 403
 Ala Ala Pro Ala Val Ala Leu Leu Ala Ala Asp Ile Asp Phe His Glu
 90 95 100

gaa atg ccc aag ctc ttc cca cct ttc cca ggc gca cgc gac atg ttc 451
 Glu Met Pro Lys Leu Phe Pro Pro Phe Pro Gly Ala Arg Asp Met Phe
 105 110 115

gaa gcc gat gaa gct tca cgt gct tcc tcc gca gaa ctc aat gct ggc 499
 Glu Ala Asp Glu Ala Ser Arg Ala Ser Ser Ala Glu Leu Asn Ala Gly
 120 125 130

ctt cag atc gga tac gcc atc atc ggt atc cgc gca gca ggt ctc gcc 547
 Leu Gln Ile Gly Tyr Ala Ile Ile Gly Ile Arg Ala Ala Gly Leu Ala
 135 140 145

gct ggc cca atg acc ggc atg gat gca gac gct atc tcc aag gag ttc 595
 Ala Gly Pro Met Thr Gly Met Asp Ala Asp Ala Ile Ser Lys Glu Phe
 150 155 160 165

ttc cca gac ggc cgc cac cgc gtt ctg gtt gcc atc aac atg ggt aag 643
 Phe Pro Asp Gly Arg His Arg Val Leu Val Ala Ile Asn Met Gly Lys
 170 175 180

cca gct gac aat gct tgg tac gac cgc ctg cca cgc ctt gag cag gac 691
 Pro Ala Asp Asn Ala Trp Tyr Asp Arg Leu Pro Arg Leu Glu Gln Asp
 185 190 195

gaa gtt gtc gaa acc ctc tagaaaccac tctagaaata gct 732
 Glu Val Val Glu Thr Leu
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<210> 326

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Thr Thr Val Thr Gln Asp Leu Leu Ala Leu Asp Glu Asp Ala Gln
 1 5 10 15

Asn Leu Leu Phe Arg Glu Ala Arg Thr Ala Asn Ala Phe Thr Asp Glu
 20 25 30

Pro Ile Ser Asp Glu Gln Ile Glu Ala Ile Phe Asp Leu Val Lys Trp
 35 40 45

Ala Pro Thr Ala Met Asn Ser Gln Pro Leu Arg Val Val Ile Val Arg
 50 55 60

Ser Glu Glu Ala Lys Ala Arg Leu Val Pro Leu Met Ala Glu Gly Asn
 65 70 75 80

Gln	Ala	Lys	Val	Ala	Ala	Ala	Pro	Ala	Val	Ala	Leu	Leu	Ala	Ala	Asp
				85					90					95	
Ile	Asp	Phe	His	Glu	Glu	Met	Pro	Lys	Leu	Phe	Pro	Pro	Phe	Pro	Gly
			100					105					110		
Ala	Arg	Asp	Met	Phe	Glu	Ala	Asp	Glu	Ala	Ser	Arg	Ala	Ser	Ser	Ala
		115					120					125			
Glu	Leu	Asn	Ala	Gly	Leu	Gln	Ile	Gly	Tyr	Ala	Ile	Ile	Gly	Ile	Arg
	130					135					140				
Ala	Ala	Gly	Leu	Ala	Ala	Gly	Pro	Met	Thr	Gly	Met	Asp	Ala	Asp	Ala
145					150					155					160
Ile	Ser	Lys	Glu	Phe	Phe	Pro	Asp	Gly	Arg	His	Arg	Val	Leu	Val	Ala
				165					170					175	
Ile	Asn	Met	Gly	Lys	Pro	Ala	Asp	Asn	Ala	Trp	Tyr	Asp	Arg	Leu	Pro
			180					185					190		
Arg	Leu	Glu	Gln	Asp	Glu	Val	Val	Glu	Thr	Leu					
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<210> 327
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum
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<220>
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<222> (101)..(1030)
<223> RXN01386
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<400> 327																
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gttcagtacg	agcgggatcc	tcccggacaa	tcgcgtccaa	atg	tgg	gag	ggc	cac	115							
				Met	Trp	Glu	Gly	His								
				1				5								
aat gct cgc gca ttg ctt ccg ctc gac att aga acc att gac gat cgc	163															
Asn Ala Arg Ala Leu Leu Pro Leu Asp Ile Arg Thr Ile Asp Asp Arg																
	10							15						20		
ccc atg cag gcc tcc gaa acc aac ctg cac ctc cca tca atg cgg atg	211															
Pro Met Gln Ala Ser Glu Thr Asn Leu His Leu Pro Ser Met Arg Met																
	25							30						35		
gcg agc gta ttc ggg act tcg caa ttt gtc gag cgt tca gag agt ttc	259															
Ala Ser Val Phe Gly Thr Ser Gln Phe Val Glu Arg Ser Glu Ser Phe																
	40							45						50		
atc tca gaa aac ccc acg ggt gtg gtt gcg atc ttc ttt gcg act gaa	307															
Ile Ser Glu Asn Pro Thr Gly Val Val Ala Ile Phe Phe Ala Thr Glu																
	55							60						65		
ggt gaa gca gtc ttc ttc cac cgt ggt gga cat gta gcg ctt cgg cca	355															
Gly Glu Ala Val Phe Phe His Arg Gly Gly His Val Ala Leu Arg Pro																

70	75	80	85	
ggt cag gcc att gtt tac gac gcc gat agg cca ttc ctc cgc gga ttc				403
Gly Gln Ala Ile Val Tyr Asp Ala Asp Arg Pro Phe Leu Arg Gly Phe				
	90	95	100	
aac aat cgc ttc cgc gag cta gtt ctc acc atc ccg aag cag cgc tac				451
Asn Asn Arg Phe Arg Glu Leu Val Leu Thr Ile Pro Lys Gln Arg Tyr				
	105	110	115	
ctt gaa att gtt ggc tca aaa ggc cct gag ctt ccc gct att ttt gag				499
Leu Glu Ile Val Gly Ser Lys Gly Pro Glu Leu Pro Ala Ile Phe Glu				
	120	125	130	
ttc gga gca aca gga acc gcc aat gaa caa gct tta gcg cga cta gtt				547
Phe Gly Ala Thr Gly Thr Ala Asn Glu Gln Ala Leu Ala Arg Leu Val				
	135	140	145	
cag gaa tct cta cac agg att gaa agt ggc gag ccg aag cat atc gat				595
Gln Glu Ser Leu His Arg Ile Glu Ser Gly Glu Pro Lys His Ile Asp				
	150	155	160	165
tcc agt gga cct tta gga aaa ccg tgg agc gat atc gag cac gag gcc				643
Ser Ser Gly Pro Leu Gly Lys Pro Trp Ser Asp Ile Glu His Glu Ala				
	170	175	180	
cac gga ctt atc cgc aat gta ctt ggc gac gcc aca agt agc gaa gaa				691
His Gly Leu Ile Arg Asn Val Leu Gly Asp Ala Thr Ser Ser Glu Glu				
	185	190	195	
ggc tta att tct gca gcc cag aga ttt att gac atc aat att tcc gaa				739
Gly Leu Ile Ser Ala Ala Gln Arg Phe Ile Asp Ile Asn Ile Ser Glu				
	200	205	210	
agt gac tta caa gcg tcg cgg att gct gca gcc gtg gga atc agc gaa				787
Ser Asp Leu Gln Ala Ser Arg Ile Ala Ala Ala Val Gly Ile Ser Glu				
	215	220	225	
cgc caa cta agt cga atc ttc tca gac tca gga caa act atc gga cgc				835
Arg Gln Leu Ser Arg Ile Phe Ser Asp Ser Gly Gln Thr Ile Gly Arg				
	230	235	240	245
tac gtc cta aac acc cga ctg gat ttt gca aag gaa gcg ctg tcg aca				883
Tyr Val Leu Asn Thr Arg Leu Asp Phe Ala Lys Glu Ala Leu Ser Thr				
	250	255	260	
ccg gag cga gac aag gtt tcg gtc agt gag atc ggt aag cgc ttt ggg				931
Pro Glu Arg Asp Lys Val Ser Val Ser Glu Ile Gly Lys Arg Phe Gly				
	265	270	275	
ttc gct tcc cca agt cat ttc agt cgc acc ttc cgc gag cgg ttt gaa				979
Phe Ala Ser Pro Ser His Phe Ser Arg Thr Phe Arg Glu Arg Phe Glu				
	280	285	290	
atg acg ccg ctt caa tgg agg aag gaa tcg cag cgt caa tcc ttt caa				1027
Met Thr Pro Leu Gln Trp Arg Lys Glu Ser Gln Arg Gln Ser Phe Gln				
	295	300	305	
gag tgagggttttt gttctcaggc gga				1053
Glu				
310				

<210> 328

<211> 310

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 328

Met Trp Glu Gly His Asn Ala Arg Ala Leu Leu Pro Leu Asp Ile Arg
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Thr Ile Asp Asp Arg Pro Met Gln Ala Ser Glu Thr Asn Leu His Leu
 20 25 30

Pro Ser Met Arg Met Ala Ser Val Phe Gly Thr Ser Gln Phe Val Glu
 35 40 45

Arg Ser Glu Ser Phe Ile Ser Glu Asn Pro Thr Gly Val Val Ala Ile
 50 55 60

Phe Phe Ala Thr Glu Gly Glu Ala Val Phe Phe His Arg Gly Gly His
 65 70 75 80

Val Ala Leu Arg Pro Gly Gln Ala Ile Val Tyr Asp Ala Asp Arg Pro
 85 90 95

Phe Leu Arg Gly Phe Asn Asn Arg Phe Arg Glu Leu Val Leu Thr Ile
 100 105 110

Pro Lys Gln Arg Tyr Leu Glu Ile Val Gly Ser Lys Gly Pro Glu Leu
 115 120 125

Pro Ala Ile Phe Glu Phe Gly Ala Thr Gly Thr Ala Asn Glu Gln Ala
 130 135 140

Leu Ala Arg Leu Val Gln Glu Ser Leu His Arg Ile Glu Ser Gly Glu
 145 150 155 160

Pro Lys His Ile Asp Ser Ser Gly Pro Leu Gly Lys Pro Trp Ser Asp
 165 170 175

Ile Glu His Glu Ala His Gly Leu Ile Arg Asn Val Leu Gly Asp Ala
 180 185 190

Thr Ser Ser Glu Glu Gly Leu Ile Ser Ala Ala Gln Arg Phe Ile Asp
 195 200 205

Ile Asn Ile Ser Glu Ser Asp Leu Gln Ala Ser Arg Ile Ala Ala Ala
 210 215 220

Val Gly Ile Ser Glu Arg Gln Leu Ser Arg Ile Phe Ser Asp Ser Gly
 225 230 235 240

Gln Thr Ile Gly Arg Tyr Val Leu Asn Thr Arg Leu Asp Phe Ala Lys
 245 250 255

Glu Ala Leu Ser Thr Pro Glu Arg Asp Lys Val Ser Val Ser Glu Ile
 260 265 270

Gly Lys Arg Phe Gly Phe Ala Ser Pro Ser His Phe Ser Arg Thr Phe
 275 280 285

Arg Glu Arg Phe Glu Met Thr Pro Leu Gln Trp Arg Lys Glu Ser Gln
 290 295 300

Arg Gln Ser Phe Gln Glu
 305 310

<210> 329

<211> 1806

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1783)

<223> RXN00073

<400> 329

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gtgacatgta cttcactagc tctttaagga ttaactcccc atg aca aca acc acc 115
                               Met Thr Thr Thr Thr
                               1 5

gga agt gcc cgg cca gca cgt gcc gcc agg aag cct aag ccc gaa ggc 163
Gly Ser Ala Arg Pro Ala Arg Ala Ala Arg Lys Pro Lys Pro Glu Gly
                               10 15 20

caa tgg aaa atc gac ggc acc gag ccg ctt aac cat gcc gag gaa att 211
Gln Trp Lys Ile Asp Gly Thr Glu Pro Leu Asn His Ala Glu Glu Ile
                               25 30 35

aag caa gaa gaa ccc gct ttt gct gtc aag cag cgg gtc att gat att 259
Lys Gln Glu Glu Pro Ala Phe Ala Val Lys Gln Arg Val Ile Asp Ile
                               40 45 50

tac tcc aag cag ggt ttt tct tcc att gca ccg gat gac att gcc cca 307
Tyr Ser Lys Lys Gln Gly Phe Ser Ser Ile Ala Pro Asp Asp Ile Ala Pro
                               55 60 65

cgc ttt aag tgg ttg ggc att tac acc cag cgt aag cag gat ctg ggc 355
Arg Phe Lys Trp Leu Gly Ile Tyr Thr Gln Arg Lys Gln Asp Leu Gly
                               70 75 80 85

ggt gaa ctg acc ggt cag ctt cct gat gat gag ctg cag gat gag tac 403
Gly Glu Leu Thr Gly Gln Leu Pro Asp Glu Leu Gln Asp Glu Tyr
                               90 95 100

ttc atg atg cgt gtg cgt ttt gat ggc gga ctg gct tcc cct gag cgc 451
Phe Met Met Arg Val Arg Phe Asp Gly Gly Leu Ala Ser Pro Glu Arg
                               105 110 115

ctg cgt gcc gtg ggt gaa att tct agg gat tat gct cgt tcc acc gcg 499
Leu Arg Ala Val Gly Glu Ile Ser Arg Asp Tyr Ala Arg Ser Thr Ala
                               120 125 130

gac ttc acc gac cgc cag aac att cag ctg cac tgg att cgt att gaa 547
Asp Phe Thr Asp Arg Gln Asn Ile Gln Leu His Trp Ile Arg Ile Glu
                               135 140 145

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gat	gtg	cct	gcg	atc	tgg	gag	aag	cta	gaa	acc	gtc	gga	ctg	tcc	acc	595
Asp	Val	Pro	Ala	Ile	Trp	Glu	Lys	Leu	Glu	Thr	Val	Gly	Leu	Ser	Thr	
150					155				160						165	
atg	ctt	ggt	tgc	ggg	gac	gtt	cca	cgt	gtt	atc	ttg	ggc	tcc	cca	gtt	643
Met	Leu	Gly	Cys	Gly	Asp	Val	Pro	Arg	Val	Ile	Leu	Gly	Ser	Pro	Val	
			170						175						180	
tct	ggc	gta	gct	gct	gaa	gag	ctg	atc	gat	gcc	acc	ccg	gct	atc	gat	691
Ser	Gly	Val	Ala	Ala	Glu	Glu	Leu	Ile	Asp	Ala	Thr	Pro	Ala	Ile	Asp	
			185						190						195	
gcg	att	cgt	gag	cgc	tac	cta	gac	aag	gaa	gag	ttc	cac	aac	ctt	cct	739
Ala	Ile	Arg	Glu	Arg	Tyr	Leu	Asp	Lys	Glu	Glu	Phe	His	Asn	Leu	Pro	
		200						205					210			
cgt	aag	ttt	aag	act	gct	atc	act	ggc	aac	cag	cgc	cag	gat	gtt	acc	787
Arg	Lys	Phe	Lys	Thr	Ala	Ile	Thr	Gly	Asn	Gln	Arg	Gln	Asp	Val	Thr	
		215					220				225					
cac	gaa	atc	cag	gac	gtt	tcc	ttc	gtt	cct	tcg	att	cac	cca	gaa	ttc	835
His	Glu	Ile	Gln	Asp	Val	Ser	Phe	Val	Pro	Ser	Ile	His	Pro	Glu	Phe	
					235					240					245	
ggc	cca	gga	ttt	gag	tgc	ttt	gtg	ggc	ggt	ggc	ctg	tcc	acc	aac	cca	883
Gly	Pro	Gly	Phe	Glu	Cys	Phe	Val	Gly	Gly	Gly	Leu	Ser	Thr	Asn	Pro	
				250					255						260	
atg	ctt	gct	cag	cca	ctt	ggt	tct	tgg	att	cca	ctt	gat	gag	gtt	cca	931
Met	Leu	Ala	Gln	Pro	Leu	Gly	Ser	Trp	Ile	Pro	Leu	Asp	Glu	Val	Pro	
			265					270							275	
gaa	gtg	tgg	gct	ggc	gtc	gcc	gga	att	ttc	cgc	gac	tac	ggc	ttc	cga	979
Glu	Val	Trp	Ala	Gly	Val	Ala	Gly	Ile	Phe	Arg	Asp	Tyr	Gly	Phe	Arg	
		280					285					290				
cgc	ctg	cgt	aac	cgt	gct	cgc	ctc	aag	ttc	ttg	gtg	gca	cag	tgg	ggt	1027
Arg	Leu	Arg	Asn	Arg	Ala	Arg	Leu	Lys	Phe	Leu	Val	Ala	Gln	Trp	Gly	
		295				300					305					
att	gag	aag	ttc	cgt	gaa	gtt	ctt	gag	acc	gaa	tac	ctc	gag	cgc	aag	1075
Ile	Glu	Lys	Phe	Arg	Glu	Val	Leu	Glu	Thr	Glu	Tyr	Leu	Glu	Arg	Lys	
					315					320					325	
ctg	atc	gat	ggc	cca	gtt	gtt	acc	acc	aac	cct	ggc	tac	cgt	gac	cac	1123
Leu	Ile	Asp	Gly	Pro	Val	Val	Thr	Thr	Asn	Pro	Gly	Tyr	Arg	Asp	His	
				330						335					340	
att	ggc	att	cac	cca	caa	aag	gac	ggc	aag	ttc	tac	ctc	ggt	gtg	aag	1171
Ile	Gly	Ile	His	Pro	Gln	Lys	Asp	Gly	Lys	Phe	Tyr	Leu	Gly	Val	Lys	
			345					350							355	
cca	acc	gtt	gga	cac	acc	acc	ggt	gag	cag	ctc	att	gcc	att	gct	gat	1219
Pro	Thr	Val	Gly	His	Thr	Thr	Gly	Glu	Gln	Leu	Ile	Ala	Ile	Ala	Asp	
			360				365					370				
gtt	gca	gaa	aag	cac	ggc	atc	acc	agg	att	cgt	acc	acg	gcg	gaa	aag	1267
Val	Ala	Glu	Lys	His	Gly	Ile	Thr	Arg	Ile	Arg	Thr	Thr	Ala	Glu	Lys	
			375				380				385					
gaa	ctg	ctc	ttc	ctc	gat	att	gag	aga	aag	aac	ctt	act	acc	gtt	gca	1315

Glu Leu Leu Phe Leu Asp Ile Glu Arg Lys Asn Leu Thr Thr Val Ala
 390 395 400 405

 cgc gac ctg gat gaa atc gga ctg tac tct tca cct tcc gag ttc cgc 1363
 Arg Asp Leu Asp Glu Ile Gly Leu Tyr Ser Ser Pro Ser Glu Phe Arg
 410 415 420

 cgc ggc atc att tcc tgc acc ggc ttg gag ttc tgc aag ctt gcg cac 1411
 Arg Gly Ile Ile Ser Cys Thr Gly Leu Glu Phe Cys Lys Leu Ala His
 425 430 435

 gca acc acc aag tca cga gca att gag ctt gtc gac gaa ctg gaa gag 1459
 Ala Thr Thr Lys Ser Arg Ala Ile Glu Leu Val Asp Glu Leu Glu Glu
 440 445 450

 cgc ctc ggc gat ttg gat gtt ccc atc aag att gca ctg aac ggt tgc 1507
 Arg Leu Gly Asp Leu Asp Val Pro Ile Lys Ile Ala Leu Asn Gly Cys
 455 460 465

 cct aac tct tgt gca cgc acc cag gtt tcc gac atc gga ttc aag gga 1555
 Pro Asn Ser Cys Ala Arg Thr Gln Val Ser Asp Ile Gly Phe Lys Gly
 470 475 480 485

 cag acc gtc act gat gct gac ggc aac cgc gtt gaa ggt ttc cag gtt 1603
 Gln Thr Val Thr Asp Ala Asp Gly Asn Arg Val Glu Gly Phe Gln Val
 490 495 500

 cac ctg ggc ggt tcc atg aac ttg gat cca aac ttc gga cgc aag ctc 1651
 His Leu Gly Gly Ser Met Asn Leu Asp Pro Asn Phe Gly Arg Lys Leu
 505 510 515

 aag ggc cac aag gtt att gcc gat gaa gtg gga gag tac gtc act cgc 1699
 Lys Gly His Lys Val Ile Ala Asp Glu Val Gly Glu Tyr Val Thr Arg
 520 525 530

 gtt gtt acc cac ttc aag gaa cag cgc cac gag gac gag cac ttc cgc 1747
 Val Val Thr His Phe Lys Glu Gln Arg His Glu Asp Glu His Phe Arg
 535 540 545

 gat tgg gtc cag cgg gcc gct gag gaa gat ttg gtg tgagtcttcg 1793
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 gaggaacccc aat 1806

<210> 330

<211> 561

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Met Thr Thr Thr Thr Gly Ser Ala Arg Pro Ala Arg Ala Ala Arg Lys
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Pro Lys Pro Glu Gly Gln Trp Lys Ile Asp Gly Thr Glu Pro Leu Asn
 20 25 30

His Ala Glu Glu Ile Lys Gln Glu Glu Pro Ala Phe Ala Val Lys Gln
 35 40 45

Arg Val Ile Asp Ile Tyr Ser Lys Gln Gly Phe Ser Ser Ile Ala Pro
 50 55 60
 Asp Asp Ile Ala Pro Arg Phe Lys Trp Leu Gly Ile Tyr Thr Gln Arg
 65 70 75 80
 Lys Gln Asp Leu Gly Gly Glu Leu Thr Gly Gln Leu Pro Asp Asp Glu
 85 90 95
 Leu Gln Asp Glu Tyr Phe Met Met Arg Val Arg Phe Asp Gly Gly Leu
 100 105 110
 Ala Ser Pro Glu Arg Leu Arg Ala Val Gly Glu Ile Ser Arg Asp Tyr
 115 120 125
 Ala Arg Ser Thr Ala Asp Phe Thr Asp Arg Gln Asn Ile Gln Leu His
 130 135 140
 Trp Ile Arg Ile Glu Asp Val Pro Ala Ile Trp Glu Lys Leu Glu Thr
 145 150 155 160
 Val Gly Leu Ser Thr Met Leu Gly Cys Gly Asp Val Pro Arg Val Ile
 165 170 175
 Leu Gly Ser Pro Val Ser Gly Val Ala Ala Glu Glu Leu Ile Asp Ala
 180 185 190
 Thr Pro Ala Ile Asp Ala Ile Arg Glu Arg Tyr Leu Asp Lys Glu Glu
 195 200 205
 Phe His Asn Leu Pro Arg Lys Phe Lys Thr Ala Ile Thr Gly Asn Gln
 210 215 220
 Arg Gln Asp Val Thr His Glu Ile Gln Asp Val Ser Phe Val Pro Ser
 225 230 235 240
 Ile His Pro Glu Phe Gly Pro Gly Phe Glu Cys Phe Val Gly Gly Gly
 245 250 255
 Leu Ser Thr Asn Pro Met Leu Ala Gln Pro Leu Gly Ser Trp Ile Pro
 260 265 270
 Leu Asp Glu Val Pro Glu Val Trp Ala Gly Val Ala Gly Ile Phe Arg
 275 280 285
 Asp Tyr Gly Phe Arg Arg Leu Arg Asn Arg Ala Arg Leu Lys Phe Leu
 290 295 300
 Val Ala Gln Trp Gly Ile Glu Lys Phe Arg Glu Val Leu Glu Thr Glu
 305 310 315 320
 Tyr Leu Glu Arg Lys Leu Ile Asp Gly Pro Val Val Thr Thr Asn Pro
 325 330 335
 Gly Tyr Arg Asp His Ile Gly Ile His Pro Gln Lys Asp Gly Lys Phe
 340 345 350
 Tyr Leu Gly Val Lys Pro Thr Val Gly His Thr Thr Gly Glu Gln Leu
 355 360 365
 Ile Ala Ile Ala Asp Val Ala Glu Lys His Gly Ile Thr Arg Ile Arg

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<400> 331
aacgcggctc gtgaagatta cctgaaaaaac caagccctcc agcgtccgct gtcggtctaa 60

accagttggc taaacaaaaa cgtattttaag gagaacacc atg acc act tct gta 115
                                     Met Thr Thr Ser Val
                                     1                               5

cct gca tcc acc aaa gct tta tct gtg gct ggc gaa aac cca ggc ctg 163
Pro Ala Ser Thr Lys Ala Leu Ser Val Ala Gly Glu Asn Pro Gly Leu
                        10                               15                               20

cgc atc ggc acc gca cct gac tcg tgg ggc gtg tqg ttc cca qaq gat 211

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Arg Ile Gly Thr Ala Pro Asp Ser Trp Gly Val Trp Phe Pro Glu Asp
 25 30 35

cca aag cag atc cct tgg gag cgt ttt ctc tac gag gtc gtg aaa gct 259
 Pro Lys Gln Ile Pro Trp Glu Arg Phe Leu Tyr Glu Val Val Lys Ala
 40 45 50

ggc tac acc tgg atc gag ctt ggc cca tac ggc tac ctg cca acc gat 307
 Gly Tyr Thr Trp Ile Glu Leu Gly Pro Tyr Gly Tyr Leu Pro Thr Asp
 55 60 65

gcc aac cag ctt gaa gat gaa ctg ggc aag cgc ggc ctg aag ctg tcc 355
 Ala Asn Gln Leu Glu Asp Glu Leu Gly Lys Arg Gly Leu Lys Leu Ser
 70 75 80 85

gct ggc acc gag ttc acc 373
 Ala Gly Thr Glu Phe Thr
 90

<210> 332
 <211> 91
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 332
 Met Thr Thr Ser Val Pro Ala Ser Thr Lys Ala Leu Ser Val Ala Gly
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Glu Asn Pro Gly Leu Arg Ile Gly Thr Ala Pro Asp Ser Trp Gly Val
 20 25 30

Trp Phe Pro Glu Asp Pro Lys Gln Ile Pro Trp Glu Arg Phe Leu Tyr
 35 40 45

Glu Val Val Lys Ala Gly Tyr Thr Trp Ile Glu Leu Gly Pro Tyr Gly
 50 55 60

Tyr Leu Pro Thr Asp Ala Asn Gln Leu Glu Asp Glu Leu Gly Lys Arg
 65 70 75 80

Gly Leu Lys Leu Ser Ala Gly Thr Glu Phe Thr
 85 90

<210> 333
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(526)
 <223> RXS00153

<400> 333
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agccctgcct ggcccttcca aattatgtag ggtggcctgc gtg gga gca ata att 115
 Val Gly Ala Ile Ile
 1 5

tgg ttt atc gga gca ttg gtt ctt gct ggc ttg gaa ttg gca gta ggt 163
 Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu Glu Leu Ala Val Gly
 10 15 20

gag ttc acc tta ttg atg ctc ggc ggt gca gct ttg gca acc gcc ggc 211
 Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala Leu Ala Thr Ala Gly
 25 30 35

gtg gca ctc atc ggt gtc cca gta tgg gct gaa ttt gtc acc ttc gcg 259
 Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu Phe Val Thr Phe Ala
 40 45 50

gtg gcc tca gct gct cta ctg atg ttc att agg ccg gcc att aga aag 307
 Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg Pro Ala Ile Arg Lys
 55 60 65

cgt ctg ctg aaa cca aag gtt ctg gac tct tca cca cga gca ctt gtt 355
 Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser Pro Arg Ala Leu Val
 70 75 80 85

ggc cac cgt gct gaa gtg ctc gaa gat gtc gga gcg acc agc ggg cag 403
 Gly His Arg Ala Glu Val Leu Glu Asp Val Gly Ala Thr Ser Gly Gln
 90 95 100

gtc cgc ctg gat ggt tca att tgg tcc gcc cgc agc atg gat ccc aca 451
 Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg Ser Met Asp Pro Thr
 105 110 115

cac acc ttc gcg gaa ggt gaa att gtc agt gtc att gat atc caa ggc 499
 His Thr Phe Ala Glu Gly Glu Ile Val Ser Val Ile Asp Ile Gln Gly
 120 125 130

acg acc gcg att gta tgg aaa gaa gcc taaattttta acaatcaaat 546
 Thr Thr Ala Ile Val Trp Lys Glu Ala
 135 140

agt 549

<210> 334

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Val Gly Ala Ile Ile Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu
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Glu Leu Ala Val Gly Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala
 20 25 30

Leu Ala Thr Ala Gly Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu
 35 40 45

Phe Val Thr Phe Ala Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg
 50 55 60

Pro Ala Ile Arg Lys Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser
 65 70 75 80

Pro Arg Ala Leu Val Gly His Arg Ala Glu Val Leu Glu Asp Val Gly
 85 90 95

Ala Thr Ser Gly Gln Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg
 100 105 110

Ser Met Asp Pro Thr His Thr Phe Ala Glu Gly Glu Ile Val Ser Val
 115 120 125

Ile Asp Ile Gln Gly Thr Thr Ala Ile Val Trp Lys Glu Ala
 130 135 140

<210> 335

<211> 509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(486)

<223> RXN01716

<400> 335

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Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile	
1 5 10 15	
gtt cgc ctg ggc aaa ggc gtc gac gcc acc ggt cag cta gac ccc gag	96
Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu	
20 25 30	
gca atc gag cgc act cgt gtc gct ttg gaa aac tac gtt gaa ctc atg	144
Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met	
35 40 45	
gaa acc cat ggg gta gag gcc gta cga atg gtt gcc acc tcc gca acc	192
Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr	
50 55 60	
cgc gat gcg tcc aac cgc gat gaa ttc ttt tcg atg acc cgc cag ctt	240
Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu	
65 70 75 80	
ctg tcc aag atc cgt cct gga tac caa gct gaa gta att tcc ggc gaa	288
Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu	
85 90 95	
gag gaa gct ctg ctg tcc ttc cga ggt gca atc gtt gac ctg cct gaa	336
Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu	
100 105 110	
gac caa ggt cct ttc tgt gtt atc gac ctt ggc ggt gga tcc act gag	384
Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu	
115 120 125	
ttc atc gtt ggc acc tac gac ggt gaa atc cta ggc tcc cac tca acc	432
Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr	
130 135 140	
caa atg gga tgc gtg cgc ctg acc gaa cga atc atg cgc agc gac cca	480

Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160

ccc gac tgaaccgaa gtggaaatcg ccc
 Pro Asp

509

<210> 336

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
 1 5 10 15

Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
 20 25 30

Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
 35 40 45

Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
 50 55 60

Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
 65 70 75 80

Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
 85 90 95

Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
 100 105 110

Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
 115 120 125

Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
 130 135 140

Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160

Pro Asp

<210> 337

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> RXN02972

<400> 337

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gaacgaatca	tgcgcagcga	cccaccccgac	tgaaaccgaa	gtg Val	gaa Glu	atc Ile	gcc Ala	cgc Arg		115
				1				5		
gac tac gtt gca gaa cgc atc cag gaa gta aaa gcc atc gtc cca att	163									
Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys Ala Ile Val Pro Ile										
	10			15				20		
tca aag gca aaa acc ttt gtg gga tgc gca ggc acc ttc acc aca atc	211									
Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly Thr Phe Thr Thr Ile										
	25			30				35		
tcc gcc tgg gtg caa ggc cta gaa agc tac gac cgc gac gcg atc cac	259									
Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp Arg Asp Ala Ile His										
	40			45				50		
ctc tct gca ctc aac ttc gat gca ctg cga gtt gtc acc gat gag atc	307									
Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val Val Thr Asp Glu Ile										
	55			60				65		
att tca gaa tca tca tca cag cgc gcc agc aac cca gtt gtt gat cca	355									
Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn Pro Val Val Asp Pro										
	70			75				80		85
ggt cgc gcc gac gtc atc ggt ggc gga tcc gtt gtt gtc caa gca gcg	403									
Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val Val Val Gln Ala Ala										
	90			95				100		
atc gac tta gcc tcc aaa gaa gcc ggt gta gac tac atc att att tcc	451									
Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp Tyr Ile Ile Ile Ser										
	105			110				115		
gaa aaa gac atc ctc gac ggc ctc atc ctt ggc ctg gta gaa gcc gac	499									
Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly Leu Val Glu Ala Asp										
	120			125				130		
tct ttg aag aaa taggacccta gttttaaac act	534									
Ser Leu Lys Lys										
	135									

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<210> 338
<211> 137
<212> PRT
<213> Corynebacterium glutamicum
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<400> 338 .  
Val Glu Ile Ala Arg Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys  
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Ala Ile Val Pro Ile Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly  
          20                25              30  
  
Thr Phe Thr Thr Ile Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp  
      35                40              45  
  
Arg Asp Ala Ile His Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val  
      50                55              60  
  
Val Thr Asp Glu Ile Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn  
  65                70              75              80
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Pro Val Val Asp Pro Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val
 85 90 95

Val Val Gln Ala Ala Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp
 100 105 110

Tyr Ile Ile Ile Ser Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly
 115 120 125

Leu Val Glu Ala Asp Ser Leu Lys Lys
 130 135

<210> 339

<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1474)

<223> RXN00663

<400> 339

ctgaacgatt ggtgaccggc tcatgaaaac ttgacgagtc cccggtattc gccagcgggtg 60

actactaccg tgggcgacaa gccacttag aggaggactt gtg aca acc acc tat 115
 Val Thr Thr Thr Tyr
 1 5

cca gat ttc ctt gga aat tct tcg ctc caa aca gat acg gag cac tgg 163
 Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr Asp Thr Glu His Trp
 10 15 20

gaa atg gaa gga ggt gcg cag gaa gtc tct gtt act tat gtt ttg gac 211
 Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val Thr Tyr Val Leu Asp
 25 30 35

acg tca gtg ttg ctg tct gat ccg ttg tcg ttg aca cgg ttc gcg gag 259
 Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu Thr Arg Phe Ala Glu
 40 45 50

cac gat gta gtt ctg cca att gtt gta att acg gaa tta gaa gcc aag 307
 His Asp Val Val Leu Pro Ile Val Val Ile Thr Glu Leu Glu Ala Lys
 55 60 65

cgt cat cac ccg gac ctt ggc ttt ttt gct cgc caa gcg ctt cgg atg 355
 Arg His His Pro Asp Leu Gly Phe Phe Ala Arg Gln Ala Leu Arg Met
 70 75 80 85

ctg gat gag ctg cgt gag atc cat ggg gat ttg tcc aag cca ctg cca 403
 Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu Ser Lys Pro Leu Pro
 90 95 100

att ggc gat gaa ggc gga cac atc cat gtt gag ctg aat cac caa aac 451
 Ile Gly Asp Glu Gly Gly His Ile His Val Glu Leu Asn His Gln Asn
 105 110 115

acg ggg tcc ttg ccc gtg gga ttc cgc ctt ggt gac aat gac acc cgc 499
 Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly Asp Asn Asp Thr Arg

120	125	130	
atc ctt gca gtg gcc aag aat ctg cag gaa gag ggc cac aat gtg gtt Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Gly His Asn Val Val 135 140 145			547
ctg gtg tcg aag gac ctg ccg atg cgg att aag gcg tcg gca agc gga Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys Ala Ser Ala Ser Gly 150 155 160 165			595
atc gcc gca cag gaa tac cgc gct gcc ctg gcg cgc gac cgt ggt tac Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala Arg Asp Arg Gly Tyr 170 175 180			643
acc ggc atg acc cac gcc aat atc acc gat gac cag ctc agc gag ctc Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp Gln Leu Ser Glu Leu 185 190 195			691
tac gac acc ggc gag gtg cgc att gag gag ctc gaa aag ctg ccc gtc Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu Glu Lys Leu Pro Val 200 205 210			739
aac cac ggc ttc acc ctc aaa tcc aac agc ggt tcg gcg ctt ggt cgt Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly Ser Ala Leu Gly Arg 215 220 225			787
atg aat tcc gac aag atc atc gag ctt gtc ccc ggc gac cag cag gta Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro Gly Asp Gln Gln Val 230 235 240 245			835
ttc ggt atc agc ggg cgt agc gct gag cag cgg gtt gcc att gat ttg Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg Val Ala Ile Asp Leu 250 255 260			883
ctt aac gac gac gcc gtc ggc atc gta tcc atc ggc ggc ccc gcg ggt Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile Gly Gly Pro Ala Gly 265 270 275			931
aca ggt aaa agc gca ctc gca ctg tgt gcc ggc ctg gaa gct gtg atg Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly Leu Glu Ala Val Met 280 285 290			979
gag cgt cgc att cag cgc aag att atc gtg ttc cgc cca ctc ttt gcc Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe Arg Pro Leu Phe Ala 295 300 305			1027
gtt ggc gga cag gaa ctt ggc tac ctg cct ggc gac caa gaa gaa aaa Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly Asp Gln Glu Glu Lys 310 315 320 325			1075
atg ggg cct tgg gcg caa gcg gtt ttt gac acc cta agc tcc atg gtc Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr Leu Ser Ser Met Val 330 335 340			1123
agc caa aac atc atc gat gaa gcc ctc tcc cgc ggc ctc atc gaa gtt Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg Gly Leu Ile Glu Val 345 350 355			1171
ctc cca ctt act cac atc cgc gga cgc tca ctc cac gat gct ttc gtc Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu His Asp Ala Phe Val 360 365 370			1219

atc gtc gac gag gcc caa tcc cta gaa cgc aac gtg ttg ctc acc atg 1267
 Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn Val Leu Leu Thr Met
 375 380 385
 ctg tct cgc atc ggc cag aat tcc cga gta gtt ctc acc cat gac gta 1315
 Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val Leu Thr His Asp Val
 390 395 400 405
 gcg cag cgc gac aac ctg cgc gtt ggt cgc tac gac ggc atc gtc tct 1363
 Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr Asp Gly Ile Val Ser
 410 415 420
 gtg gtg gaa gca ctc aag gat cac gaa ctg ttt ggc cac atc acg ttg 1411
 Val Val Glu Ala Leu Lys Asp His Glu Leu Phe Gly His Ile Thr Leu
 425 430 435
 cag cgt tcc gaa cgc tcc cga atc gct gag ttg gtc acc caa gtt ttg 1459
 Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu Val Thr Gln Val Leu
 440 445 450
 gat gcg ccg tct ctg tagtcgcgca gtctgtggcg att 1497
 Asp Ala Pro Ser Leu
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<210> 340
 <211> 458
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 340
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 20 25 30
 Thr Tyr Val Leu Asp Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu
 35 40 45
 Thr Arg Phe Ala Glu His Asp Val Val Leu Pro Ile Val Val Ile Thr
 50 55 60
 Glu Leu Glu Ala Lys Arg His His Pro Asp Leu Gly Phe Phe Ala Arg
 65 70 75 80
 Gln Ala Leu Arg Met Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu
 85 90 95
 Ser Lys Pro Leu Pro Ile Gly Asp Glu Gly Gly His Ile His Val Glu
 100 105 110
 Leu Asn His Gln Asn Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly
 115 120 125
 Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu
 130 135 140
 Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys
 145 150 155 160

Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala
 165 170 175
 Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp
 180 185 190
 Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu
 195 200 205
 Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly
 210 215 220
 Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro
 225 230 235 240
 Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg
 245 250 255
 Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile
 260 265 270
 Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly
 275 280 285
 Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe
 290 295 300
 Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly
 305 310 315 320
 Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr
 325 330 335
 Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg
 340 345 350
 Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu
 355 360 365
 His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn
 370 375 380
 Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val
 385 390 395 400
 Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr
 405 410 415
 Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu Leu Phe
 420 425 430
 Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu
 435 440 445
 Val Thr Gln Val Leu Asp Ala Pro Ser Leu
 450 455

<210> 341

<211> 1248

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1225)

<223> RXN00778 .

<400> 341

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gctcagacga tgtcttcaact taaaccggaa aggccttcccc gtg aac ctc act ctt 115
                               Val Asn Leu Thr Leu
                               1      5

aag cgc tcc atc gcc ctt gtg ggc gca gtt act gca ggc tcc ttc gct 163
Lys Arg Ser Ile Ala Leu Val Gly Ala Val Thr Ala Gly Ser Phe Ala
                10                15                20

ctt gta gct tgc tcc gac tcc aat gag tct gat tcc acc tcc tca tct 211
Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp Ser Thr Ser Ser Ser
                25                30                35

gca gct tcc acc ggt tct tcc gat gct gca tcc att gag ggc ctt tcc 259
Ala Ala Ser Thr Gly Ser Ser Asp Ala Ala Ser Ile Glu Gly Leu Ser
                40                45                50

ggg gtt acc ggt cag ctc gtt gct gaa ggt gca tct tcc cag cag tcc 307
Gly Val Thr Gly Gln Leu Val Ala Glu Gly Ala Ser Ser Gln Gln Ser
                55                60                65

gca atg gac tac ttt ggt atc cgt tac tcc gag gct gtc agc ggt gca 355
Ala Met Asp Tyr Phe Gly Ile Arg Tyr Ser Glu Ala Val Ser Gly Ala
                70                75                80                85

tct ctg gct tac acc cct tca ggt tcc ggt tcc ggc cgc acc aac ttc 403
Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser Gly Arg Thr Asn Phe
                90                95                100

gct gca ggc cag gtt gct ttc ggt ggc tcc gac tcc gca atg aag gac 451
Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp Ser Ala Met Lys Asp
                105                110                115

gac cag gct gca gaa gca gaa gca cgt tgc aac ggc aac gaa gca tgg 499
Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly Asn Glu Ala Trp
                120                125                130

cac ctg cca ttc gtt atc ggc cca gtt gca gtt gct tac aac ctg cct 547
His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala Tyr Asn Leu Pro
                135                140                145

ggc gtt gac acc ctg aac ctg gac acc aac atc atc gct cag atc ttc 595
Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile Ala Gln Ile Phe
                150                155                160                165

aag ggc gag atc acc aag tgg aac gac gaa gca atc gct tcc cag aac 643
Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile Ala Ser Gln Asn
                170                175                180

gag ggc acc gac ctc cca gac cag gac atc tcc gtt ctg tac cgt tcc 691
Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val Leu Tyr Arg Ser

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185	190	195	
gaa gag tcc ggt acc tcc gac aac ttc cag aag ttc ctc gga gct tcc			739
Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe Leu Gly Ala Ser			
200	205	210	
acc gac atc tgg gag acc gaa ggc cag cag ttc cca acc gag gtt ggc			787
Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro Thr Glu Val Gly			
215	220	225	
tcc ggt gcg cag ggc tcc aac ggt gta gct tct gag gct tcc aac atc			835
Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu Ala Ser Asn Ile			
230	235	240	245
gag ggt gca atc acc tac gtt gaa gct ggt ttc gct aac cag tcc ggc			883
Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala Asn Gln Ser Gly			
	250	255	260
ctg ggc gtt gca aac atc gac ttc ggt tcc ggc cca gtt gaa ctc aac			931
Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro Val Glu Leu Asn			
	265	270	275
gct gag tcc gtt ggc gtt gca ctt ggt gca ctc gac ttc ctg act gag			979
Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp Phe Leu Thr Glu			
	280	285	290
ggc cac aac atg gtt gtt gac acc gac gct atg ttc gca atg aac gaa			1027
Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe Ala Met Asn Glu			
	295	300	305
gcc ggt gct tac cca ctg atc ctc acc acc tac gaa atc gtc tgc tcc			1075
Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu Ile Val Cys Ser			
310	315	320	325
gca ggc tac gac gag acc acc cgc gac cag gtc aag gac ttc ctg acc			1123
Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys Asp Phe Leu Thr			
	330	335	340
gtt gca ctg gac tcc cag gat gac cag ctc gag gct ctc ggc tac atc			1171
Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala Leu Gly Tyr Ile			
	345	350	355
cca gtt acc ggc gag cac tac gat cgc ctc gtt gca gca gtt gaa gca			1219
Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala Ala Val Glu Ala			
	360	365	370
att cag taataaacgcg ctgccgtagc ttc			1248
Ile Gln			
375			

<210> 342

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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Ala Gly Ser Phe Ala Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp

20										25					30				
Ser	Thr	Ser	Ser	Ser	Ala	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ala	Ala	Ser				
		35					40					45							
Ile	Glu	Gly	Leu	Ser	Gly	Val	Thr	Gly	Gln	Leu	Val	Ala	Glu	Gly	Ala				
	50					55					60								
Ser	Ser	Gln	Gln	Ser	Ala	Met	Asp	Tyr	Phe	Gly	Ile	Arg	Tyr	Ser	Glu				
	65				70					75					80				
Ala	Val	Ser	Gly	Ala	Ser	Leu	Ala	Tyr	Thr	Pro	Ser	Gly	Ser	Gly	Ser				
				85				90						95					
Gly	Arg	Thr	Asn	Phe	Ala	Ala	Gly	Gln	Val	Ala	Phe	Gly	Gly	Ser	Asp				
			100					105						110					
Ser	Ala	Met	Lys	Asp	Asp	Gln	Ala	Ala	Glu	Ala	Glu	Ala	Arg	Cys	Asn				
		115					120					125							
Gly	Asn	Glu	Ala	Trp	His	Leu	Pro	Phe	Val	Ile	Gly	Pro	Val	Ala	Val				
	130					135					140								
Ala	Tyr	Asn	Leu	Pro	Gly	Val	Asp	Thr	Leu	Asn	Leu	Asp	Thr	Asn	Ile				
	145				150					155					160				
Ile	Ala	Gln	Ile	Phe	Lys	Gly	Glu	Ile	Thr	Lys	Trp	Asn	Asp	Glu	Ala				
				165					170					175					
Ile	Ala	Ser	Gln	Asn	Glu	Gly	Thr	Asp	Leu	Pro	Asp	Gln	Asp	Ile	Ser				
			180					185						190					
Val	Leu	Tyr	Arg	Ser	Glu	Glu	Ser	Gly	Thr	Ser	Asp	Asn	Phe	Gln	Lys				
		195					200					205							
Phe	Leu	Gly	Ala	Ser	Thr	Asp	Ile	Trp	Glu	Thr	Glu	Gly	Gln	Gln	Phe				
	210					215					220								
Pro	Thr	Glu	Val	Gly	Ser	Gly	Ala	Gln	Gly	Ser	Asn	Gly	Val	Ala	Ser				
	225				230					235					240				
Glu	Ala	Ser	Asn	Ile	Glu	Gly	Ala	Ile	Thr	Tyr	Val	Glu	Ala	Gly	Phe				
			245						250					255					
Ala	Asn	Gln	Ser	Gly	Leu	Gly	Val	Ala	Asn	Ile	Asp	Phe	Gly	Ser	Gly				
		260						265						270					
Pro	Val	Glu	Leu	Asn	Ala	Glu	Ser	Val	Gly	Val	Ala	Leu	Gly	Ala	Leu				
		275					280					285							
Asp	Phe	Leu	Thr	Glu	Gly	His	Asn	Met	Val	Val	Asp	Thr	Asp	Ala	Met				
	290					295					300								
Phe	Ala	Met	Asn	Glu	Ala	Gly	Ala	Tyr	Pro	Leu	Ile	Leu	Thr	Thr	Tyr				
	305				310					315					320				
Glu	Ile	Val	Cys	Ser	Ala	Gly	Tyr	Asp	Glu	Thr	Thr	Arg	Asp	Gln	Val				
			325						330					335					
Lys	Asp	Phe	Leu	Thr	Val	Ala	Leu	Asp	Ser	Gln	Asp	Asp	Gln	Leu	Glu				
		340						345						350					

Ala Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val
 355 360 365

Ala Ala Val Glu Ala Ile Gln
 370 375

<210> 343

<211> 870

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(847)

<223> RXN00250

<400> 343

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 ccgtatagaa attcagtcaa ccaagagtac tctgtccacc atg gtt ttt act ctt 115
 Met Val Phe Thr Leu
 1 5
 gcg gac tcc gtc tcc cag gtt gcg cta ggt ccg tcc tgg ctg gac cct 163
 Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro Ser Trp Leu Asp Pro
 10 15 20
 atg gaa ctt ctt tcc ggc tcc ggc ccg ttc ggt agc ttc att ctt ccg 211
 Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro
 25 30 35
 gcg atg ctt gcc att gtc ttt atc gaa tca ggc cta ctt ttc cca ctt 259
 Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu
 40 45 50
 cta cca ggt gat tct ctc ctt ttc acc ggt ggt ctc cta gct aac cag 307
 Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln
 55 60 65
 gct gac cct ttt gca ccg ctg tgg ctg gtg ctg atc ctc tgc cct atc 355
 Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu Ile Leu Cys Pro Ile
 70 75 80 85
 gcc gca att ctt ggc gat cag gtg ggt tac tgg att ggc cac aag ttc 403
 Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp Ile Gly His Lys Phe
 90 95 100
 cac cct cgc ctg gtc aat cgt ccg gat ggc agg att ttc aag cag gaa 451
 His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu
 105 110 115
 tac ctc aag cag act gag gat ttc ttt gag aag cat ggc ccc gtg acg 499
 Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys His Gly Pro Val Thr
 120 125 130
 atc att ttg tgc cgt ttc gtg ccc atc gtc cgt act tac gca cct ctg 547
 Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg Thr Tyr Ala Pro Leu
 135 140 145

gtc gca ggt atg gct ggc atg cgt tac cgc acg ttc att att tac aac 595
 Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr Phe Ile Ile Tyr Asn
 150 155 160 165

 atg atc ggt ggc att ttg tgg ggt tcc ggc gtg gtg gct ttg ggt gct 643
 Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val Val Ala Leu Gly Ala
 170 175 180

 gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att gat ctg att ttc 691
 Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile Asp Leu Ile Phe
 185 190 195

 ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg gtc ggc atg gcc 739
 Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu Val Gly Met Ala
 200 205 210

 cgc aag ctg gct gac ggc cac aag caa gcc aac acc gag cca caa gaa 787
 Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr Glu Pro Gln Glu
 215 220 225

 aac ccc gca gtc cag aca gcc cca gta aaa acc cag gaa gcc cag gaa 835
 Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln Glu Ala Gln Glu
 230 235 240 245

 gcc ccc cag aac taatctttcc ggtccgccag ttc 870
 Ala Pro Gln Asn

<210> 344

<211> 249

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 344

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 20 25 30

 Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly
 35 40 45

 Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly
 50 55 60

 Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu
 65 70 75 80

 Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp
 85 90 95

 Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg
 100 105 110

 Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys
 115 120 125

 His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg
 130 135 140

Thr Tyr Ala Pro Leu Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr
 145 150 155 160
 Phe Ile Ile Tyr Asn Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val
 165 170 175
 Val Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn
 180 185 190
 Ile Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly
 195 200 205
 Leu Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn
 210 215 220
 Thr Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr
 225 230 235 240
 Gln Glu Ala Gln Glu Ala Pro Gln Asn
 245

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 <211> 541
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(541)
 <223> RXA00072

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 aagaatctct cgaaagacac aaaagaggtg agtcgcaaca atg agc ttt caa cta 115
 Met Ser Phe Gln Leu
 1 5
 gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser
 10 15 20
 ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys
 25 30 35
 cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala
 40 45 50
 agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala
 55 60 65
 att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355
 Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala
 70 75 80 85
 gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403

Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr
 90 95 100

cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr
 105 110 115

tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499
 Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln
 120 125 130

gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541
 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala
 135 140 145

<210> 346

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Met Ser Phe Gln Leu Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys
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Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser
 20 25 30

Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala
 35 40 45

Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu
 50 55 60

His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val
 65 70 75 80

Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe
 85 90 95

Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln
 100 105 110

Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu
 115 120 125

Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser
 130 135 140

Asn Pro Ala
 145

<210> 347

<211> 1299

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1276)

<223> RXA00793

<400> 347

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acctttgaga tcaatataga ccgtgtggtc tactcgagga atg agt gaa aac aat 115
Met Ser Glu Asn Asn
1 5

ccc act acc ttg cac tgg ttc cta ccc acc tat ggc gat tct cgc gga 163
Pro Thr Thr Leu His Trp Phe Leu Pro Thr Tyr Gly Asp Ser Arg Gly
10 15 20

atc aca gcc ggc ggg cat ggc ttc ggc ttc cac tcc gga agc cgg aca 211
Ile Thr Ala Gly Gly His Gly Phe Gly Phe His Ser Gly Ser Arg Thr
25 30 35

gca gac ctc gat tac ctc tcc caa att gcc ctg gcc gct gaa cga aac 259
Ala Asp Leu Asp Tyr Leu Ser Gln Ile Ala Leu Ala Ala Glu Arg Asn
40 45 50

ggg ttt gaa tcc gtc ctg act ccc act gga ttg tgg tgc gaa gat gcg 307
Gly Phe Glu Ser Val Leu Thr Pro Thr Gly Leu Trp Cys Glu Asp Ala
55 60 65

tgg atc acc acc gca gcg ctg ctg tct agg aca tca aaa ctg aaa ttc 355
Trp Ile Thr Thr Ala Ala Leu Leu Ser Arg Thr Ser Lys Leu Lys Phe
70 75 80 85

ctc gtt gct att cga cca ggc caa gtt agc ccc acc atc atc gcg cag 403
Leu Val Ala Ile Arg Pro Gly Gln Val Ser Pro Thr Ile Ile Ala Gln
90 95 100

cag ggt gct gcc ttc cag aaa ttc tca aat aac cgc ctg ctc atc aac 451
Gln Gly Ala Ala Phe Gln Lys Phe Ser Asn Asn Arg Leu Leu Ile Asn
105 110 115

gtc gtg gtg ggt ggc gaa gac cat gaa cag cgc gct ttc gct gat tat 499
Val Val Val Gly Gly Glu Asp His Glu Gln Arg Ala Phe Ala Asp Tyr
120 125 130

tct tcc aaa gag gag cgc tac cac aag gct gat gaa acc tta gag atc 547
Ser Ser Lys Glu Glu Arg Tyr His Lys Ala Asp Glu Thr Leu Glu Ile
135 140 145

atc gat cac cta tgg aac agc gca gaa cct cta aat ttc cag ggt gaa 595
Ile Asp His Leu Trp Asn Ser Ala Glu Pro Leu Asn Phe Gln Gly Glu
150 155 160 165

ttc ctc agt gtg gaa aac gcg gta ttg aag gaa cag ccc gag gtt tcc 643
Phe Leu Ser Val Glu Asn Ala Val Leu Lys Glu Gln Pro Glu Val Ser
170 175 180

cca ccg att tac ttt ggc gga tcc tca caa ctc ggc atc gaa atc gca 691
Pro Pro Ile Tyr Phe Gly Gly Ser Ser Gln Leu Gly Ile Glu Ile Ala
185 190 195

gcc caa cat tcc gat gtt tat ctc acc tgg ggt gaa cct gcg gaa aag 739
Ala Gln His Ser Asp Val Tyr Leu Thr Trp Gly Glu Pro Ala Glu Lys
200 205 210

gta gag gag aag ctt gcc cgg gtg cgc gcc gaa gca gat aag cga aac 787
 Val Glu Glu Lys Leu Ala Arg Val Arg Ala Glu Ala Asp Lys Arg Asn
 215 220 225

cgc gaa cta gac tat ggc atc cgc ctg cat gtc att gct cga cca act 835
 Arg Glu Leu Asp Tyr Gly Ile Arg Leu His Val Ile Ala Arg Pro Thr
 230 235 240 245

gag gat gaa gcc tgg tca gtg gct caa aat ctt ctt gac caa ctt gat 883
 Glu Asp Glu Ala Trp Ser Val Ala Gln Asn Leu Leu Asp Gln Leu Asp
 250 255 260

cag gaa gag gtt gcc cgc att cag gaa ggg ctt gcg cgt tct caa tcg 931
 Gln Glu Glu Val Ala Arg Ile Gln Glu Gly Leu Ala Arg Ser Gln Ser
 265 270 275

gaa ggt cag cgt cgc atg acg gaa ctt cat gga caa ggg gca gca ttc 979
 Glu Gly Gln Arg Arg Met Thr Glu Leu His Gly Gln Gly Ala Ala Phe
 280 285 290

aca gca gga gca gat gct cgc tcc ctt gaa att gca ccg aat ctc tgg 1027
 Thr Ala Gly Ala Asp Ala Arg Ser Leu Glu Ile Ala Pro Asn Leu Trp
 295 300 305

gca ggt gtt ggg cta gtc cgc ggt ggc gcc ggc aca gcg ttg gtg ggt 1075
 Ala Gly Val Gly Leu Val Arg Gly Gly Ala Gly Thr Ala Leu Val Gly
 310 315 320 325

tcc tat gag caa gtc gcg caa gca att ttg cga tac cgc gat att ggt 1123
 Ser Tyr Glu Gln Val Ala Gln Ala Ile Leu Arg Tyr Arg Asp Ile Gly
 330 335 340

ctg agc cac ttc att ttc tcc ggc tat cca cat ttg gag gaa acc tat 1171
 Leu Ser His Phe Ile Phe Ser Gly Tyr Pro His Leu Glu Glu Thr Tyr
 345 350 355

cac gtg ggc gaa gga gtg gta cct gag ctc ctc aaa ttg ggt gtt ccg 1219
 His Val Gly Glu Gly Val Val Pro Glu Leu Leu Lys Leu Gly Val Pro
 360 365 370

gtg aac aac cat gaa gaa caa cgc aac gac gtg gta gcg act ccg ttt 1267
 Val Asn Asn His Glu Glu Gln Arg Asn Asp Val Val Ala Thr Pro Phe
 375 380 385

att tcc aga tagatcacgg atcggctgct tta 1299
 Ile Ser Arg
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<210> 348

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Ser Glu Asn Asn Pro Thr Thr Leu His Trp Phe Leu Pro Thr Tyr
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Gly Asp Ser Arg Gly Ile Thr Ala Gly Gly His Gly Phe Gly Phe His
 20 25 30

Ser Gly Ser Arg Thr Ala Asp Leu Asp Tyr Leu Ser Gln Ile Ala Leu
 35 40 45
 Ala Ala Glu Arg Asn Gly Phe Glu Ser Val Leu Thr Pro Thr Gly Leu
 50 55 60
 Trp Cys Glu Asp Ala Trp Ile Thr Thr Ala Ala Leu Leu Ser Arg Thr
 65 70 75 80
 Ser Lys Leu Lys Phe Leu Val Ala Ile Arg Pro Gly Gln Val Ser Pro
 85 90 95
 Thr Ile Ile Ala Gln Gln Gly Ala Ala Phe Gln Lys Phe Ser Asn Asn
 100 105 110
 Arg Leu Leu Ile Asn Val Val Val Gly Gly Glu Asp His Glu Gln Arg
 115 120 125
 Ala Phe Ala Asp Tyr Ser Ser Lys Glu Glu Arg Tyr His Lys Ala Asp
 130 135 140
 Glu Thr Leu Glu Ile Ile Asp His Leu Trp Asn Ser Ala Glu Pro Leu
 145 150 155 160
 Asn Phe Gln Gly Glu Phe Leu Ser Val Glu Asn Ala Val Leu Lys Glu
 165 170 175
 Gln Pro Glu Val Ser Pro Pro Ile Tyr Phe Gly Gly Ser Ser Gln Leu
 180 185 190
 Gly Ile Glu Ile Ala Ala Gln His Ser Asp Val Tyr Leu Thr Trp Gly
 195 200 205
 Glu Pro Ala Glu Lys Val Glu Glu Lys Leu Ala Arg Val Arg Ala Glu
 210 215 220
 Ala Asp Lys Arg Asn Arg Glu Leu Asp Tyr Gly Ile Arg Leu His Val
 225 230 235 240
 Ile Ala Arg Pro Thr Glu Asp Glu Ala Trp Ser Val Ala Gln Asn Leu
 245 250 255
 Leu Asp Gln Leu Asp Gln Glu Glu Val Ala Arg Ile Gln Glu Gly Leu
 260 265 270
 Ala Arg Ser Gln Ser Glu Gly Gln Arg Arg Met Thr Glu Leu His Gly
 275 280 285
 Gln Gly Ala Ala Phe Thr Ala Gly Ala Asp Ala Arg Ser Leu Glu Ile
 290 295 300
 Ala Pro Asn Leu Trp Ala Gly Val Gly Leu Val Arg Gly Gly Ala Gly
 305 310 315 320
 Thr Ala Leu Val Gly Ser Tyr Glu Gln Val Ala Gln Ala Ile Leu Arg
 325 330 335
 Tyr Arg Asp Ile Gly Leu Ser His Phe Ile Phe Ser Gly Tyr Pro His
 340 345 350
 Leu Glu Glu Thr Tyr His Val Gly Glu Gly Val Val Pro Glu Leu Leu

355

360

365

Lys Leu Gly Val Pro Val Asn Asn His Glu Glu Gln Arg Asn Asp Val
 370 375 380

Val Ala Thr Pro Phe Ile Ser Arg
 385 390

<210> 349

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA01192

<400> 349

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 Val Ala Ala Arg Tyr
 1 5

gcg gac acc tat ctc acg tgg ggt gaa act ccc gat cag gtg gcg cag 163
 Ala Asp Thr Tyr Leu Thr Trp Gly Glu Thr Pro Asp Gln Val Ala Gln
 10 15 20

aaa atc aac tgg atc aac gag cta gca gca cag cgc ggc cgg gaa ctg 211
 Lys Ile Asn Trp Ile Asn Glu Leu Ala Ala Gln Arg Gly Arg Glu Leu
 25 30 35

cgc cat gga atc cgc ttc cat gtg atc acc cgc gat acg tct gaa gaa 259
 Arg His Gly Ile Arg Phe His Val Ile Thr Arg Asp Thr Ser Glu Glu
 40 45 50

gca tgg gtg gtg gca gag aag ttg att agc ggg gtc act cca gaa cag 307
 Ala Trp Val Val Ala Glu Lys Leu Ile Ser Gly Val Thr Pro Glu Gln
 55 60 65

gtc gct aag gct caa gcc ggg ttt gca acg tct aag tcg gag ggg cag 355
 Val Ala Lys Ala Gln Ala Gly Phe Ala Thr Ser Lys Ser Glu Gly Gln
 70 75 80 85

cgc cgg atg gct gag ctg cac agc aag ggt cgt gcc ttt act agt ggc 403
 Arg Arg Met Ala Glu Leu His Ser Lys Gly Arg Ala Phe Thr Ser Gly
 90 95 100

tca act gct cgt gat ctg gag gtg tat ccc aat gtg tgg gca ggc gtc 451
 Ser Thr Ala Arg Asp Leu Glu Val Tyr Pro Asn Val Trp Ala Gly Val
 105 110 115

ggg ttg ctt cgc gga ggt gca gga aca gcc ctt gtg ggc tcg cat gaa 499
 Gly Leu Leu Arg Gly Gly Ala Gly Thr Ala Leu Val Gly Ser His Glu
 120 125 130

gag gtc gcc gat cgc atc gaa gaa tac gca gca ctc ggc ttg gat cag 547
 Glu Val Ala Asp Arg Ile Glu Glu Tyr Ala Ala Leu Gly Leu Asp Gln
 135 140 145

ttt gta ctg tcg ggt tat cca aac ttg gag gag gcc ttc cac ttc ggt 595
 Phe Val Leu Ser Gly Tyr Pro Asn Leu Glu Glu Ala Phe His Phe Gly
 150 155 160 165

gag ggt gtg att ccg aaa ctg ctg cgc cgc ggt gtg gat atc aaa aat 643
 Glu Gly Val Ile Pro Lys Leu Leu Arg Arg Gly Val Asp Ile Lys Asn
 170 175 180

caa gaa tca cga gtt ttg gaa cct gtt ggg taaacggg 681
 Gln Glu Ser Arg Val Leu Glu Pro Val Gly
 185 190

<210> 350

<211> 191

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 350

Val Ala Ala Arg Tyr Ala Asp Thr Tyr Leu Thr Trp Gly Glu Thr Pro
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Asp Gln Val Ala Gln Lys Ile Asn Trp Ile Asn Glu Leu Ala Ala Gln
 20 25 30

Arg Gly Arg Glu Leu Arg His Gly Ile Arg Phe His Val Ile Thr Arg
 35 40 45

Asp Thr Ser Glu Glu Ala Trp Val Val Ala Glu Lys Leu Ile Ser Gly
 50 55 60

Val Thr Pro Glu Gln Val Ala Lys Ala Gln Ala Gly Phe Ala Thr Ser
 65 70 75 80

Lys Ser Glu Gly Gln Arg Arg Met Ala Glu Leu His Ser Lys Gly Arg
 85 90 95

Ala Phe Thr Ser Gly Ser Thr Ala Arg Asp Leu Glu Val Tyr Pro Asn
 100 105 110

Val Trp Ala Gly Val Gly Leu Leu Arg Gly Gly Ala Gly Thr Ala Leu
 115 120 125

Val Gly Ser His Glu Glu Val Ala Asp Arg Ile Glu Glu Tyr Ala Ala
 130 135 140

Leu Gly Leu Asp Gln Phe Val Leu Ser Gly Tyr Pro Asn Leu Glu Glu
 145 150 155 160

Ala Phe His Phe Gly Glu Gly Val Ile Pro Lys Leu Leu Arg Arg Gly
 165 170 175

Val Asp Ile Lys Asn Gln Glu Ser Arg Val Leu Glu Pro Val Gly
 180 185 190

<210> 351

<211> 918

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(895)

<223> RXA00715

<400> 351

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tgcaaccaat aacaatgatg cccattttcc tgaaggtcca gtg gta acc gtt gac 115
                               Val Val Thr Val Asp
                               1 5

tgg ttg tca cac aac ctt gac cgg gat gat gtc atc gtg ttg tgt gcc 163
Trp Leu Ser His Asn Leu Asp Arg Asp Asp Val Ile Val Leu Cys Ala
                               10 15 20

aca atg gag gat gat gaa att gca cgt caa gcg gga att ccg ggg gca 211
Thr Met Glu Asp Asp Glu Ile Ala Arg Gln Ala Gly Ile Pro Gly Ala
                               25 30 35

ttt ctc gct gac ttg gaa gga gat ttc tca gat cca cat tcc gag ctt 259
Phe Leu Ala Asp Leu Glu Gly Asp Phe Ser Asp Pro His Ser Glu Leu
                               40 45 50

cca cac acc gcg cca cca aat ttg gtg ggt ttg cta gaa agc tac ggc 307
Pro His Thr Ala Pro Pro Asn Leu Val Gly Leu Leu Glu Ser Tyr Gly
                               55 60 65

att agc acc gat tcc acg gtg gtt gtt tat gat ctg cac ggc ctc atg 355
Ile Ser Thr Asp Ser Thr Val Val Val Tyr Asp Leu His Gly Leu Met
                               70 75 80 85

gtt gca ccg cgg gtg tgg tgg ctt ctc cgt gtt gct gga tta agc agc 403
Val Ala Pro Arg Val Trp Trp Leu Leu Arg Val Ala Gly Leu Ser Ser
                               90 95 100

att ggc gtg ctt gat ggc gga ttg cca gcc tgg gtt gat gct ggc ctt 451
Ile Gly Val Leu Asp Gly Gly Leu Pro Ala Trp Val Asp Ala Gly Leu
                               105 110 115

cca acg gaa ccg ctg tcg cta cct aca agt ggt gga agg atc agc gca 499
Pro Thr Glu Pro Leu Ser Leu Pro Thr Ser Gly Gly Arg Ile Ser Ala
                               120 125 130

gaa cca cag cca gat tta ctc gtt ggt gcc tcc ggc gtt gaa cgg gcg 547
Glu Pro Gln Pro Asp Leu Leu Val Gly Ala Ser Gly Val Glu Arg Ala
                               135 140 145

atc gcg cgc tca agc aag gca gtg att gat gct cgt aat gcg agc cga 595
Ile Ala Arg Ser Ser Lys Ala Val Ile Asp Ala Arg Asn Ala Ser Arg
                               150 155 160 165

ttc gct ggc gtt gaa gaa gag ccc cgt cca ggc ctt cga aaa ggg tcg 643
Phe Ala Gly Val Glu Glu Glu Pro Arg Pro Gly Leu Arg Lys Gly Ser
                               170 175 180

atc cct gga agc gtc aac att ccc ttc act gac att tct gat gag cat 691
Ile Pro Gly Ser Val Asn Ile Pro Phe Thr Asp Ile Ser Asp Glu His
                               185 190 195

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ggt ttt gtc cgg cca gca gaa gaa ctg aag gaa ttg atc ttc agc cgc 739
 Gly Phe Val Arg Pro Ala Glu Glu Leu Lys Glu Leu Ile Phe Ser Arg
 200 205 210
 aca aat gga gcg cag tcg ttg gtc ttt agc tgt ggc tcc gga gtc acg 787
 Thr Asn Gly Ala Gln Ser Leu Val Phe Ser Cys Gly Ser Gly Val Thr
 215 220 225
 gca tgt gtt gat gcc tac gct gca gtt atc gca ggt tat gac gac gtt 835
 Ala Cys Val Asp Ala Tyr Ala Ala Val Ile Ala Gly Tyr Asp Asp Val
 230 235 240 245
 gta gtg tat gaa ggc tct tgg gcg gag tgg ggc aac ccg gca aac caa 883
 Val Val Tyr Glu Gly Ser Trp Ala Glu Trp Gly Asn Pro Ala Asn Gln
 250 255 260
 aag ccg att gct taacgcccgc tatgataacc act 918
 Lys Pro Ile Ala
 265

<210> 352
 <211> 265
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 352
 Val Val Thr Val Asp Trp Leu Ser His Asn Leu Asp Arg Asp Asp Val
 1 5 10 15
 Ile Val Leu Cys Ala Thr Met Glu Asp Asp Glu Ile Ala Arg Gln Ala
 20 25 30
 Gly Ile Pro Gly Ala Phe Leu Ala Asp Leu Glu Gly Asp Phe Ser Asp
 35 40 45
 Pro His Ser Glu Leu Pro His Thr Ala Pro Pro Asn Leu Val Gly Leu
 50 55 60
 Leu Glu Ser Tyr Gly Ile Ser Thr Asp Ser Thr Val Val Val Tyr Asp
 65 70 75 80
 Leu His Gly Leu Met Val Ala Pro Arg Val Trp Trp Leu Leu Arg Val
 85 90 95
 Ala Gly Leu Ser Ser Ile Gly Val Leu Asp Gly Gly Leu Pro Ala Trp
 100 105 110
 Val Asp Ala Gly Leu Pro Thr Glu Pro Leu Ser Leu Pro Thr Ser Gly
 115 120 125
 Gly Arg Ile Ser Ala Glu Pro Gln Pro Asp Leu Leu Val Gly Ala Ser
 130 135 140
 Gly Val Glu Arg Ala Ile Ala Arg Ser Ser Lys Ala Val Ile Asp Ala
 145 150 155 160
 Arg Asn Ala Ser Arg Phe Ala Gly Val Glu Glu Glu Pro Arg Pro Gly
 165 170 175
 Leu Arg Lys Gly Ser Ile Pro Gly Ser Val Asn Ile Pro Phe Thr Asp

180 185 190

Ile Ser Asp Glu His Gly Phe Val Arg Pro Ala Glu Glu Leu Lys Glu
195 200 205

Leu Ile Phe Ser Arg Thr Asn Gly Ala Gln Ser Leu Val Phe Ser Cys
210 215 220

Gly Ser Gly Val Thr Ala Cys Val Asp Ala Tyr Ala Ala Val Ile Ala
225 230 235 240

Gly Tyr Asp Asp Val Val Val Tyr Glu Gly Ser Trp Ala Glu Trp Gly
245 250 255

Asn Pro Ala Asn Gln Lys Pro Ile Ala
260 265

<210> 353
<211> 945
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(922)
<223> RXA01664

<400> 353
cgggttacca aagtgaatgg taggggaagt ttccgtgtct tataccggtt aggttttggc 60

cgcgctgcgc ttggtcacat taacgcctag gctcggggct atg acc gtg ttg att 115
Met Thr Val Leu Ile
1 5

tct ccg.tcc acc ctt gct gaa tca atc cac gct ggt aag aaa caa act 163
Ser Pro Ser Thr Leu Ala Glu Ser Ile His Ala Gly Lys Lys Gln Thr
10 15 20

gtt ctc gct gct ttc tgg gct cca att gaa gga gca ggc cgc aca gtt 211
Val Leu Ala Ala Phe Trp Ala Pro Ile Glu Gly Ala Gly Arg Thr Val
25 30 35

ttc tgc tct gag cac atc cca act tcc att ttc tgc gac cct gcc.ctt 259
Phe Cys Ser Glu His Ile Pro Thr Ser Ile Phe Cys Asp Pro Ala Leu
40 45 50

gag ctt tcc gga gtt cct tcc tct gaa gat ggc cgc aac cca ctg cca 307
Glu Leu Ser Gly Val Pro Ser Ser Glu Asp Gly Arg Asn Pro Leu Pro
55 60 65

ccg ctg aat gtg ttg gca cgt tct ttc agg acc tgg ggt ttg aat acc 355
Pro Leu Asn Val Leu Ala Arg Ser Phe Arg Thr Trp Gly Leu Asn Thr
70 75 80 85

gat cgt gaa atc gtg ttt tac gat cag gga cgt ggc ctt ttt gct gca 403
Asp Arg Glu Ile Val Phe Tyr Asp Gln Gly Arg Gly Leu Phe Ala Ala
90 95 100

cgc gcc tgg tgg atc ctc cga tgg gcg ggc atg ccc aac gtt cgc atc 451
Arg Ala Trp Trp Ile Leu Arg Trp Ala Gly Met Pro Asn Val Arg Ile

105	110	115	
ctt gac ggt ggt ttc cag aag tgg gaa gac cat gag ctg gga cac gct			499
Leu Asp Gly Gly Phe Gln Lys Trp Glu Asp His Glu Leu Gly His Ala			
120	125	130	
ggc ggg cct gga aac ttc ccg cac ttt tgc aat gtg cgt ccc aac cca			547
Gly Gly Pro Gly Asn Phe Pro His Phe Cys Asn Val Arg Pro Asn Pro			
135	140	145	
ggt cag ctg tcg gta gcg acc atc gaa gat gtc aag gca cat cag ggc			595
Gly Gln Leu Ser Val Ala Thr Ile Glu Asp Val Lys Ala His Gln Gly			
150	155	160	165
att ttg att gat tct cgc gat gaa caa cga ttt gcg ggt cgc agt gaa			643
Ile Leu Ile Asp Ser Arg Asp Glu Gln Arg Phe Ala Gly Arg Ser Glu			
170	175	180	
aag ctc gat ctg aaa gcc gga cac att cca ggc gct atc aac atc aac			691
Lys Leu Asp Leu Lys Ala Gly His Ile Pro Gly Ala Ile Asn Ile Asn			
185	190	195	
gct aaa tct ttg ctg gaa gat gat ttc acc ttc aaa tca cca gaa gaa			739
Ala Lys Ser Leu Leu Glu Asp Asp Phe Thr Phe Lys Ser Pro Glu Glu			
200	205	210	
atc cgc cag att ttt gcg gac aag ggg gta acc agc gga gag aac gtc			787
Ile Arg Gln Ile Phe Ala Asp Lys Gly Val Thr Ser Gly Glu Asn Val			
215	220	225	
atc gtt tat tcc ggt tcc ggt aac cac tcg tcc cag ttg ctg gct ggc			835
Ile Val Tyr Ser Gly Ser Gly Asn His Ser Ser Gln Leu Leu Ala Gly			
230	235	240	245
atg gag cac gcg ggg cta acc ggt gcg agc cat tat ttt gct ggt tgg			883
Met Glu His Ala Gly Leu Thr Gly Ala Ser His Tyr Phe Ala Gly Trp			
250	255	260	
tca cag tgg agc gct aac ccc gag aat cct atc gag gcc taaaatcgtg			932
Ser Gln Trp Ser Ala Asn Pro Glu Asn Pro Ile Glu Ala			
265	270		
gcttgagtac gca			945

<210> 354

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

Met Thr Val Leu Ile Ser Pro Ser Thr Leu Ala Glu Ser Ile His Ala	
1 5 10 15	

Gly Lys Lys Gln Thr Val Leu Ala Ala Phe Trp Ala Pro Ile Glu Gly	
20 25 30	

Ala Gly Arg Thr Val Phe Cys Ser Glu His Ile Pro Thr Ser Ile Phe	
35 40 45	

Cys Asp Pro Ala Leu Glu Leu Ser Gly Val Pro Ser Ser Glu Asp Gly	
---	--

50 55 60
 Arg Asn Pro Leu Pro Pro Leu Asn Val Leu Ala Arg Ser Phe Arg Thr
 65 70 75 80
 Trp Gly Leu Asn Thr Asp Arg Glu Ile Val Phe Tyr Asp Gln Gly Arg
 85 90 95
 Gly Leu Phe Ala Ala Arg Ala Trp Trp Ile Leu Arg Trp Ala Gly Met
 100 105 110
 Pro Asn Val Arg Ile Leu Asp Gly Gly Phe Gln Lys Trp Glu Asp His
 115 120 125
 Glu Leu Gly His Ala Gly Gly Pro Gly Asn Phe Pro His Phe Cys Asn
 130 135 140
 Val Arg Pro Asn Pro Gly Gln Leu Ser Val Ala Thr Ile Glu Asp Val
 145 150 155 160
 Lys Ala His Gln Gly Ile Leu Ile Asp Ser Arg Asp Glu Gln Arg Phe
 165 170 175
 Ala Gly Arg Ser Glu Lys Leu Asp Leu Lys Ala Gly His Ile Pro Gly
 180 185 190
 Ala Ile Asn Ile Asn Ala Lys Ser Leu Leu Glu Asp Asp Phe Thr Phe
 195 200 205
 Lys Ser Pro Glu Glu Ile Arg Gln Ile Phe Ala Asp Lys Gly Val Thr
 210 215 220
 Ser Gly Glu Asn Val Ile Val Tyr Ser Gly Ser Gly Asn His Ser Ser
 225 230 235 240
 Gln Leu Leu Ala Gly Met Glu His Ala Gly Leu Thr Gly Ala Ser His
 245 250 255
 Tyr Phe Ala Gly Trp Ser Gln Trp Ser Ala Asn Pro Glu Asn Pro Ile
 260 265 270
 Glu Ala

<210> 355

<211> 746

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(723)

<223> RXN02334

<400> 355

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 Val Lys Asp Leu Asn Asp Pro Leu Thr Arg Asp Phe Ile Asp Gly Glu
 1 5 10 15

gct ttc gct gag ctg atg aac cgc aag ggc atc gct cgc gat gac acc 96

Ala	Phe	Ala	Glu	Leu	Met	Asn	Arg	Lys	Gly	Ile	Ala	Arg	Asp	Asp	Thr		
			20					25					30				
gtt	gtt	gtc	tac	ggt	gac	aag	tcc	aac	tgg	tgg	gct	gcg	ttc	acc	ctg	144	
Val	Val	Val	Tyr	Gly	Asp	Lys	Ser	Asn	Trp	Trp	Ala	Ala	Phe	Thr	Leu		
		35					40					45					
tgg	gtc	ttc	gaa	ctg	ttc	ggc	cac	tcc	gat	gtc	cgc	ctg	ctc	aac	ggc	192	
Trp	Val	Phe	Glu	Leu	Phe	Gly	His	Ser	Asp	Val	Arg	Leu	Leu	Asn	Gly		
	50					55				60							
ggc	cgc	gac	gcg	tgg	atg	gct	gaa	gag	cgc	gac	acc	tcc	tac	gtg	gtt	240	
Gly	Arg	Asp	Ala	Trp	Met	Ala	Glu	Glu	Arg	Asp	Thr	Ser	Tyr	Val	Val		
65					70				75						80		
ccg	gag	tac	ccc	tcc	gcc	aac	tac	ccc	gtc	gtg	gag	cgt	gtc	gac	gaa	288	
Pro	Glu	Tyr	Pro	Ser	Ala	Asn	Tyr	Pro	Val	Val	Glu	Arg	Val	Asp	Glu		
				85					90					95			
aac	cag	cgc	gcg	ttc	gtg	gct	gag	gtg	ctc	ggg	tcg	ctc	acg	caa	tcc	336	
Asn	Gln	Arg	Ala	Phe	Val	Ala	Glu	Val	Leu	Gly	Ser	Leu	Thr	Gln	Ser		
			100					105					110				
ggg	ggc	atg	acg	ctt	gtc	gac	gtc	agg	acc	cct	tcg	gag	ttc	tcc	gga	384	
Gly	Gly	Met	Thr	Leu	Val	Asp	Val	Arg	Thr	Pro	Ser	Glu	Phe	Ser	Gly		
		115					120					125					
ttg	gat	gag	cac	ggc	aac	cca	acc	tca	aac	acc	ggc	gtg	ctt	cgt	ggg	432	
Leu	Asp	Glu	His	Gly	Asn	Pro	Thr	Ser	Asn	Thr	Gly	Val	Leu	Arg	Gly		
	130					135					140						
gga	cac	atc	cca	ggc	gcg	atc	aac	ctg	gat	tgg	tcg	gac	gct	gtt	ctt	480	
Gly	His	Ile	Pro	Gly	Ala	Ile	Asn	Leu	Asp	Trp	Ser	Asp	Ala	Val	Leu		
145					150					155					160		
ccc	aac	gga	aac	ttc	cgc	acc	cgt	gca	gag	ttg	gac	aag	ctc	tac	gcc	528	
Pro	Asn	Gly	Asn	Phe	Arg	Thr	Arg	Ala	Glu	Leu	Asp	Lys	Leu	Tyr	Ala		
				165					170					175			
gat	ctc	aac	cca	gct	gac	gat	acc	gtt	gtc	tac	tgc	cag	gtt	ggc	gac	576	
Asp	Leu	Asn	Pro	Ala	Asp	Asp	Thr	Val	Val	Tyr	Cys	Gln	Val	Gly	Asp		
			180					185					190				
cgc	gcg	gcc	cac	acc	tgg	ttc	gtg	ctg	aag	tat	ctg	ctc	ggg	ttc	aac	624	
Arg	Ala	Ala	His	Thr	Trp	Phe	Val	Leu	Lys	Tyr	Leu	Leu	Gly	Phe	Asn		
		195					200					205					
aac	gtc	cga	aac	tat	gac	gga	tcg	tgg	gca	gaa	tgg	ggc	aat	atg	gtt	672	
Asn	Val	Arg	Asn	Tyr	Asp	Gly	Ser	Trp	Ala	Glu	Trp	Gly	Asn	Met	Val		
	210					215					220						
cgc	atg	ccg	atc	gaa	act	ggc	gaa	aac	acc	aaa	aat	aac	gtt	tcg	gtg	720	
Arg	Met	Pro	Ile	Glu	Thr	Gly	Glu	Asn	Thr	Lys	Asn	Asn	Val	Ser	Val		
225					230					235					240		
tca	taga	taggc	gtat	cccc	ttt											746	
Ser																	

<210> 356

<211> 241

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 356

Val Lys Asp Leu Asn Asp Pro Leu Thr Arg Asp Phe Ile Asp Gly Glu
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Ala Phe Ala Glu Leu Met Asn Arg Lys Gly Ile Ala Arg Asp Asp Thr
 20 25 30

Val Val Val Tyr Gly Asp Lys Ser Asn Trp Trp Ala Ala Phe Thr Leu
 35 40 45

Trp Val Phe Glu Leu Phe Gly His Ser Asp Val Arg Leu Leu Asn Gly
 50 55 60

Gly Arg Asp Ala Trp Met Ala Glu Glu Arg Asp Thr Ser Tyr Val Val
 65 70 75 80

Pro Glu Tyr Pro Ser Ala Asn Tyr Pro Val Val Glu Arg Val Asp Glu
 85 90 95

Asn Gln Arg Ala Phe Val Ala Glu Val Leu Gly Ser Leu Thr Gln Ser
 100 105 110

Gly Gly Met Thr Leu Val Asp Val Arg Thr Pro Ser Glu Phe Ser Gly
 115 120 125

Leu Asp Glu His Gly Asn Pro Thr Ser Asn Thr Gly Val Leu Arg Gly
 130 135 140

Gly His Ile Pro Gly Ala Ile Asn Leu Asp Trp Ser Asp Ala Val Leu
 145 150 155 160

Pro Asn Gly Asn Phe Arg Thr Arg Ala Glu Leu Asp Lys Leu Tyr Ala
 165 170 175

Asp Leu Asn Pro Ala Asp Asp Thr Val Val Tyr Cys Gln Val Gly Asp
 180 185 190

Arg Ala Ala His Thr Trp Phe Val Leu Lys Tyr Leu Leu Gly Phe Asn
 195 200 205

Asn Val Arg Asn Tyr Asp Gly Ser Trp Ala Glu Trp Gly Asn Met Val
 210 215 220

Arg Met Pro Ile Glu Thr Gly Glu Asn Thr Lys Asn Asn Val Ser Val
 225 230 235 240

Ser

<210> 357

<211> 377

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(354)

<223> FRXA02334

<400> 357

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Gly Val Leu Pro Asp Trp Met Ser Thr Ala Thr Gln Pro Ser Asn Thr
  1             5             10             15

ggc gtg ctt cgt ggt gaa cac atc cca ggc gcg atc aac ctg gat tgg 96
Gly Val Leu Arg Gly Glu His Ile Pro Gly Ala Ile Asn Leu Asp Trp
             20             25             30

tcg gac gct gtt ctt ccc aac gga aac ttc cgc acc cgt gca gag ttg 144
Ser Asp Ala Val Leu Pro Asn Gly Asn Phe Arg Thr Arg Ala Glu Leu
             35             40             45

gac aag ctc tac gcc gat ctc aac cca gct gac gat acc gtt gtc tac 192
Asp Lys Leu Tyr Ala Asp Leu Asn Pro Ala Asp Asp Thr Val Val Tyr
             50             55             60

tgc cag gtt ggc gac cgc gcg gcc cac acc tgg ttc gtg ctg aag tat 240
Cys Gln Val Gly Asp Arg Ala Ala His Thr Trp Phe Val Leu Lys Tyr
             65             70             75             80

ctg ctc ggt ttc aac aac gtc cga aac tat gac gga tcg tgg gca gaa 288
Leu Leu Gly Phe Asn Asn Val Arg Asn Tyr Asp Gly Ser Trp Ala Glu
             85             90             95

tgg ggc aat atg gtt cgc atg ccg atc gaa act ggc gaa aac acc aaa 336
Trp Gly Asn Met Val Arg Met Pro Ile Glu Thr Gly Glu Asn Thr Lys
             100             105             110

aat aac gtt tcg gtg tca tagaataggc gtatccccctt ttt 377
Asn Asn Val Ser Val Ser
             115

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<210> 358

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

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Gly Val Leu Pro Asp Trp Met Ser Thr Ala Thr Gln Pro Ser Asn Thr
  1             5             10             15

Gly Val Leu Arg Gly Glu His Ile Pro Gly Ala Ile Asn Leu Asp Trp
             20             25             30

Ser Asp Ala Val Leu Pro Asn Gly Asn Phe Arg Thr Arg Ala Glu Leu
             35             40             45

Asp Lys Leu Tyr Ala Asp Leu Asn Pro Ala Asp Asp Thr Val Val Tyr
             50             55             60

Cys Gln Val Gly Asp Arg Ala Ala His Thr Trp Phe Val Leu Lys Tyr
             65             70             75             80

Leu Leu Gly Phe Asn Asn Val Arg Asn Tyr Asp Gly Ser Trp Ala Glu
             85             90             95

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Trp Gly Asn Met Val Arg Met Pro Ile Glu Thr Gly Glu Asn Thr Lys
 100 105 110

Asn Asn Val Ser Val Ser
 115

<210> 359

<211> 3945

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(3922)

<223> RXN01499

<400> 359

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 acagttcctg agatccgccc aggcgcccc gaagcgtact ttg tgg gac gtc tta 115
 Leu Trp Asp Val Leu
 1 5
 gaa tcc gtc gcc tct act tat cct gag gca gca gct att gac gat ggc 163
 Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala Ala Ile Asp Asp Gly
 10 15 20
 cag gtg ttg acc tac gca gag ttg atg gaa gaa gtc acc gcg ttg gct 211
 Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu Val Thr Ala Leu Ala
 25 30 35
 gat tcc att cat gca cag ggc att cgc cgt ggt gat cgc atc ggt att 259
 Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly Asp Arg Ile Gly Ile
 40 45 50
 cgc atg ccg tct ggt acg cgt gac ctt tac atc gct att ttg gcc act 307
 Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile Ala Ile Leu Ala Thr
 55 60 65
 ctc gct gct ggt gct gct tac gtg cca gtt gat gca gat gat cct gaa 355
 Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp Ala Asp Asp Pro Glu
 70 75 80 85
 gag cgc gcc gag atg gtg ttt ggt gaa gca aat att aat gcg ctt ttc 403
 Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn Ile Asn Ala Leu Phe
 90 95 100
 gac gcc acc ggc ttc cat atg ctt cgc ccg acc gcg ggc ggc gat acc 451
 Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr Ala Gly Gly Asp Thr
 105 110 115
 cgt aga cca cgc ttg gat gat acg gcg tgg att atc ttt act tcc ggt 499
 Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile Ile Phe Thr Ser Gly
 120 125 130
 tcc acc ggc aag cct aag ggt gtg gct gtg tcc cac cgt tca gct gcg 547
 Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser His Arg Ser Ala Ala
 135 140 145
 gct ttc gtg gat gcc gaa gca caa atg ttc ctt gtc gat cac cct tcc 595

Ala 150	Phe	Val	Asp	Ala	Glu 155	Ala	Gln	Met	Phe	Leu 160	Val	Asp	His	Pro	Ser 165	
ggc Gly	ccc Pro	ctt Leu	ggc Gly	cca Pro 170	gaa Glu	gac Asp	cga Arg	gtc Val	ctt Leu 175	gcg Ala	gga Gly	ttg Leu	tct Ser	gta Val 180	gcc Ala	643
ttt Phe	gac Asp	gca Ala	tct Ser 185	tgt Cys	gag Glu	gaa Glu	atg Met	tgg Trp 190	ttg Leu	gcc Ala	tgg Trp	ggc Gly	cac His 195	ggc Gly	gcc Ala	691
tgc Cys	ttg Leu	gtg Val 200	cca Pro	gca Ala	cca Pro	cgc Arg	tcc Ser 205	cta Leu	gtc Val	cgt Arg	tcc Ser 210	ggt Gly	atg Met	gac Asp	ttg Leu	739
ggc Gly	cca Pro 215	tgg Trp	ctg Leu	att Ile	cgc Arg	cgc Arg	gac Asp 220	atc Ile	agt Ser	gtc Val	gtc Val 225	tcc Ser	acc Thr	gtc Val	cca Pro	787
act Thr 230	ctg Leu	gct Ala	ggt Gly	ctg Leu	tgg Trp 235	cca Pro	gca Ala	gaa Glu	gca Ala	ttg Leu 240	tca Ser	cag Gln	gtc Val	cgc Arg	ttg Leu 245	835
ctc Leu	atc Ile	gtc Val	ggc Gly 250	ggc Gly	gag Glu	gct Ala	tgc Cys	tgc Ser	cag Gln 255	gag Glu	ctc Leu	ggt Val	gaa Glu	cgc Arg 260	tta Leu	883
tcg Ser	acg Thr	cct Pro	gac Asp 265	cgc Arg	gag Glu	gtg Val	tgg Trp	aac Asn 270	act Thr	tac Tyr	ggc Gly	ccc Pro	acc Thr 275	gaa Glu	gca Ala	931
acg Thr	gtg Val	ggt Val 280	gcc Ala	tgt Cys	ggc Gly	act Thr	caa Gln 285	ctc Leu	tat Tyr	gct Ala	ggt Gly	cag Gln 290	cca Pro	gtg Val	ggc Gly	979
att Ile 295	ggt Gly	ttg Leu	cca Pro	ctt Leu	gct Ala	ggt Gly 300	tgg Trp	gat Asp	ctt Leu	ggt Val 305	ggt Val	gtc Val	gac Asp	gat Asp	gcc Ala	1027
ggc Gly 310	gaa Glu	cct Pro	gtc Val	gga Gly	atc Ile 315	ggc Gly	gag Glu	gtc Val	ggc Gly	gaa Glu 320	ttg Leu	gtc Val	atc Ile	ggt Gly	ggt Gly 325	1075
gtg Val	ggt Gly	ctt Leu	gca Ala	cgc Arg 330	tac Tyr	ctt Leu	gat Asp	cca Pro	gaa Glu 335	aaa Lys	gac Asp	cgc Arg	gag Glu	aag Lys 340	tat Tyr	1123
gcg Ala	cca Pro	ctg Leu	aag Lys 345	tct Ser	gtt Val	ggt Gly	tgg Trp	acc Thr 350	cgc Arg	gct Ala	tat Tyr	cgt Arg	tcc Ser 355	ggt Gly	gac Asp	1171
cac His	ggt Val	cgt Arg 360	ctg Leu	gaa Glu	gaa Glu	gat Asp	ggc Gly 365	ctc Leu	tac Tyr	ttt Phe	gtg Val	ggc Gly 370	cgc Arg	ggt Val	gat Asp	1219
gat Asp	cag Gln 375	gtg Val	aaa Lys	atc Ile	ggc Gly	ggt Gly 380	cga Arg	cgc Arg	atc Ile	gag Glu	ctc Leu 385	ggt Gly	gaa Glu	ggt Val	gat Asp	1267
gcc Ala	aat Asn	gtg Val	gca Ala	gcg Ala	ctt Leu	tcc Ser	aac Asn	ggt Val	cgt Arg	tcc Ser	tcc Ser	gca Ala	gtg Val	ggt Val	ggt Val	1315

390	395	400	405	
cag acc act ggt gcg gat caa aaa gtt ctg gtt gca tac gtt tct ttg				1363
Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val Ala Tyr Val Ser Leu	410	415	420	
gaa gat gct gca gct gga ttt gat cac aac gtc gcg act gcc cga ctc				1411
Glu Asp Ala Ala Ala Gly Phe Asp His Asn Val Ala Thr Ala Arg Leu	425	430	435	
acc gaa acc atg cct gct gct ttg gtt ccg cgc att cac gtg atg gat				1459
Thr Glu Thr Met Pro Ala Ala Leu Val Pro Arg Ile His Val Met Asp	440	445	450	
gat ctg cct gtc acc acc tcc ggc aag gtt gat aag aag tct ttg ccg				1507
Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp Lys Lys Ser Leu Pro	455	460	465	
tgg cct ctt cct ggc acc gtg gtg gaa gct aat gac ctc agc gca acg				1555
Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn Asp Leu Ser Ala Thr	470	475	480	485
gaa gcg tgg att gct cag gaa tgg gtc gat atc ctc ggc act tct gtg				1603
Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile Leu Gly Thr Ser Val	490	495	500	
agc agc aaa gac gcc gac ttc ttc tcc ctt ggc ggt acc tct ctc gcg				1651
Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly Gly Thr Ser Leu Ala	505	510	515	
gct gcg act ttg gtt ggc cgg gta cgc gca aag gtt ccc acc gct gcg				1699
Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys Val Pro Thr Ala Ala	520	525	530	
gtg cgt gat ctt tac gat cac cct cgc ttg gag aaa ttc gcc gag cgt				1747
Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu Lys Phe Ala Glu Arg	535	540	545	
gtc gag gct atc gcc gcc gac act ggc att tct ttg gag gcg cca aac				1795
Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser Leu Glu Ala Pro Asn	550	555	560	565
cag gtg gag gag cgc gtc gtc aag cct gtt tct ttt ggc act cgt gtg				1843
Gln Val Glu Glu Arg Val Val Lys Pro Val Ser Phe Gly Thr Arg Val	570	575	580	
atg cag acc ctc atc cag att ccg atc atg acg ctg caa gca gca cag				1891
Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr Leu Gln Ala Ala Gln	585	590	595	
tgg att gca tgg ttg ctg ttg ggc aac aac atc atg gca gcg ctt gat				1939
Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile Met Ala Ala Leu Asp	600	605	610	
ttc gat tgg gct gtt cat gtc tcc tgg tgg ctt gtc atc ggc atg att				1987
Phe Asp Trp Ala Val His Val Ser Trp Trp Leu Val Ile Gly Met Ile	615	620	625	
ttg gtg ttc gct acc ccg att ggt cgc ttg ccg atc ggc ggt tgg ggc				2035
Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro Ile Gly Gly Trp Gly	630	635	640	645

gcc cgc atc atc acc cgt ggc ata act cct ggc tcc tac cct cgt ggc	2083
Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly Ser Tyr Pro Arg Gly	
650 655 660	
ggt tcc act cac ctg cgc att tgg tcc gcc gag cgc ctt gct gat gcc	2131
Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu Arg Leu Ala Asp Ala	
665 670 675	
tct ggc tct cgc aat att tct ggc gca acc tgg gtg aac tac ttc gcg	2179
Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp Val Asn Tyr Phe Ala	
680 685 690	
cgt tcc ctg ggt gtg aag atg ggc aag ggc gtg gat ctt cac tcc ctg	2227
Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val Asp Leu His Ser Leu	
695 700 705	
cca cca atc act ggc ctt ttg acc ttg ggc aac aat gtt tcc atc gag	2275
Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn Asn Val Ser Ile Glu	
710 715 720 725	
caa gaa gtt gac ctt cgt ggc tac tgg ctc gac ggc gat atc ctg cgt	2323
Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp Gly Asp Ile Leu Arg	
730 735 740	
gta ggc acc att gag gtc cat gac aac gct cgc atc ggc gct cgt tcc	2371
Val Gly Thr Ile Glu Val His Asp Asn Ala Arg Ile Gly Ala Arg Ser	
745 750 755	
acc ctg ctt ccc ggc acc gtg gtg ggc acc ggc gct cac ctg ctg cct	2419
Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly Ala His Leu Leu Pro	
760 765 770	
ggt tca aca gtg act ggt gat aag acc atc aag cct ggt tct cgt tgg	2467
Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys Pro Gly Ser Arg Trp	
775 780 785	
gct ggc tcc cct gca caa aag gtg ggt cgt gca aag cac cgg ttc cca	2515
Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala Lys His Arg Phe Pro	
790 795 800 805	
acc tcc cat cct cca cgc agg tcc cgg tgg gtt ccg gtg ttc ggc gcg	2563
Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val Pro Val Phe Gly Ala	
810 815 820	
acc tcc atc gtg ttg tcg ctg ctg cca ctt cag gct ctc gct att ggc	2611
Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln Ala Leu Ala Ile Gly	
825 830 835	
gct gct atc acc ttg tgg ctg gcc acg att agc ccg ctt cca ctg atc	2659
Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser Pro Leu Pro Leu Ile	
840 845 850	
tgg ggt gtg ctg gtt ttt gct acc gtc ggc gcg ttg gct gcg ttc ttt	2707
Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala Leu Ala Ala Phe Phe	
855 860 865	
gct tac acc gtg acc atc tgg gtg ctt gtc cgt ttg atc cag atc ggc	2755
Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg Leu Ile Gln Ile Gly	
870 875 880 885	

atc aag ggc ggc acc gca cca gtg agg tcc cgt ctt ggt tgg cag gtc	2803
Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg Leu Gly Trp Gln Val	
890 895 900	
tgg gca gtt caa cgc ctc atg gac gat gcc cgc acc tat ctc ttc ccg	2851
Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg Thr Tyr Leu Phe Pro	
905 910 915	
ctc tac gca tcc caa ctg acc cca ctg tgg ttc cgc agc ttg ggc gcg	2899
Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe Arg Ser Leu Gly Ala	
920 925 930	
aag atc ggc aag gat gtt gag atc tcc acc gcg gtg atg gtt cct aaa	2947
Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala Val Met Val Pro Lys	
935 940 945	
ctg gct gat atc cgc gaa ggc gca ttc ctg gcc gat gac acc ctc atc	2995
Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala Asp Asp Thr Leu Ile	
950 955 960 965	
ggt ggc tat gag ctg ggt aat ggt tgg ctg ctc agt ggt gaa acc cgc	3043
Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu Ser Gly Glu Thr Arg	
970 975 980	
gtg ggt aag cgt tcc ttc att ggt aac tct ggc atc gca gga cct gag	3091
Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly Ile Ala Gly Pro Glu	
985 990 995	
cgc aag ctc gct aag aac tcc ctg gtt gca gtg ctc tcc tcc acc ccg	3139
Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val Leu Ser Ser Thr Pro	
1000 1005 1010	
aag aag gct aag gcc aac tcc aac tgg tgg ggt tcc cct cca gag cgc	3187
Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly Ser Pro Pro Glu Arg	
1015 1020 1025	
atg cgt cgt gtc act gtc gaa gtt gat gag ggc gaa gca aag acc tac	3235
Met Arg Arg Val Thr Val Glu Val Asp Glu Gly Glu Ala Lys Thr Tyr	
1030 1035 1040 1045	
agc cct ggc ttt ggt gtg aag ttt gca cgt ggc gcg gtg gaa acc gca	3283
Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly Ala Val Glu Thr Ala	
1050 1055 1060	
cgt ctg ctt gct cca ata acc tct ggt gtg ttg gct gcg ctg tca ctg	3331
Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu Ala Ala Leu Ser Leu	
1065 1070 1075	
ctg ctc atg cag tac ctg ctc act gag ttc aac atg tgg atc acc tgg	3379
Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn Met Trp Ile Thr Trp	
1080 1085 1090	
ttg ctt ggc gga ctg atc ctc atg acg gtt ggt gtg ctc gcc atg ggc	3427
Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly Val Leu Ala Met Gly	
1095 1100 1105	
att acg gtt gtg atg aag tgg gtt tgc gtc ggc aag cat aag ccg tct	3475
Ile Thr Val Val Met Lys Trp Val Cys Val Gly Lys His Lys Pro Ser	
1110 1115 1120 1125	
gag cac cct ctc ttc agc cgc ttt gtg tgg ctg aat gag ctg caa gat	3523

Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu Asn Glu Leu Gln Asp
 1130 1135 1140

gcg ttc gtg gaa tcc gtg gct ggc cca tgg ttc ctc gtg ccc aac ctg 3571
 Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe Leu Val Pro Asn Leu
 1145 1150 1155

ggc acc ggc gcg ctg aac gcc ggc atg agc gcg ctt ggc gca cac atc 3619
 Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala Leu Gly Ala His Ile
 1160 1165 1170

ggc cgt ggc gca tgg atc gaa tcc tac tgg ctg ccg gaa acc gac ctc 3667
 Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu Pro Glu Thr Asp Leu
 1175 1180 1185

tgc tac atc ggc aag ggc gca acc gtg ggc cct ggc gtg gtc gtg cag 3715
 Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro Gly Val Val Val Gln
 1190 1195 1200 1205

acc cac ctc ttc cag gac cgc gtg atg agc cta gat acg gtg acc gtc 3763
 Thr His Leu Phe Gln Asp Arg Val Met Ser Leu Asp Thr Val Thr Val
 1210 1215 1220

gct gac ggc gcc acc cta gcg gac cac tcc gtt gcc ctt cct gct tcg 3811
 Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val Ala Leu Pro Ala Ser
 1225 1230 1235

ctt atc gac gcc tcc gcc acc atc ggc cca ggc tcg ctg gtg atg cgc 3859
 Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly Ser Leu Val Met Arg
 1240 1245 1250

ggc gac aag gta cca gcg cat acc cgc tgg caa ggc aac cca att gag 3907
 Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln Gly Asn Pro Ile Glu
 1255 1260 1265

ccg tgg agc aac tct taaataacaa caatcagccg gat 3945
 Pro Trp Ser Asn Ser
 1270

<210> 360

<211> 1274

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Leu Trp Asp Val Leu Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala
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Ala Ile Asp Asp Gly Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu
 20 25 30

Val Thr Ala Leu Ala Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly
 35 40 45

Asp Arg Ile Gly Ile Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile
 50 55 60

Ala Ile Leu Ala Thr Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp
 65 70 75 80

Ala Asp Asp Pro Glu Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn
 85 90 95
 Ile Asn Ala Leu Phe Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr
 100 105 110
 Ala Gly Gly Asp Thr Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile
 115 120 125
 Ile Phe Thr Ser Gly Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser
 130 135 140
 His Arg Ser Ala Ala Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu
 145 150 155 160
 Val Asp His Pro Ser Gly Pro Leu Gly Pro Glu Asp Arg Val Leu Ala
 165 170 175
 Gly Leu Ser Val Ala Phe Asp Ala Ser Cys Glu Glu Met Trp Leu Ala
 180 185 190
 Trp Gly His Gly Ala Cys Leu Val Pro Ala Pro Arg Ser Leu Val Arg
 195 200 205
 Ser Gly Met Asp Leu Gly Pro Trp Leu Ile Arg Arg Asp Ile Ser Val
 210 215 220
 Val Ser Thr Val Pro Thr Leu Ala Gly Leu Trp Pro Ala Glu Ala Leu
 225 230 235 240
 Ser Gln Val Arg Leu Leu Ile Val Gly Gly Glu Ala Cys Ser Gln Glu
 245 250 255
 Leu Val Glu Arg Leu Ser Thr Pro Asp Arg Glu Val Trp Asn Thr Tyr
 260 265 270
 Gly Pro Thr Glu Ala Thr Val Val Ala Cys Gly Thr Gln Leu Tyr Ala
 275 280 285
 Gly Gln Pro Val Gly Ile Gly Leu Pro Leu Ala Gly Trp Asp Leu Val
 290 295 300
 Val Val Asp Asp Ala Gly Glu Pro Val Gly Ile Gly Glu Val Gly Glu
 305 310 315 320
 Leu Val Ile Gly Gly Val Gly Leu Ala Arg Tyr Leu Asp Pro Glu Lys
 325 330 335
 Asp Arg Glu Lys Tyr Ala Pro Leu Lys Ser Val Gly Trp Thr Arg Ala
 340 345 350
 Tyr Arg Ser Gly Asp His Val Arg Leu Glu Glu Asp Gly Leu Tyr Phe
 355 360 365
 Val Gly Arg Val Asp Asp Gln Val Lys Ile Gly Gly Arg Arg Ile Glu
 370 375 380
 Leu Gly Glu Val Asp Ala Asn Val Ala Ala Leu Ser Asn Val Arg Ser
 385 390 395 400
 Ser Ala Val Val Val Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val

482

Gly Asp Ile Leu Arg Val Gly Thr Ile Glu Val His Asp Asn Ala Arg
 740 745 750
 Ile Gly Ala Arg Ser Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly
 755 760 765
 Ala His Leu Leu Pro Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys
 770 775 780
 Pro Gly Ser Arg Trp Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala
 785 790 795 800
 Lys His Arg Phe Pro Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val
 805 810 815
 Pro Val Phe Gly Ala Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln
 820 825 830
 Ala Leu Ala Ile Gly Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser
 835 840 845
 Pro Leu Pro Leu Ile Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala
 850 855 860
 Leu Ala Ala Phe Phe Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg
 865 870 875 880
 Leu Ile Gln Ile Gly Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg
 885 890 895
 Leu Gly Trp Gln Val Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg
 900 905 910
 Thr Tyr Leu Phe Pro Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe
 915 920 925
 Arg Ser Leu Gly Ala Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala
 930 935 940
 Val Met Val Pro Lys Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala
 945 950 955 960
 Asp Asp Thr Leu Ile Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu
 965 970 975
 Ser Gly Glu Thr Arg Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly
 980 985 990
 Ile Ala Gly Pro Glu Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val
 995 1000 1005
 Leu Ser Ser Thr Pro Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly
 1010 1015 1020
 Ser Pro Pro Glu Arg Met Arg Arg Val Thr Val Glu Val Asp Glu Gly
 1025 1030 1035 1040
 Glu Ala Lys Thr Tyr Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly
 1045 1050 1055

Ala Val Glu Thr Ala Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu
1060 1065 1070

Ala Ala Leu Ser Leu Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn
1075 1080 1085

Met Trp Ile Thr Trp Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly
1090 1095 1100

Val Leu Ala Met Gly Ile Thr Val Val Met Lys Trp Val Cys Val Gly
1105 1110 1115 1120

Lys His Lys Pro Ser Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu
1125 1130 1135

Asn Glu Leu Gln Asp Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe
1140 1145 1150

Leu Val Pro Asn Leu Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala
1155 1160 1165

Leu Gly Ala His Ile Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu
1170 1175 1180

Pro Glu Thr Asp Leu Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro
1185 1190 1195 1200

Gly Val Val Val Gln Thr His Leu Phe Gln Asp Arg Val Met Ser Leu
1205 1210 1215

Asp Thr Val Thr Val Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val
1220 1225 1230

Ala Leu Pro Ala Ser Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly
1235 1240 1245

Ser Leu Val Met Arg Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln
1250 1255 1260

Gly Asn Pro Ile Glu Pro Trp Ser Asn Ser
1265 1270

<210> 361

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN01997

<400> 361

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tatgctgaca gccttgcgga agttgtgtac gttaggggcc atg aca atc aac gag 115

Met Thr Ile Asn Glu

1 5

aag atc gca tca gct ttc aac aac caa gtg act gca gag ctt gaa gct 163

Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr Ala Glu Leu Glu Ala
 10 15 20
 tca atg gtg tac ctt cag ctc tcc tac gtt cta gac gat ctg ggc ctc 211
 Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu Asp Asp Leu Gly Leu
 25 30 35
 acc ggc atg cgc gac tgg atg aag gca cag agc aaa gaa gag ctc gaa 259
 Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser Lys Glu Glu Leu Glu
 40 45 50
 cac gca cag aag ttc gct cag cac ctt ctt gac cgt gac tac acc cca 307
 His Ala Gln Lys Phe Ala Gln His Leu Leu Asp Arg Asp Tyr Thr Pro
 55 60 65
 cag atc ggt gac att gca cca cca aag ctt gat gtc acc tcc gct atc 355
 Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp Val Thr Ser Ala Ile
 70 75 80 85
 gag gct ttc gag gct tcc ctg gca cac gag cag aag atc tcc ggc ctg 403
 Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln Lys Ile Ser Gly Leu
 90 95 100
 atc cgc gag ctc gct gcc atc cag gac gct gag aag gac tac gat tcc 451
 Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu Lys Asp Tyr Asp Ser
 105 110 115
 cgc gca ctg atc gac tgg ttc ctc aac gag cag atc gaa gaa gaa gca 499
 Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln Ile Glu Glu Glu Ala
 120 125 130
 acc gtc ggc gag atc atc gac cgc ctc cgt atc gct ggt gat tcc ggt 547
 Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile Ala Gly Asp Ser Gly
 135 140 145
 tcc gga atc ctg cgc atc gac ggc gaa ctc ggc tcc cgc taaattcccc 596
 Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Gly Ser Arg
 150 155 160
 gcagttttta atg 609

<210> 362

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Met Thr Ile Asn Glu Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr
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 Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu
 20 25 30
 Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser
 35 40 45
 Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp
 50 55 60
 Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp

65		70		75		80
Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln						
	85		90		95	
Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu						
	100		105		110	
Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln						
	115		120		125	
Ile Glu Glu Glu Ala Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile						
	130		135		140	
Ala Gly Asp Ser Gly Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Gly						
	145		150		155	160
Ser Arg						

<210> 363
 <211> 867
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(844)
 <223> RXA01848

<400> 363
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ggcgaccctt ttcgctccta ggcatttgcg cctggcgctcc atg ggg gag gag gac 115
 Met Gly Glu Glu Asp
 1 5

tcc acc cca ggt agg cgt tcc aag gcg tat tcg cgc cag ggc gct gat 163
 Ser Thr Pro Gly Arg Arg Ser Lys Ala Tyr Ser Arg Gln Gly Ala Asp
 10 15 20

gtc cgc ccc atg aag ggt gga cac ggc atc aac tta gtg ggc acg ctc 211
 Val Arg Pro Met Lys Gly Gly His Gly Ile Asn Leu Val Gly Thr Leu
 25 30 35

atg gcg gct acg gaa cgc ggc gcc aac att gtt gaa ggc gtg gtc gat 259
 Met Ala Ala Thr Glu Arg Gly Ala Asn Ile Val Glu Gly Val Val Asp
 40 45 50

ttc cgg ccc acg gac ctg cgg ggt tcg ctg cgc cgt ggg cgc gaa gcc 307
 Phe Arg Pro Thr Asp Leu Arg Gly Ser Leu Arg Arg Gly Arg Glu Ala
 55 60 65

aac ctc atc gtg ttc gtc gtc gac aca tcg ggg tcg atg gct gcg cgt 355
 Asn Leu Ile Val Phe Val Val Asp Thr Ser Gly Ser Met Ala Ala Arg
 70 75 80 85

tcc agg gtg cgt gcg gtc acc ggg act att acc tct atg ctt aac gac 403
 Ser Arg Val Arg Ala Val Thr Gly Thr Ile Thr Ser Met Leu Asn Asp
 90 95 100

gcc tac cag cgc cgc gac aag gtt gcg gtt atc gcg gtc aac ggc aac 451
 Ala Tyr Gln Arg Arg Asp Lys Val Ala Val Ile Ala Val Asn Gly Asn
 105 110 115

aag ccg aca ctg gtg ttg aat cca aca aat tct gtg gag caa gct cag 499
 Lys Pro Thr Leu Val Leu Asn Pro Thr Asn Ser Val Glu Gln Ala Gln
 120 125 130

cag aaa tta aag gat atg ccg atg ggt ggt cgc act cca ctg gca gag 547
 Gln Lys Leu Lys Asp Met Pro Met Gly Gly Arg Thr Pro Leu Ala Glu
 135 140 145

ggg ctg ctc atg gcc aag gat ctc atg gca agg gaa ctc cga aag gaa 595
 Gly Leu Leu Met Ala Lys Asp Leu Met Ala Arg Glu Leu Arg Lys Glu
 150 155 160 165

ccc ggc cga cgc gcg atc ctc atg gtg atg acc gat ggc caa gac acc 643
 Pro Gly Arg Arg Ala Ile Leu Met Val Met Thr Asp Gly Gln Asp Thr
 170 175 180

tcc gat gcc ggc gaa gca ggc att gcc acc gcg gcg gaa aca gtg gtg 691
 Ser Asp Ala Gly Glu Ala Gly Ile Ala Thr Ala Ala Glu Thr Val Val
 185 190 195

aaa tca cga ctg tcc ggc aac gtg gtc atc gac tgc gaa ggc cga ctc 739
 Lys Ser Arg Leu Ser Gly Asn Val Val Ile Asp Cys Glu Gly Arg Leu
 200 205 210

aaa gtg cgc aaa gag cgc gcc ggg gtg ttg gct gaa atg ctc ggt ggt 787
 Lys Val Arg Lys Glu Arg Ala Gly Val Leu Ala Glu Met Leu Gly Gly
 215 220 225

gtg tgc gtg aga ttg cgt gat ctt aac tcc gag cac atc aaa atg gtg 835
 Val Cys Val Arg Leu Arg Asp Leu Asn Ser Glu His Ile Lys Met Val
 230 235 240 245

att aac gcc tagacaacca gagtgagggt ttc 867
 Ile Asn Ala

<210> 364

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Met Gly Glu Glu Asp Ser Thr Pro Gly Arg Arg Ser Lys Ala Tyr Ser
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Arg Gln Gly Ala Asp Val Arg Pro Met Lys Gly Gly His Gly Ile Asn
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Leu Val Gly Thr Leu Met Ala Ala Thr Glu Arg Gly Ala Asn Ile Val
 35 40 45

Glu Gly Val Val Asp Phe Arg Pro Thr Asp Leu Arg Gly Ser Leu Arg
 50 55 60

Arg Gly Arg Glu Ala Asn Leu Ile Val Phe Val Val Asp Thr Ser Gly

65	70	75	80
Ser Met Ala Ala Arg Ser Arg Val Arg Ala Val Thr Gly Thr Ile Thr	85	90	95
Ser Met Leu Asn Asp Ala Tyr Gln Arg Arg Asp Lys Val Ala Val Ile	100	105	110
Ala Val Asn Gly Asn Lys Pro Thr Leu Val Leu Asn Pro Thr Asn Ser	115	120	125
Val Glu Gln Ala Gln Gln Lys Leu Lys Asp Met Pro Met Gly Gly Arg	130	135	140
Thr Pro Leu Ala Glu Gly Leu Leu Met Ala Lys Asp Leu Met Ala Arg	145	150	155
Glu Leu Arg Lys Glu Pro Gly Arg Arg Ala Ile Leu Met Val Met Thr	165	170	175
Asp Gly Gln Asp Thr Ser Asp Ala Gly Glu Ala Gly Ile Ala Thr Ala	180	185	190
Ala Glu Thr Val Val Lys Ser Arg Leu Ser Gly Asn Val Val Ile Asp	195	200	205
Cys Glu Gly Arg Leu Lys Val Arg Lys Glu Arg Ala Gly Val Leu Ala	210	215	220
Glu Met Leu Gly Gly Val Cys Val Arg Leu Arg Asp Leu Asn Ser Glu	225	230	235
His Ile Lys Met Val Ile Asn Ala	245		

<210> 365
 <211> 1224
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1201)
 <223> RXN01849

<400> 365
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 caccaaaaaa tctcaagaaa actcacatta aaggacagta atg gcg tca caa cag 115
 Met Ala Ser Gln Gln
 1 5
 atc cgc tat cca ttc tcc gcg gtt gtg gga caa gac gag ctt cgg ctt 163
 Ile Arg Tyr Pro Phe Ser Ala Val Val Gly Gln Asp Glu Leu Arg Leu
 10 15 20
 gcg ttg atc ctc act gcg att tcc cca cgc att ggt ggc gtg gtg att 211
 Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile Gly Gly Val Val Ile
 25 30 35

cga ggt gag aag ggt aca gcg aaa act acc act gtg cgt gct ttt gct	259
Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr Val Arg Ala Phe Ala	
40 45 50	
ggt ctt tta ggt gat gcc cct ttg gtg aac ttg cct ctc gga tcc acg	307
Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu Pro Leu Gly Ser Thr	
55 60 65	
gag gat cgt gtg gtg ggt tcc ctc aac atg gaa act gtg ttg acc acc	355
Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu Thr Val Leu Thr Thr	
70 75 80 85	
ggc cgt gcg gaa tat cag cca ggt ttg ctc gcg cag gct gat ggc ggt	403
Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala Gln Ala Asp Gly Gly	
90 95 100	
gtg ctg tat gtc gat gag gtc aac ctc ttg gcg gat cac ctg gtg gat	451
Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala Asp His Leu Val Asp	
105 110 115	
gct ctg ctc gat gca gct gca agc ggt cgc gtc agc att gag cgt gac	499
Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val Ser Ile Glu Arg Asp	
120 125 130	
ggt att tcg cat tct tca cca gca aac ttt gtg ttg gtg ggc acc atg	547
Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val Leu Val Gly Thr Met	
135 140 145	
aat ccg gag gaa ggc gag ctg cgc ccg cag ctg ctg gac cgt ttc ggt	595
Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu Leu Asp Arg Phe Gly	
150 155 160 165	
ttg gct gtg gac gtt gct gcg tct acg aac cct gag gtg cgc gtg gag	643
Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro Glu Val Arg Val Glu	
170 175 180	
atc att cgc cgc cgg ctt gat ttt gaa aac gct cct gag cag ttc atg	691
Ile Ile Arg Arg Arg Leu Asp Phe Glu Asn Ala Pro Glu Gln Phe Met	
185 190 195	
gct aag tgg gct gag caa gat gcg gac acc tcc aac cgt att ttg gcg	739
Ala Lys Trp Ala Glu Gln Asp Ala Asp Thr Ser Asn Arg Ile Leu Ala	
200 205 210	
gct aag gat ttg ctg cct ggt gtg gag ctg ccg gat ctg atc ttg tcg	787
Ala Lys Asp Leu Leu Pro Gly Val Glu Leu Pro Asp Leu Ile Leu Ser	
215 220 225	
cag att gcg tgg ttg tgt gca cgt att gaa gtc gac ggt atg cgc gct	835
Gln Ile Ala Trp Leu Cys Ala Arg Ile Glu Val Asp Gly Met Arg Ala	
230 235 240 245	
gac ctg gtg atc acg cgt acc gca ctt gct cac gcc gcg tgg gct gga	883
Asp Leu Val Ile Thr Arg Thr Ala Leu Ala His Ala Ala Trp Ala Gly	
250 255 260	
cgc act gtg gtt acg gaa gaa gac gtg gag atc gca gct cgc cta gcg	931
Arg Thr Val Val Thr Glu Glu Asp Val Glu Ile Ala Ala Arg Leu Ala	
265 270 275	
ttg ccg cac cgc cgt cgc cgt aat cct ttc gat gct cca gaa atg gag	979

Leu Pro His Arg Arg Arg Arg Asn Pro Phe Asp Ala Pro Glu Met Glu
 280 285 290
 gag cgc aag ctt cag gaa acc ctg cag gaa gct cgg gac ttc ttc aaa 1027
 Glu Arg Lys Leu Gln Glu Thr Leu Gln Glu Ala Arg Asp Phe Phe Lys
 295 300 305
 gac aat gaa gat aaa gga cct gcc gcc aag atc acc gat gag gaa acc 1075
 Asp Asn Glu Asp Lys Gly Pro Ala Ala Lys Ile Thr Asp Glu Glu Thr
 310 315 320 325
 ggt gca gag gcc ttt acc gat acc gac aat ccc acc gag gaa gac ggt 1123
 Gly Ala Glu Ala Phe Thr Asp Thr Asp Asn Pro Thr Glu Glu Asp Gly
 330 335 340
 ctg caa gga act gcg cag gcg aag gcg cag act act gga aag gta ggt 1171
 Leu Gln Gly Thr Ala Gln Ala Lys Ala Gln Thr Thr Gly Lys Val Gly
 345 350 355
 act gcc gga tcc ggc gac ccc ttt cgc tcc taggcatttg cgcctggcgt 1221
 Thr Ala Gly Ser Gly Asp Pro Phe Arg Ser
 360 365
 cca 1224

<210> 366

<211> 367

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 366

Met Ala Ser Gln Gln Ile Arg Tyr Pro Phe Ser Ala Val Val Gly Gln
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 Asp Glu Leu Arg Leu Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile
 20 25 30
 Gly Gly Val Val Ile Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr
 35 40 45
 Val Arg Ala Phe Ala Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu
 50 55 60
 Pro Leu Gly Ser Thr Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu
 65 70 75 80
 Thr Val Leu Thr Thr Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala
 85 90 95
 Gln Ala Asp Gly Gly Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala
 100 105 110
 Asp His Leu Val Asp Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val
 115 120 125
 Ser Ile Glu Arg Asp Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val
 130 135 140
 Leu Val Gly Thr Met Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu
 145 150 155 160

Leu Asp Arg Phe Gly Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro
 165 170 175
 Glu Val Arg Val Glu Ile Ile Arg Arg Arg Leu Asp Phe Glu Asn Ala
 180 185 190
 Pro Glu Gln Phe Met Ala Lys Trp Ala Glu Gln Asp Ala Asp Thr Ser
 195 200 205
 Asn Arg Ile Leu Ala Ala Lys Asp Leu Leu Pro Gly Val Glu Leu Pro
 210 215 220
 Asp Leu Ile Leu Ser Gln Ile Ala Trp Leu Cys Ala Arg Ile Glu Val
 225 230 235 240
 Asp Gly Met Arg Ala Asp Leu Val Ile Thr Arg Thr Ala Leu Ala His
 245 250 255
 Ala Ala Trp Ala Gly Arg Thr Val Val Thr Glu Glu Asp Val Glu Ile
 260 265 270
 Ala Ala Arg Leu Ala Leu Pro His Arg Arg Arg Arg Asn Pro Phe Asp
 275 280 285
 Ala Pro Glu Met Glu Glu Arg Lys Leu Gln Glu Thr Leu Gln Glu Ala
 290 295 300
 Arg Asp Phe Phe Lys Asp Asn Glu Asp Lys Gly Pro Ala Ala Lys Ile
 305 310 315 320
 Thr Asp Glu Glu Thr Gly Ala Glu Ala Phe Thr Asp Thr Asp Asn Pro
 325 330 335
 Thr Glu Glu Asp Gly Leu Gln Gly Thr Ala Gln Ala Lys Ala Gln Thr
 340 345 350
 Thr Gly Lys Val Gly Thr Ala Gly Ser Gly Asp Pro Phe Arg Ser
 355 360 365

<210> 367

<211> 473

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(450)

<223> FRXA01849

<400> 367

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 Leu Pro Gly Val Glu Leu Pro Asp Leu Ile Leu Ser Gln Ile Ala Trp
 1 5 10 15
 ttg tgt gca cgt att gaa gtc gac ggt atg cgc gct gac ctg gtg atc 96
 Leu Cys Ala Arg Ile Glu Val Asp Gly Met Arg Ala Asp Leu Val Ile
 20 25 30
 acg cgt acc gca ctt gct cac gcc gcg tgg gct gga cgc act gtg gtt 144

Thr Arg Thr Ala Leu Ala His Ala Ala Trp Ala Gly Arg Thr Val Val
 35 40 45

acg gaa gaa gac gtg gag atc gca gct cgc cta gcg ttg ccg cac cgc 192
 Thr Glu Glu Asp Val Glu Ile Ala Ala Arg Leu Ala Leu Pro His Arg
 50 55 60

cgt cgc cgt aat cct ttc gat gct cca gaa atg gag gag cgc aag ctt 240
 Arg Arg Arg Asn Pro Phe Asp Ala Pro Glu Met Glu Glu Arg Lys Leu
 65 70 75 80

cag gaa acc ctg cag gaa gct cgg gac ttc ttc aaa gac aat gaa gat 288
 Gln Glu Thr Leu Gln Glu Ala Arg Asp Phe Phe Lys Asp Asn Glu Asp
 85 90 95

aaa gga cct gcc gcc aag atc acc gat gag gaa acc ggt gca gag gcc 336
 Lys Gly Pro Ala Ala Lys Ile Thr Asp Glu Glu Thr Gly Ala Glu Ala
 100 105 110

ttt acc gat acc gac aat ccc acc gag gaa gac ggt ctg caa gga act 384
 Phe Thr Asp Thr Asp Asn Pro Thr Glu Glu Asp Gly Leu Gln Gly Thr
 115 120 125

gcg cag gcg aag gcg cag act act gga aag gta ggt act gcc gga tcc 432
 Ala Gln Ala Lys Ala Gln Thr Thr Gly Lys Val Gly Thr Ala Gly Ser
 130 135 140

ggc gac ccc ttt cgc tcc taggcatttg cgcctggcgt cca 473
 Gly Asp Pro Phe Arg Ser
 145 150

<210> 368

<211> 150

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 368

Leu Pro Gly Val Glu Leu Pro Asp Leu Ile Leu Ser Gln Ile Ala Trp
 1 5 10 15

Leu Cys Ala Arg Ile Glu Val Asp Gly Met Arg Ala Asp Leu Val Ile
 20 25 30

Thr Arg Thr Ala Leu Ala His Ala Ala Trp Ala Gly Arg Thr Val Val
 35 40 45

Thr Glu Glu Asp Val Glu Ile Ala Ala Arg Leu Ala Leu Pro His Arg
 50 55 60

Arg Arg Arg Asn Pro Phe Asp Ala Pro Glu Met Glu Glu Arg Lys Leu
 65 70 75 80

Gln Glu Thr Leu Gln Glu Ala Arg Asp Phe Phe Lys Asp Asn Glu Asp
 85 90 95

Lys Gly Pro Ala Ala Lys Ile Thr Asp Glu Glu Thr Gly Ala Glu Ala
 100 105 110

Phe Thr Asp Thr Asp Asn Pro Thr Glu Glu Asp Gly Leu Gln Gly Thr
 115 120 125

Ala Gln Ala Lys Ala Gln Thr Thr Gly Lys Val Gly Thr Ala Gly Ser
 130 135 140

Gly Asp Pro Phe Arg Ser
 145 150

<210> 369

<211> 667

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(667)

<223> FRXA01691

<400> 369

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caccaaaaaa tctcaagaaa actcacatta aaggacagta atg gcg tca caa cag 115
 Met Ala Ser Gln Gln
 1 5

atc cgc tat cca ttc tcc gcg gtt gtg gga caa gac gag ctt cgg ctt 163
 Ile Arg Tyr Pro Phe Ser Ala Val Val Gly Gln Asp Glu Leu Arg Leu
 10 15 20

gcg ttg atc ctc act gcg att tcc cca cgc att ggt ggc gtg gtg att 211
 Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile Gly Gly Val Val Ile
 25 30 35

cga ggt gag aag ggt aca gcg aaa act acc act gtg cgt gct ttt gct 259
 Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr Val Arg Ala Phe Ala
 40 45 50

ggt ctt tta ggt gat gcc cct ttg gtg aac ttg cct ctc gga tcc acg 307
 Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu Pro Leu Gly Ser Thr
 55 60 65

gag gat cgt gtg gtg ggt tcc ctc aac atg gaa act gtg ttg acc acc 355
 Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu Thr Val Leu Thr Thr
 70 75 80 85

ggc cgt gcg gaa tat cag cca ggt ttg ctc gcg cag gct gat ggc ggt 403
 Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala Gln Ala Asp Gly Gly
 90 95 100

gtg ctg tat gtc gat gag gtc aac ctc ttg gcg gat cac ctg gtg gat 451
 Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala Asp His Leu Val Asp
 105 110 115

gct ctg ctc gat gca gct gca agc ggt cgc gtc agc att gag cgt gac 499
 Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val Ser Ile Glu Arg Asp
 120 125 130

ggt att tcg cat tct tca cca gca aac ttt gtg ttg gtg ggc acc atg 547
 Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val Leu Val Gly Thr Met
 135 140 145

aat ccg gag gaa ggc gag ctg cgc ccg cag ctg ctg gac cgt ttc ggt 595
 Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu Leu Asp Arg Phe Gly
 150 155 160 165

ttg gct gtg gac gtt gct gcg tct acg aac cct gag gtg cgc gtg gag 643
 Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro Glu Val Arg Val Glu
 170 175 180

atc att cgc cgc cgg ctt gat ttt 667
 Ile Ile Arg Arg Arg Leu Asp Phe
 185

<210> 370

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

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Asp Glu Leu Arg Leu Ala Leu Ile Leu Thr Ala Ile Ser Pro Arg Ile
 20 25 30

Gly Gly Val Val Ile Arg Gly Glu Lys Gly Thr Ala Lys Thr Thr Thr
 35 40 45

Val Arg Ala Phe Ala Gly Leu Leu Gly Asp Ala Pro Leu Val Asn Leu
 50 55 60

Pro Leu Gly Ser Thr Glu Asp Arg Val Val Gly Ser Leu Asn Met Glu
 65 70 75 80

Thr Val Leu Thr Thr Gly Arg Ala Glu Tyr Gln Pro Gly Leu Leu Ala
 85 90 95

Gln Ala Asp Gly Gly Val Leu Tyr Val Asp Glu Val Asn Leu Leu Ala
 100 105 110

Asp His Leu Val Asp Ala Leu Leu Asp Ala Ala Ala Ser Gly Arg Val
 115 120 125

Ser Ile Glu Arg Asp Gly Ile Ser His Ser Ser Pro Ala Asn Phe Val
 130 135 140

Leu Val Gly Thr Met Asn Pro Glu Glu Gly Glu Leu Arg Pro Gln Leu
 145 150 155 160

Leu Asp Arg Phe Gly Leu Ala Val Asp Val Ala Ala Ser Thr Asn Pro
 165 170 175

Glu Val Arg Val Glu Ile Ile Arg Arg Arg Leu Asp Phe
 180 185

<210> 371

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN00665

<400> 371

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tcgggatctc aaagtttcga gaaacacaga aagggcagca atg agc agc tca aca 115
                                         Met Ser Ser Ser Thr
                                         1 5

ctt ctc ctg gct tca gga caa gtc acg gca tta gcc gct gac tac acg 163
Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu Ala Ala Asp Tyr Thr
                        10                        15                        20

ctc agc cac acc ccc tca gat ggc atc ctg gta gtc ctt ggc ttc gcc 211
Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val Val Leu Gly Phe Ala
                        25                        30                        35

atg atc ctc acc ttc atg acc ctg atc atg ctg ggt cga ctc acc cca 259
Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu Gly Arg Leu Thr Pro
                        40                        45                        50

atg gtg gcc atg ctg ttg gtc ccc acc atc ttc ggt ctc atc gcc gcc 307
Met Val Ala Met Leu Leu Val Pro Thr Ile Phe Gly Leu Ile Ala Gly
                        55                        60                        65

gca gga ctc ggc ctt ggt gac atg gcg ctt gac gcc atc aag gac atg 355
Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp Ala Ile Lys Asp Met
70                        75                        80                        85

gcg cct acc gcg gca ctc ctg atg ttc gcg att atg ttc ttc gga atc 403
Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile Met Phe Phe Gly Ile
                        90                        95                        100

atg atc gac gtc gga ctc ttc gac ccc ctg atc cgc gtg atc acc cgc 451
Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile Arg Val Ile Thr Arg
105                        110                        115

gtt ctt cac gat gac ccc gca aag gtc gtc atc ggc acc gca gta ctt 499
Val Leu His Asp Asp Pro Ala Lys Val Val Ile Gly Thr Ala Val Leu
120                        125                        130

gca ggt gtt gtc tcc ctc gac ggc gac ggc tcc acc acc ttc atc att 547
Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser Thr Thr Phe Ile Ile
135                        140                        145

acc acc ttc cgc gat gct gcc cat cta cct gcg cct tgg cat gag ccc 595
Thr Thr Phe Arg Asp Ala Ala His Leu Pro Ala Pro Trp His Glu Pro
150                        155                        160                        165

tgt ggt
Cys Gly 601

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<210> 372

<211> 167

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 372

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Met Ser Ser Ser Thr Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu
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Ala Ala Asp Tyr Thr Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val
      20           25           30

Val Leu Gly Phe Ala Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu
      35           40           45

Gly Arg Leu Thr Pro Met Val Ala Met Leu Leu Val Pro Thr Ile Phe
      50           55           60

Gly Leu Ile Ala Gly Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp
      65           70           75           80

Ala Ile Lys Asp Met Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile
      85           90           95

Met Phe Phe Gly Ile Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile
      100          105          110

Arg Val Ile Thr Arg Val Leu His Asp Asp Pro Ala Lys Val Val Ile
      115          120          125

Gly Thr Ala Val Leu Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser
      130          135          140

Thr Thr Phe Ile Ile Thr Thr Phe Arg Asp Ala Ala His Leu Pro Ala
      145          150          155          160

Pro Trp His Glu Pro Cys Gly
      165

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<210> 373

<211> 390

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(367)

<223> RXN03026

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cgaactagcc cccaacaac aattagaaat ggaacctaaa atg cct gga aaa att 115
                                   Met Pro Gly Lys Ile
                                   1           5

ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
      10           15           20

gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
      25           30           35

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gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
 Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
 40 45 50

cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307
 His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His
 55 60 65

atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85

ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 374
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 374
 Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu
 1 5 10 15

Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val
 20 25 30

Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
 35 40 45

Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
 50 55 60

Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
 65 70 75 80

Thr Leu Arg Trp Arg Phe Trp Met Leu
 85

<210> 375
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(361)
 <223> RXN02908

<400> 375
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gtgactggtc gcgtggatac ccgtcattga ttccggtgga ttg aag ttg cac cca 115
 Leu Lys Leu His Pro
 1 5

gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala

10										15					20					
tgt	ggt	gtg	ggt	att	ccc	gat	ccc	cga	tta	ggc	caa	gca	att	gtg	gcc	211				
Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly	Gln	Ala	Ile	Val	Ala					
			25					30						35						
gcg	tac	tcc	gga	tcg	atc	agt	ccg	tct	gaa	ggt	att	gaa	ggc	ctc	gac	259				
Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val	Ile	Glu	Gly	Leu	Asp					
		40					45					50								
gat	cta	cct	cgt	tgg	cag	ctt	ccc	aaa	cgg	ctg	aag	cat	ctg	gaa	tct	307				
Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu	Lys	His	Leu	Glu	Ser					
		55				60					65									
ttg	ccc	agc	att	ggt	cct	gga	aaa	gct	gat	cga	cgt	gct	atc	gcg	aag	355				
Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg	Arg	Ala	Ile	Ala	Lys					
	70					75				80					85					
ctg	ttt	tagtcttcat	tcttgctggc	tgc												384				
Leu	Phe																			

<210> 376

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Leu	Lys	Leu	His	Pro	Glu	Val	Leu	Glu	Arg	Ala	Ile	Ala	Asp	Ile	Lys
1				5					10					15	

Gly	Val	Thr	Ala	Ala	Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly
			20					25					30		

Gln	Ala	Ile	Val	Ala	Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val
		35					40					45			

Ile	Glu	Gly	Leu	Asp	Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu
	50					55					60				

Lys	His	Leu	Glu	Ser	Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg
	65				70				75					80	

Arg	Ala	Ile	Ala	Lys	Leu	Phe
				85		

<210> 377

<211> 667

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(667)

<223> RXN03000

<400> 377

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ctaaccacct ttttcaactc acagtttagga aacttcaccc atg tct ctt cca cat 115
Met Ser Leu Pro His
1 5

tct gat gaa ctc cgc ggc caa aag atc att att tcc ggt ggc gga att 163
Ser Asp Glu Leu Arg Gly Gln Lys Ile Ile Ile Ser Gly Gly Gly Ile
10 15 20

ggt ggc gca gca ggt gca ctt gcg ctt gct ttg cgc ggt gcc gat gtc 211
Gly Gly Ala Ala Gly Ala Leu Ala Leu Ala Leu Arg Gly Ala Asp Val
25 30 35

act ttg tac gaa cgc gca gct gag ttc aag gag gtc ggc gct ggc ctc 259
Thr Leu Tyr Glu Arg Ala Ala Glu Phe Lys Glu Val Gly Ala Gly Leu
40 45 50

cag atc ggt ccg cac ggc tgg cga atg ctg gaa tcc tgg ggt ctg ctc 307
Gln Ile Gly Pro His Gly Trp Arg Met Leu Glu Ser Trp Gly Leu Leu
55 60 65

gac caa att gtc gtg gcc ggc tac ctc cca gaa gac atg cag ttc cgc 355
Asp Gln Ile Val Val Ala Gly Tyr Leu Pro Glu Asp Met Gln Phe Arg
70 75 80 85

gac gct gtc aac cgc gaa acc atc ctg acc atg cgt ttc gat gaa gaa 403
Asp Ala Val Asn Arg Glu Thr Ile Leu Thr Met Arg Phe Asp Glu Glu
90 95 100

ttc cag cag cac tac ggc ggt cgc tac ctg gtg att cac cgc tct gac 451
Phe Gln Gln His Tyr Gly Gly Arg Tyr Leu Val Ile His Arg Ser Asp
105 110 115

ctg ctc aac atc ctg gtc acc aac gcc gaa gca gcg ggc gcg aag ctc 499
Leu Leu Asn Ile Leu Val Thr Asn Ala Glu Ala Ala Gly Ala Lys Leu
120 125 130

cac aat ggc gtc ctg gtc acc gat tcc cgc acc gtc gac ggc ggt atc 547
His Asn Gly Val Leu Val Thr Asp Ser Arg Thr Val Asp Gly Gly Ile
135 140 145

gag gtg gac atc gaa tcc tcc atc aac aag ggc gaa gat aac aag act 595
Glu Val Asp Ile Glu Ser Ser Ile Asn Lys Gly Glu Asp Asn Lys Thr
150 155 160 165

ttg ctt gtc gac gcc ttc ctc gcc ttc gac ggc atc cac tcg gtc atg 643
Leu Leu Val Asp Ala Phe Leu Ala Phe Asp Gly Ile His Ser Val Met
170 175 180

cgc aaa aag ctt gtc gac gac gcc 667
Arg Lys Lys Leu Val Asp Asp Ala
185

<210> 378

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

Met Ser Leu Pro His Ser Asp Glu Leu Arg Gly Gln Lys Ile Ile Ile
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Ser Gly Gly Gly Ile Gly Gly Ala Ala Gly Ala Leu Ala Leu Ala Leu
 20 25 30

Arg Gly Ala Asp Val Thr Leu Tyr Glu Arg Ala Ala Glu Phe Lys Glu
 35 40 45

Val Gly Ala Gly Leu Gln Ile Gly Pro His Gly Trp Arg Met Leu Glu
 50 55 60

Ser Trp Gly Leu Leu Asp Gln Ile Val Val Ala Gly Tyr Leu Pro Glu
 65 70 75 80

Asp Met Gln Phe Arg Asp Ala Val Asn Arg Glu Thr Ile Leu Thr Met
 85 90 95

Arg Phe Asp Glu Glu Phe Gln Gln His Tyr Gly Gly Arg Tyr Leu Val
 100 105 110

Ile His Arg Ser Asp Leu Leu Asn Ile Leu Val Thr Asn Ala Glu Ala
 115 120 125

Ala Gly Ala Lys Leu His Asn Gly Val Leu Val Thr Asp Ser Arg Thr
 130 135 140

Val Asp Gly Gly Ile Glu Val Asp Ile Glu Ser Ser Ile Asn Lys Gly
 145 150 155 160

Glu Asp Asn Lys Thr Leu Leu Val Asp Ala Phe Leu Ala Phe Asp Gly
 165 170 175

Ile His Ser Val Met Arg Lys Lys Leu Val Asp Asp Ala
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(766)
 <223> RXN03036

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 Met Ala Glu Gln Leu
 1 5

cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa 163
 Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln Ser Glu Asp Leu Glu
 10 15 20

gat cag ggt ttg gga ttt gac ctg gga acc gtt ttc tcc cgc agg aag 211
 Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val Phe Ser Arg Arg Lys
 25 30 35

gtt ttg gga ttc atc ggt gtt ggt gga gca ggt gtg gca ctt gct gct 259

Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly Val Ala Leu Ala Ala
40 45 50

tgt tca cct tct ggt tct tcc gcg gca tcg agc acc tca agc gcg tcc 307
Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser Thr Ser Ser Ala Ser
55 60 65

agc agc gca gct gca acc acc agt gca gca gca gag act ttg act gag 355
Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala Glu Thr Leu Thr Glu
70 75 80 85

atg aag tcg gag act gct ggt ccg tac ccg ggc gat ggt tcg aat ggt 403
Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly Asp Gly Ser Asn Gly
90 95 100

ccg gat gtg ttg gag gtc tcc ggt gtg gag cgc cag gac atc acc aag 451
Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg Gln Asp Ile Thr Lys
105 110 115

tcg att gat tct gac acc gtg gca gag ggc gta cct ctg acg ttg act 499
Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val Pro Leu Thr Leu Thr
120 125 130

atg acc att ttg gac atg aac aac aac aat cag cca atg gag ggt gct 547
Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln Pro Met Glu Gly Ala
135 140 145

gcg gtg tac gtg tgg cac tgt gat gcg ccg ggt cga tat tcg atg tac 595
Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly Arg Tyr Ser Met Tyr
150 155 160 165

gac tct gag ctg gaa gat gag acc tat tta cgc ggt gtg cag att acc 643
Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg Gly Val Gln Ile Thr
170 175 180

gat aag tat ggc cag gtc acg ttc gat acc att ttc cct ggt tgt tat 691
Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile Phe Pro Gly Cys Tyr
185 190 195

gcg ggc cgt tgg gtg cat att cat ttc gag gtg ttc ccg gat cga gac 739
Ala Gly Arg Trp Val His Ile His Phe Glu Val Phe Pro Asp Arg Asp
200 205 210

agc atc acg gat tcc acg aac aac att 766
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215 220

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<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

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Phe Ser Arg Arg Lys Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly

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                                     Met Gln Asp Leu Tyr
                                     1          5

agc gat  ccg  ggc  gag  ctc  aag  cca  ggt  gcc  cag  ggc  ggt  ttt  tca  gcg      163
Ser Asp  Pro  Gly  Glu  Leu  Lys  Pro  Gly  Ala  Gln  Gly  Gly  Phe  Ser  Ala
                        10                        15                        20

ctt atc  gac  ggc  gac  acc  ctg  gtc  att  tcc  ggc  ggc  gat  gcc  ggc  gca      211
Leu Ile  Asp  Gly  Asp  Thr  Leu  Val  Ile  Ser  Gly  Gly  Asp  Ala  Gly  Ala
                        25                        30                        35

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act ccg gtt gca gca ctc cgc act gcg ttg gat gtg gcc tgg gcg gcc 259
 Thr Pro Val Ala Ala Leu Arg Thr Ala Leu Asp Val Ala Trp Ala Ala
 40 45 50

aca gag cag tca ccg agg tac gcg ctg att cag agg tagctgctac 305
 Thr Glu Gln Ser Pro Arg Tyr Ala Leu Ile Gln Arg
 55 60 65

tgcattgcag agc 318

<210> 382

<211> 65

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

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 20 25 30

Gly Asp Ala Gly Ala Thr Pro Val Ala Ala Leu Arg Thr Ala Leu Asp
 35 40 45

Val Ala Trp Ala Ala Thr Glu Gln Ser Pro Arg Tyr Ala Leu Ile Gln
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Arg
 65

<210> 383

<211> 1017

<212> DNA

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<222> (101)..(994)

<223> RXN00393

<400> 383

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aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50

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Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
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tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
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Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
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Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

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 Ala Leu Ala Phe Ser
 295.

1017

<210> 384

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

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			20					25					30		
Ile	Ala	Gly	Ser	Gly	Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp
		35					40					45			
Lys	Ala	Leu	Leu	Ala	Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val
	50					55					60				
Asn	Tyr	Ala	Asn	Asp	Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp
65				70						75				80	
Arg	Thr	Gly	Pro	Leu	Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys
				85					90					95	
Lys	Val	Lys	Ala	Ala	Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala
			100					105					110		
Gly	Thr	Ala	Leu	Ser	Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly
		115					120					125			
Ile	Leu	Cys	Val	Leu	Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro
	130					135					140				
Tyr	Gly	Tyr	Arg	Gly	Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly
145					150					155					160
Leu	Val	Ala	Val	Met	Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser
				165					170					175	
Trp	Ala	Gly	Leu	Ala	Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly
			180					185					190		
Val	Asn	Leu	Ala	Asn	Asn	Ile	Arg	Asp	Ile	Pro	Thr	Asp	Ser	Lys	Thr
		195					200					205			
Gly	Lys	Ile	Thr	Leu	Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys
	210					215					220				
Leu	Phe	Leu	Ala	Leu	Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu
225					230					235				240	
Ala	Phe	Val	Ala	Trp	Pro	Ala	Leu	Ile	Ala	Ile	Ile	Val	Phe	Pro	Leu
			245						250					255	
Ala	Leu	Lys	Ala	Ala	Gly	Pro	Ile	Arg	Asn	Asn	Ala	Thr	Gly	Lys	Asp
		260						265					270		

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Val Leu Thr Gly Leu Ala Leu Ala Phe Ser
 290 295

<210> 385

<211> 1242

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1219)

<223> RXN00948

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                                         Met Ala Asn Val Val
                                         1 5

cta gtc gat cga atg gag cct ttg gtg tcc aag ctg ttt acc cca att 163
Leu Val Asp Arg Met Glu Pro Leu Val Ser Lys Leu Phe Thr Pro Ile
                        10 15 20

caa atc cgc gac atc acc atc ccc aac cgc gtg tgg atg tca ccg atg 211
Gln Ile Arg Asp Ile Thr Ile Pro Asn Arg Val Trp Met Ser Pro Met
                        25 30 35

tgc acc tac tct gca gcc acc ggt tca ggt ctt ccc acc gat ttt cac 259
Cys Thr Tyr Ser Ala Ala Thr Gly Ser Gly Leu Pro Thr Asp Phe His
                        40 45 50

cag gct cat tac gca gct cgc gca gca ggt ggt gtc gga tta gtc atg 307
Gln Ala His Tyr Ala Ala Arg Ala Ala Gly Gly Val Gly Leu Val Met
                        55 60 65

gtt gaa gca act gga gtg aac ccc gta gct ccc atc tcc cca gtc gac 355
Val Glu Ala Thr Gly Val Asn Pro Val Ala Pro Ile Ser Pro Val Asp
70 75 80 85

ctt gga ctt tgg agc cat gac caa att gaa cca ttc tcc cga gtg aca 403
Leu Gly Leu Trp Ser His Asp Gln Ile Glu Pro Phe Ser Arg Val Thr
90 95 100

gca gct att cgc gcc ggt ggg gca gta ccg gcc gtt caa tta gcc cat 451
Ala Ala Ile Arg Ala Gly Gly Ala Val Pro Ala Val Gln Leu Ala His
105 110 115

gct ggc cgc aag gca tcc acc gat gct ccg tgg aat ggt ggc gga tat 499
Ala Gly Arg Lys Ala Ser Thr Asp Ala Pro Trp Asn Gly Gly Tyr
120 125 130

gtt gga cca gaa acc aat gga tgg gag act gtc ggc ccc agc cct ctg 547
Val Gly Pro Glu Thr Asn Gly Trp Glu Thr Val Gly Pro Ser Pro Leu
135 140 145

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gca ttc cca ggt ttg cct gct ccg cgc gag ctg acg gtt tca gaa atc 595
 Ala Phe Pro Gly Leu Pro Ala Pro Arg Glu Leu Thr Val Ser Glu Ile
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 caa gag gtt gtg cag cag ttc gct ggc gcc gcc gtt cgt gcc gat cag 643
 Gln Glu Val Val Gln Gln Phe Ala Gly Ala Ala Val Arg Ala Asp Gln
 170 175 180

 gct ggt ttt gat gtc gtg gaa att cac gca gca cac ggc tac ctt ttg 691
 Ala Gly Phe Asp Val Val Glu Ile His Ala Ala His Gly Tyr Leu Leu
 185 190 195

 cat aac ttc ctt tct ccg atc tcc aac aag cgc acc gat tca tac ggc 739
 His Asn Phe Leu Ser Pro Ile Ser Asn Lys Arg Thr Asp Ser Tyr Gly
 200 205 210

 gga tct tta gaa aac cgc gct cgc atc gtg ctc gaa gtc att gat gca 787
 Gly Ser Leu Glu Asn Arg Ala Arg Ile Val Leu Glu Val Ile Asp Ala
 215 220 225

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 Ile Arg Ala Val Trp Pro Glu Glu Lys Pro Val Phe Met Arg Ile Ser
 230 235 240 245

 acc acc gac tgg gtg gag gaa aac cca cag gat gat cgc gag tcc tgg 883
 Thr Thr Asp Trp Val Glu Glu Asn Pro Gln Asp Asp Arg Glu Ser Trp
 250 255 260

 acg ctg agc caa agc agg cag ctg gct ttg tgg gca tcc gag cac gga 931
 Thr Leu Ser Gln Ser Arg Gln Leu Ala Leu Trp Ala Ser Glu His Gly
 265 270 275

 gtt gat ttg atc gat gcc tct tct ggt ggc ctc gac atc gtc ccc att 979
 Val Asp Leu Ile Asp Ala Ser Ser Gly Gly Leu Asp Ile Val Pro Ile
 280 285 290

 ccg cat gac cgc gat tac caa acc gcg aag gcc gca gat ctt cac gca 1027
 Pro His Asp Arg Asp Tyr Gln Thr Ala Lys Ala Ala Asp Leu His Ala
 295 300 305

 agt acc gga gtg aca gtc gct gct gtg ggg cgc att gat gac gcc caa 1075
 Ser Thr Gly Val Thr Val Ala Ala Val Gly Arg Ile Asp Asp Ala Gln
 310 315 320 325

 act gcg cac aat ttg gtt gat tct ggc gat gtc aat gca gtt ttc ctc 1123
 Thr Ala His Asn Leu Val Asp Ser Gly Asp Val Asn Ala Val Phe Leu
 330 335 340

 ggc cgt cca ctg ctc aag gat cct tcc tgg gca aac caa gca gcc ctc 1171
 Gly Arg Pro Leu Leu Lys Asp Pro Ser Trp Ala Asn Gln Ala Ala Leu
 345 350 355

 gca cta ggt gcg gaa ccc agg tat gtt cac caa tac gac tac gta ctt 1219
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<210> 386

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

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 35 40 45
 Pro Thr Asp Phe His Gln Ala His Tyr Ala Ala Arg Ala Ala Gly Gly
 50 55 60
 Val Gly Leu Val Met Val Glu Ala Thr Gly Val Asn Pro Val Ala Pro
 65 70 75 80
 Ile Ser Pro Val Asp Leu Gly Leu Trp Ser His Asp Gln Ile Glu Pro
 85 90 95
 Phe Ser Arg Val Thr Ala Ala Ile Arg Ala Gly Gly Ala Val Pro Ala
 100 105 110
 Val Gln Leu Ala His Ala Gly Arg Lys Ala Ser Thr Asp Ala Pro Trp
 115 120 125
 Asn Gly Gly Gly Tyr Val Gly Pro Glu Thr Asn Gly Trp Glu Thr Val
 130 135 140
 Gly Pro Ser Pro Leu Ala Phe Pro Gly Leu Pro Ala Pro Arg Glu Leu
 145 150 155 160
 Thr Val Ser Glu Ile Gln Glu Val Val Gln Gln Phe Ala Gly Ala Ala
 165 170 175
 Val Arg Ala Asp Gln Ala Gly Phe Asp Val Val Glu Ile His Ala Ala
 180 185 190
 His Gly Tyr Leu Leu His Asn Phe Leu Ser Pro Ile Ser Asn Lys Arg
 195 200 205
 Thr Asp Ser Tyr Gly Gly Ser Leu Glu Asn Arg Ala Arg Ile Val Leu
 210 215 220
 Glu Val Ile Asp Ala Ile Arg Ala Val Trp Pro Glu Glu Lys Pro Val
 225 230 235 240
 Phe Met Arg Ile Ser Thr Thr Asp Trp Val Glu Glu Asn Pro Gln Asp
 245 250 255
 Asp Arg Glu Ser Trp Thr Leu Ser Gln Ser Arg Gln Leu Ala Leu Trp
 260 265 270
 Ala Ser Glu His Gly Val Asp Leu Ile Asp Ala Ser Ser Gly Gly Leu
 275 280 285
 Asp Ile Val Pro Ile Pro His Asp Arg Asp Tyr Gln Thr Ala Lys Ala
 290 295 300

Ala Asp Leu His Ala Ser Thr Gly Val Thr Val Ala Ala Val Gly Arg
 305 310 315 320

Ile Asp Asp Ala Gln Thr Ala His Asn Leu Val Asp Ser Gly Asp Val
 325 330 335

Asn Ala Val Phe Leu Gly Arg Pro Leu Leu Lys Asp Pro Ser Trp Ala
 340 345 350

Asn Gln Ala Ala Leu Ala Leu Gly Ala Glu Pro Arg Tyr Val His Gln
 355 360 365

Tyr Asp Tyr Val Leu
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<210> 387
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(850)
 <223> RXN01923

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 Met Ser Ala Leu Ile
 1 5

aaa ggt tca gga cct cat cat gtg gtt gtc tta aat ggt tgg ttt ggt 163
 Lys Gly Ser Gly Pro His His Val Val Val Leu Asn Gly Trp Phe Gly
 10 15 20

cat gct gcg ggc tgg gga gct ttc gct gac tat ctt gac ctc ggc aac 211
 His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr Leu Asp Leu Gly Asn
 25 30 35

tac acc tgg cac ttt tgg gat tac cga ggt tac ggc aac aga aaa gac 259
 Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr Gly Asn Arg Lys Asp
 40 45 50

gac gca gga gaa ttt act ctg gag gaa att tca gcg gat atc gtt gca 307
 Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser Ala Asp Ile Val Ala
 55 60 65

tac atc gac tcg att gag gca gaa aag gtt tcc atc ctg ggc cat tcc 355
 Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser Ile Leu Gly His Ser
 70 75 80 85

atg ggt gga gtg ttc atg cag aaa gtc ctt gca gac agc gcc acc ccc 403
 Met Gly Gly Val Phe Met Gln Lys Val Leu Ala Asp Ser Ala Thr Pro
 90 95 100

atc gct tca ctg gtt gga att tct gcc gtt gct gca gct gga aca cca 451
 Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala Ala Ala Gly Thr Pro
 105 110 115

ttc gat gag gat tct cgg aag ctt ttc acc tca gca ggg cac aac ccg 499
 Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser Ala Gly His Asn Pro
 120 125 130

 gac tcg agg cga gcc atc atc gat ttc acc tca gga tct cgc caa cct 547
 Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr Ser Gly Ser Arg Gln Pro
 135 140 145

 gcc gcg tgg ttg gat gat ctc acc gac tcg gcg gtg cag aat tcc act 595
 Ala Ala Trp Leu Asp Asp Leu Thr Asp Ser Ala Val Gln Asn Ser Thr
 150 155 160 165

 cca gag gcc gtt gaa aag tac ttt ttt gcg tgg gct gat tgt aat ttc 643
 Pro Glu Ala Val Glu Lys Tyr Phe Phe Ala Trp Ala Asp Cys Asn Phe
 170 175 180

 gca gcg gat tta ggc acc caa gat ttg ccc gtg gac att ctc acc ggc 691
 Ala Ala Asp Leu Gly Thr Gln Asp Leu Pro Val Asp Ile Leu Thr Gly
 185 190 195

 gat ctc gac ccc gcg gtc act aaa act gcc gtg gaa tcc gca ttc ggc 739
 Asp Leu Asp Pro Ala Val Thr Lys Thr Ala Val Glu Ser Ala Phe Gly
 200 205 210

 ccg atc tat caa aat ctg acc gtt gaa gaa ctc cac gat gtc gga cac 787
 Pro Ile Tyr Gln Asn Leu Thr Val Glu Glu Leu His Asp Val Gly His
 215 220 225

 tac gca att ttc gag cac ccc tta ggc ctt gcc gcc agg gtg ctt cga 835
 Tyr Ala Ile Phe Glu His Pro Leu Gly Leu Ala Ala Arg Val Leu Arg
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 Phe Leu Asp Ala Val
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<210> 388

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

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 20 25 30

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 35 40 45

 Gly Asn Arg Lys Asp Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser
 50 55 60

 Ala Asp Ile Val Ala Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser
 65 70 75 80

 Ile Leu Gly His Ser Met Gly Gly Val Phe Met Gln Lys Val Leu Ala
 85 90 95

Asp Ser Ala Thr Pro Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala
 100 105 110
 Ala Ala Gly Thr Pro Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser
 115 120 125
 Ala Gly His Asn Pro Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr Ser
 130 135 140
 Gly Ser Arg Gln Pro Ala Ala Trp Leu Asp Asp Leu Thr Asp Ser Ala
 145 150 155 160
 Val Gln Asn Ser Thr Pro Glu Ala Val Glu Lys Tyr Phe Phe Ala Trp
 165 170 175
 Ala Asp Cys Asn Phe Ala Ala Asp Leu Gly Thr Gln Asp Leu Pro Val
 180 185 190
 Asp Ile Leu Thr Gly Asp Leu Asp Pro Ala Val Thr Lys Thr Ala Val
 195 200 205
 Glu Ser Ala Phe Gly Pro Ile Tyr Gln Asn Leu Thr Val Glu Glu Leu
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 225 230 235 240
 Ala Arg Val Leu Arg Phe Leu Asp Ala Val
 245 250

<210> 389
 <211> 873
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(850)
 <223> RXN00398

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 Met Ala Lys Leu Phe
 1 5
 gat tcc cat ttc cat atc atc gat ccc cag cac cca ctg atc gaa aac 163
 Asp Ser His Phe His Ile Ile Asp Pro Gln His Pro Leu Ile Glu Asn
 10 15 20
 aac ggc tac ctc ccc gag cct ttc acc gtg gag gat tac act gcg cgt 211
 Asn Gly Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg
 25 30 35
 gtt gaa ggc ctc gaa gtt gct gcc gga gcg att gtt tcc ggt tct ttc 259
 Val Glu Gly Leu Glu Val Ala Ala Gly Ala Ile Val Ser Gly Ser Phe
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 cag gct ttc gac cag ggc tac ctc aaa gat gct ctc gca gtg ctt ggc 307

Gln Ala Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly
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 cca ggc tat gtc ggt gtc act cag atc ccc gca gat acc tct gat cag 355
 Pro Gly Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln
 70 75 80 85
 gag att ctt gat ctg gac aaa gct ggc gtg aag gct gtg cgt tta aac 403
 Glu Ile Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn
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 ttg aag cgc ggt ggt tcg gca ggt ctt gac gat ctg gag acc ttg gca 451
 Leu Lys Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala
 105 110 115
 cgc cga gtc cac gac cta gcc ggt tgg cac acc gaa ctg tat gtg gat 499
 Arg Arg Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp
 120 125 130
 gct cgc gaa cta gac gag ttg gaa tca acc ttg gcc tcc ctg cct gct 547
 Ala Arg Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala
 135 140 145
 gtc agc att gat cac tta ggg ctg cac cgc gat gga ctt ccc gca ctt 595
 Val Ser Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu
 150 155 160 165
 ctt cgc ttg gta gaa aat ggc att aaa gtc aaa gca acc gga ttc gga 643
 Leu Arg Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly
 170 175 180
 cgg gta gaa cta gat cca act gaa gtc atc cag gca atc atg gct gtc 691
 Arg Val Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val
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 gat ccc act gct ttg atg atc gga act gat ctt cca tcc acc cgc act 739
 Asp Pro Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr
 200 205 210
 aag cga cct ttc gaa gac gct gac cta gat ttg atc gct gaa acg gtt 787
 Lys Arg Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val
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 ggc gaa gat cat gtc gac aac gtc ttc tgg aac aac gct gca gcg ttc 835
 Gly Glu Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe
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 tac ctg gga gac cag tagttttaag acccgaaatg tct 873
 Tyr Leu Gly Asp Gln
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<210> 390

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 390

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PCT/TB00/00911

513

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Ala Val Ala Ala Ala Pro Glu His Ala Ala Met Ala Lys Ala Thr Ile	
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Asp Ser Tyr Gln Leu Asp Val Glu Glu Leu Ser Arg Arg Ala Ala Glu	
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Gly Gly Asn Pro Leu Ile Pro Leu Val Thr Asp Leu Lys Ala Ile Asn	
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ccg gca ggc atc cac att ggc gca acg agc cag gac atc att gat tct	307
Pro Ala Gly Ile His Ile Gly Ala Thr Ser Gln Asp Ile Ile Asp Ser	
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Ala Leu Met Leu Cys Met Lys Glu Gly Val Gly Glu Val Val Asp Lys	
70 75 80 85	
ctt aaa aag ctt gcg cga gat ttg gcc gag ctc acc gcg gag cat aaa	403
Leu Lys Lys Leu Ala Arg Asp Leu Ala Glu Leu Thr Ala Glu His Lys	
90 95 100	
gca acc ccg atc atg ggg cgc acg ttg ggg cag atc gcg acg ccg acg	451
Ala Thr Pro Ile Met Gly Arg Thr Leu Gly Gln Ile Ala Thr Pro Thr	
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Thr Phe Gly Ala Leu Thr Gly Gly Trp Leu Val Ala Val Asp Asn Ala	
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Ala Arg Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala	
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Ser Gly Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala	
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Lys Leu Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His	
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Ser Asp Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala	
185 190 195	
gct ggt gtg gta cgc aaa att gct ggt gac gtg gtg ttt tac tca caa	739
Ala Gly Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln	
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acc gag gtc ggc gag ttg ccg gag aaa tcc ccc ggc ggc agc tcc gcg	787
Thr Glu Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala	
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Met Pro His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr	
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gcg cgc cgg gca cct ggc ctt ctt gca acg ctt ttc gac gcc ctc gac 883
 Ala Arg Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp
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tgc cgt ttg cag cgc ggc acc ggc agc tgg cac gcg gag tgg gca acg 931
 Cys Arg Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr
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ctg cgc gag ttg gct gct gtc act cac tca gca gtg agc agg gct gca 979
 Leu Arg Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala
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acc agc atc gat ggc atc acc gtc aac gtt gat gtg atg gca agt cgc 1027
 Thr Ser Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg
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gtc aat gga cca acc ggg cac gcc gaa gat ttg gcg gag cgg gca cta 1075
 Val Asn Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu
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gaa att tat gga aaa gga cgc agt taatggatc 1108
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<210> 392

<211> 333

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 392

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Arg Arg Ala Ala Glu Gly Gly Asn Pro Leu Ile Pro Leu Val Thr Asp
 35 40 45

Leu Lys Ala Ile Asn Pro Ala Gly Ile His Ile Gly Ala Thr Ser Gln
 50 55 60

Asp Ile Ile Asp Ser Ala Leu Met Leu Cys Met Lys Glu Gly Val Gly
 65 70 75 80

Glu Val Val Asp Lys Leu Lys Lys Leu Ala Arg Asp Leu Ala Glu Leu
 85 90 95

Thr Ala Glu His Lys Ala Thr Pro Ile Met Gly Arg Thr Leu Gly Gln
 100 105 110

Ile Ala Thr Pro Thr Thr Phe Gly Ala Leu Thr Gly Gly Trp Leu Val
 115 120 125

Ala Val Asp Asn Ala Ala Arg Ala Leu Glu Ala Leu Glu Phe Pro Val
 130 135 140

Ser Tyr Gly Gly Ala Ser Gly Asn Met Thr Ala Val His Pro Arg Gly
 145 150 155 160

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<400> 393
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cccggttttct tcctattaca agcgaaaggc aacgtgcccc atg agc gca gtg cag 115
                                         Met Ser Ala Val Gln
                                         1           5

att ttc aac acc gtc cac gtc aat gga tct tcc ccc tat gat gtc cac 163
Ile Phe Asn Thr Val His Val Asn Gly Ser Ser Pro Tyr Asp Val His
          10                15                20

att ggt tcc ggc ctc aac gag ctc att gtt cag cgc gca gcg gaa tca 211
Ile Gly Ser Gly Leu Asn Glu Leu Ile Val Gln Arg Ala Ala Glu Ser
          25                30                35

ggc gcg gag cag gta gcg att ttg cac cag ccc agc atg gat gac att 259

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Gly	Ala	Glu	Gln	Val	Ala	Ile	Leu	His	Gln	Pro	Ser	Met	Asp	Asp	Ile		
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gca	tcc	gag	ttg	gat	gca	gca	cta	gtc	gct	gct	ggg	ttg	aag	gtc	ctg	307	
Ala	Ser	Glu	Leu	Asp	Ala	Ala	Leu	Val	Ala	Ala	Gly	Leu	Lys	Val	Leu		
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cac	ctt	aat	gtt	ccc	gat	gcg	gaa	aac	ggc	aag	tcc	ttg	gaa	gta	gcg	355	
His	Leu	Asn	Val	Pro	Asp	Ala	Glu	Asn	Gly	Lys	Ser	Leu	Glu	Val	Ala		
	70					75				80					85		
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Gly	Gln	Cys	Trp	Asp	Glu	Leu	Gly	Gly	Ala	Ala	Phe	Gly	Arg	Arg	Asp		
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Ile	Val	Ile	Gly	Leu	Gly	Gly	Gly	Ala	Ala	Thr	Asp	Leu	Ala	Gly	Phe		
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gtc	gct	gct	gca	tgg	atg	cgt	ggc	gtg	cgc	gtc	att	cag	gtt	cca	acc	499	
Val	Ala	Ala	Ala	Trp	Met	Arg	Gly	Val	Arg	Val	Ile	Gln	Val	Pro	Thr		
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acc	ttg	ttg	gcc	atg	gtg	gac	gct	gcg	gtg	ggc	ggc	aag	act	ggc	atc	547	
Thr	Leu	Leu	Ala	Met	Val	Asp	Ala	Ala	Val	Gly	Gly	Lys	Thr	Gly	Ile		
	135					140						145					
aat	acc	gcc	gca	ggc	aag	aac	ctt	gtg	ggc	gcg	ttc	cac	gag	cct	gac	595	
Asn	Thr	Ala	Ala	Gly	Lys	Asn	Leu	Val	Gly	Ala	Phe	His	Glu	Pro	Asp		
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gca	gta	ttc	att	gac	acc	gat	cgc	cta	gcc	acc	ctg	cct	gac	gcg	gaa	643	
Ala	Val	Phe	Ile	Asp	Thr	Asp	Arg	Leu	Ala	Thr	Leu	Pro	Asp	Ala	Glu		
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atc	atc	gcg	gga	tcc	gcc	gaa	atc	atc	aaa	act	ggg	ttc	atc	gcc	gac	691	
Ile	Ile	Ala	Gly	Ser	Ala	Glu	Ile	Ile	Lys	Thr	Gly	Phe	Ile	Ala	Asp		
			185					190					195				
cca	gaa	atc	ctg	cgc	ctt	tac	gaa	act	gat	ccc	gca	gcc	tgc	ctg	aag	739	
Pro	Glu	Ile	Leu	Arg	Leu	Tyr	Glu	Thr	Asp	Pro	Ala	Ala	Cys	Leu	Lys		
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aaa	gaa	gtc	gaa	ggc	tcc	cac	cta	cct	gaa	ctg	att	tgg	cgc	tcc	gtc	787	
Lys	Glu	Val	Glu	Gly	Ser	His	Leu	Pro	Glu	Leu	Ile	Trp	Arg	Ser	Val		
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Thr	Val	Lys	Gly	Ser	Val	Val	Gly	Gln	Asp	Leu	Lys	Glu	Ser	Ser	Leu		
	230				235					240					245		
cgc	gaa	atc	ctc	aac	tac	gga	cac	acc	ttt	gcc	cac	gcc	gtc	gaa	ctc	883	
Arg	Glu	Ile	Leu	Asn	Tyr	Gly	His	Thr	Phe	Ala	His	Ala	Val	Glu	Leu		
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cgc	gaa	aac	ttc	cgc	tgg	cgc	cac	ggc	aat	gcc	gtt	gca	gtg	ggc	atg	931	
Arg	Glu	Asn	Phe	Arg	Trp	Arg	His	Gly	Asn	Ala	Val	Ala	Val	Gly	Met		
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atg	ttc	atc	gcc	aac	ctc	tcc	cac	aag	ctc	ggg	ctt	atc	gac	gcg	ccc	979	
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Leu Leu Glu Arg His Arg Ser Ile Leu Ala Ala Ile Gly Leu Pro Thr			
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tcc tac gaa ggc gga gcc ttc gac gag ctt tac gac ggt atg acc cgc			1075
Ser Tyr Glu Gly Gly Ala Phe Asp Glu Leu Tyr Asp Gly Met Thr Arg			
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gac aag aaa aac cgc gac ggc aac atc cgc ttc gtc gca ctg acc gcc			1123
Asp Lys Lys Asn Arg Asp Gly Asn Ile Arg Phe Val Ala Leu Thr Ala			
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gtg ggc gag gtt acc cgc att gag ggg ccc tca aaa caa gat tta cag			1171
Val Gly Glu Val Thr Arg Ile Glu Gly Pro Ser Lys Gln Asp Leu Gln			
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Arg Ala Ala Glu Ser Gly Ala Glu Gln Val Ala Ile Leu His Gln Pro			
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Ser Met Asp Asp Ile Ala Ser Glu Leu Asp Ala Ala Leu Val Ala Ala			
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Gly Leu Lys Val Leu His Leu Asn Val Pro Asp Ala Glu Asn Gly Lys			
65	70	75	80
Ser Leu Glu Val Ala Gly Gln Cys Trp Asp Glu Leu Gly Gly Ala Ala			
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Phe Gly Arg Arg Asp Ile Val Ile Gly Leu Gly Gly Gly Ala Ala Thr			
	100	105	110
Asp Leu Ala Gly Phe Val Ala Ala Ala Trp Met Arg Gly Val Arg Val			
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Ile Gln Val Pro Thr Thr Leu Leu Ala Met Val Asp Ala Ala Val Gly			
	130	135	140
Gly Lys Thr Gly Ile Asn Thr Ala Ala Gly Lys Asn Leu Val Gly Ala			
145	150	155	160
Phe His Glu Pro Asp Ala Val Phe Ile Asp Thr Asp Arg Leu Ala Thr			
	165	170	175

Leu Pro Asp Ala Glu Ile Ile Ala Gly Ser Ala Glu Ile Ile Lys Thr
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 Gly Phe Ile Ala Asp Pro Glu Ile Leu Arg Leu Tyr Glu Thr Asp Pro
 195 200 205
 Ala Ala Cys Leu Lys Lys Glu Val Glu Gly Ser His Leu Pro Glu Leu
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 Ile Trp Arg Ser Val Thr Val Lys Gly Ser Val Val Gly Gln Asp Leu
 225 230 235 240
 Lys Glu Ser Ser Leu Arg Glu Ile Leu Asn Tyr Gly His Thr Phe Ala
 245 250 255
 His Ala Val Glu Leu Arg Glu Asn Phe Arg Trp Arg His Gly Asn Ala
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 Val Ala Val Gly Met Met Phe Ile Ala Asn Leu Ser His Lys Leu Gly
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 Asp Gly Met Thr Arg Asp Lys Lys Asn Arg Asp Gly Asn Ile Arg Phe
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1954)
 <223> RXN02508

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 Met Arg Thr Ser Ile
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 gcc act gtt tgt ttg tcc gga act ctt gct gaa aag ctg cgc gca gct 163
 Ala Thr Val Cys Leu Ser Gly Thr Leu Ala Glu Lys Leu Arg Ala Ala
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 gca gat gct gga ttt gat ggt gtg gaa atc ttc gag cag gac ttg gtg 211
 Ala Asp Ala Gly Phe Asp Gly Val Glu Ile Phe Glu Gln Asp Leu Val

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gtg ggc acc gcg acc atc aat gat gat gac ctt ttc gtg gag cag ttg Val Gly Thr Ala Thr Ile Asn Asp Asp Asp Leu Phe Val Glu Gln Leu 105 110 115	451		
cat cgt gca gca gat ttg gct gag aag tac aac gtc aag att gct tat His Arg Ala Ala Asp Leu Ala Glu Lys Tyr Asn Val Lys Ile Ala Tyr 120 125 130	499		
gaa gcg ttg gcg tgg ggc aag ttt gtc aat gat ttt gag cat gcg cat Glu Ala Leu Ala Trp Gly Lys Phe Val Asn Asp Phe Glu His Ala His 135 140 145	547		
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Pro Ser Ala Leu Glu Leu Arg Ala Leu Pro Glu Val Ala Glu Pro Glu	
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Gly Val Asp Phe Ile Glu Ile Ala Thr Gly Arg Leu Gly Glu Thr Ile	
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cgg gtt ctt cat caa ttg ggt ttc cgc ttg ggt ggt cat cac tgc agt	1075
Arg Val Leu His Gln Leu Gly Phe Arg Leu Gly Gly His His Cys Ser	
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Lys Gln Asp Tyr Gln Val Trp Thr Gln Gly Asp Val Arg Ile Val Val	
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Cys Asp Arg Gly Val Thr Gly Ala Pro Thr Thr Ile Ser Ala Met Gly	
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Phe Asp Thr Pro Asp Pro Glu Ala Ala His Ala Arg Ala Glu Leu Leu	
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Arg Ala Gln Thr Ile Asp Arg Pro His Ile Glu Gly Glu Val Asp Leu	
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Lys Gly Val Tyr Ala Pro Asp Gly Val Glu Leu Phe Phe Ala Gly Pro	
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Ser Pro Asp Gly Met Pro Glu Trp Leu Pro Glu Phe Gly Val Glu Lys	
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caa gaa gct ggt ctc att gaa gcc atc gac cac gtc aat ttc gcc cag	1411
Gln Glu Ala Gly Leu Ile Glu Ala Ile Asp His Val Asn Phe Ala Gln	
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Pro Trp Gln His Phe Asp Glu Ala Val Leu Phe Tyr Thr Ala Leu Met	
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Ala Leu Glu Thr Val Arg Glu Asp Glu Phe Pro Ser Pro Ile Gly Leu	
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Val Arg Asn Gln Val Met Arg Ser Pro Asn Asp Ala Val Arg Leu Leu	
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Leu Ser Val Ala Pro Glu Asp Gly Glu Gln Gly Asp Phe Leu Asn Ala	
490 495 500	
gcc tac ccg gag cac att gcg ttg gcc acg gcg gac atc gtg gcg gtg	1651
Ala Tyr Pro Glu His Ile Ala Leu Ala Thr Ala Asp Ile Val Ala Val	
505 510 515	

gct gaa cgt gcg cgc aaa cga ggc ctg gat ttc ttg ccc gtc cca gag 1699
 Ala Glu Arg Ala Arg Lys Arg Gly Leu Asp Phe Leu Pro Val Pro Glu
 520 525 530

aat tac tac gac gat gtg cag gcg cgt ttt gat ttg ccg cag gaa ttc 1747
 Asn Tyr Tyr Asp Asp Val Gln Ala Arg Phe Asp Leu Pro Gln Glu Phe
 535 540 545

ttg gac aca ctc aag gaa aac cac ctg ctt tac gac cgc gac gag aac 1795
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 550 555 560 565

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 570 575 580

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 Glu Val Val Glu Arg Arg Gly Gly Phe Ala Gly Trp Gly Glu Thr Asn
 585 590 595

gct ccg gtg cgg ttg gcg gcg cag tat cgt gag gtg cgg gac ctc gag 1939
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<213> Corynebacterium glutamicum

<400> 396

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 35 40 45

Arg Ala Gln Asp Leu Gly Leu Thr Leu Asp Leu Phe Gln Pro Phe Arg
 50 55 60

Asp Phe Glu Gly Val Glu Glu Glu Gln Phe Leu Lys Asn Leu His Arg
 65 70 75 80

Leu Glu Glu Lys Phe Lys Leu Met Asn Arg Leu Gly Ile Glu Met Ile
 85 90 95

Leu Leu Cys Ser Asn Val Gly Thr Ala Thr Ile Asn Asp Asp Asp Leu
 100 105 110

Phe Val Glu Gln Leu His Arg Ala Ala Asp Leu Ala Glu Lys Tyr Asn
 115 120 125

Val Lys Ile Ala Tyr Glu Ala Leu Ala Trp Gly Lys Phe Val Asn Asp
 130 135 140

Phe Glu His Ala His Ala Leu Val Glu Lys Val Asn His Lys Ala Leu
 145 150 155 160
 Gly Thr Cys Leu Asp Thr Phe His Ile Leu Ser Arg Gly Trp Glu Thr
 165 170 175
 Asp Glu Val Glu Asn Ile Pro Ala Glu Lys Ile Phe Phe Val Gln Leu
 180 185 190
 Ala Asp Ala Pro Lys Leu Ser Met Asp Ile Leu Ser Trp Ser Arg His
 195 200 205
 His Arg Val Phe Pro Gly Glu Gly Asp Phe Asp Leu Val Lys Phe Met
 210 215 220
 Val His Leu Ala Lys Thr Gly Tyr Asp Gly Pro Ile Ser Leu Glu Ile
 225 230 235 240
 Phe Asn Asp Ser Phe Arg Lys Ala Glu Val Gly Arg Thr Ala Ile Asp
 245 250 255
 Gly Leu Arg Ser Leu Arg Trp Leu Glu Asp Gln Thr Trp His Ala Leu
 260 265 270
 Asn Ala Glu Asp Arg Pro Ser Ala Leu Glu Leu Arg Ala Leu Pro Glu
 275 280 285
 Val Ala Glu Pro Glu Gly Val Asp Phe Ile Glu Ile Ala Thr Gly Arg
 290 295 300
 Leu Gly Glu Thr Ile Arg Val Leu His Gln Leu Gly Phe Arg Leu Gly
 305 310 315 320
 Gly His His Cys Ser Lys Gln Asp Tyr Gln Val Trp Thr Gln Gly Asp
 325 330 335
 Val Arg Ile Val Val Cys Asp Arg Gly Val Thr Gly Ala Pro Thr Thr
 340 345 350
 Ile Ser Ala Met Gly Phe Asp Thr Pro Asp Pro Glu Ala Ala His Ala
 355 360 365
 Arg Ala Glu Leu Leu Arg Ala Gln Thr Ile Asp Arg Pro His Ile Glu
 370 375 380
 Gly Glu Val Asp Leu Lys Gly Val Tyr Ala Pro Asp Gly Val Glu Leu
 385 390 395 400
 Phe Phe Ala Gly Pro Ser Pro Asp Gly Met Pro Glu Trp Leu Pro Glu
 405 410 415
 Phe Gly Val Glu Lys Gln Glu Ala Gly Leu Ile Glu Ala Ile Asp His
 420 425 430
 Val Asn Phe Ala Gln Pro Trp Gln His Phe Asp Glu Ala Val Leu Phe
 435 440 445
 Tyr Thr Ala Leu Met Ala Leu Glu Thr Val Arg Glu Asp Glu Phe Pro
 450 455 460

Ser Pro Ile Gly Leu Val Arg Asn Gln Val Met Arg Ser Pro Asn Asp
 465 470 475 480

Ala Val Arg Leu Leu Leu Ser Val Ala Pro Glu Asp Gly Glu Gln Gly
 485 490 495

Asp Phe Leu Asn Ala Ala Tyr Pro Glu His Ile Ala Leu Ala Thr Ala
 500 505 510

Asp Ile Val Ala Val Ala Glu Arg Ala Arg Lys Arg Gly Leu Asp Phe
 515 520 525

Leu Pro Val Pro Glu Asn Tyr Tyr Asp Asp Val Gln Ala Arg Phe Asp
 530 535 540

Leu Pro Gln Glu Phe Leu Asp Thr Leu Lys Glu Asn His Leu Leu Tyr
 545 550 555 560

Asp Arg Asp Glu Asn Gly Glu Phe Leu His Phe Tyr Thr Arg Thr Leu
 565 570 575

Gly Thr Leu Phe Phe Glu Val Val Glu Arg Arg Gly Gly Phe Ala Gly
 580 585 590

Trp Gly Glu Thr Asn Ala Pro Val Arg Leu Ala Ala Gln Tyr Arg Glu
 595 600 605

Val Arg Asp Leu Glu Arg Gly Ile Pro Asn
 610 615

<210> 397

<211> 470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(447)

<223> RXN02839

<400> 397

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Cys	Val	Val	Asn	Asp	Tyr	Ala	Asp	Arg	Lys	Phe	Asp	Gly	His	Val	Lys	
1				5					10					15		
cgc	acg	gcg	aac	cga	cca	ctt	ccc	agc	ggc	gcg	gta	aca	gag	aaa	gag	96
Arg	Thr	Ala	Asn	Arg	Pro	Leu	Pro	Ser	Gly	Ala	Val	Thr	Glu	Lys	Glu	
			20					25					30			
gcg	cgc	gcg	ctg	ttt	gtc	gtg	ctg	gta	ctg	att	tcg	ttt	tta	ctg	gtg	144
Ala	Arg	Ala	Leu	Phe	Val	Val	Leu	Val	Leu	Ile	Ser	Phe	Leu	Leu	Val	
			35				40					45				
ctg	acg	ctg	aat	acg	atg	acc	att	ctg	ttg	tcg	att	gcc	gcg	cta	gcg	192
Leu	Thr	Leu	Asn	Thr	Met	Thr	Ile	Leu	Leu	Ser	Ile	Ala	Ala	Leu	Ala	
			50			55				60						
ctg	gcg	tgg	gtg	tac	ccg	ttt	atg	aag	cgg	tat	acc	cat	cta	ccg	caa	240
Leu	Ala	Trp	Val	Tyr	Pro	Phe	Met	Lys	Arg	Tyr	Thr	His	Leu	Pro	Gln	
65					70				75						80	

gtg gtg ctg ggc gcg gcg ttt ggc tgg tcg att cca atg gct ttt gcc 288
 Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

gct gtg agt gag tcg gtg cca ttg agt tgc tgg tta atg ttc ctc gcc 336
 Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac 384
 Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

cgc gat gat gat gtg aag att ggc att aaa tcc acg gca atc ctg ttg 432
 Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
 130 135 140

gcc aat acg ata aat tgatattggg attttgcaga ttg 470
 Ala Asn Thr Ile Asn
 145

<210> 398

<211> 149

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
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Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30

Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45

Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60

Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80

Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
 130 135 140

Ala Asn Thr Ile Asn
 145

<210> 399

<211> 978

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(955)

<223> RXN00639

<400> 399

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gcaccccccta cttcaccccc aaagtctcta ggagtatgac atg act tca gct gaa 115
                                         Met Thr Ser Ala Glu
                                         1           5

cag atc gtt gat cca aca gcc cac gat tcg ggc aac aag gca act gac 163
Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp
                10                15                20

aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca 211
Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala
                25                30                35

aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac 259
Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His
                40                45                50

aag cac gaa gtc acc tac gaa gag tac gca gtg ctc aag cag tgg atg 307
Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val Leu Lys Gln Trp Met
                55                60                65

atc gac gtt gga gaa tac ggc gag tgg cca ctg tgg ttg gac gtt ttc 355
Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu Trp Leu Asp Val Phe
                70                75                80                85

gtt gag cat gag atc gaa gag atc aac tac aac cgc cac gac tac acc 403
Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn Arg His Asp Tyr Thr
                90                95                100

gga acc aag ggt tcc atc gaa ggc cct tat tac gta gag aac tct ccg 451
Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr Val Glu Asn Ser Pro
                105                110                115

aag ctc cct tgg gat gct gaa atg cca atg cgt gac aag gac cgc gca 499
Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg Asp Lys Asp Arg Ala
                120                125                130

tgc acc cca ctg atc ttc gag ggg cag gtt act gac ctc gac ggc aac 547
Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr Asp Leu Asp Gly Asn
                135                140                145

ggt ctt gat gga gca gaa gtt gag ctc tgg cac gca gat gag gac gga 595
Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His Ala Asp Glu Asp Gly
                150                155                160                165

tac tac tcc cag ttc gcg cct gga atc cca gag tgg aac ctg cgt ggc 643
Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu Trp Asn Leu Arg Gly
                170                175                180

acc atc gtt acc gat gag gaa ggc cgc tac aag atc aag acc ctg cag 691
Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys Ile Lys Thr Leu Gln

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185 190 195
 cct gcg cct tac cag atc cct cat gat ggc cca acc ggt tgg ttc att 739
 Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro Thr Gly Trp Phe Ile
 200 205 210
 gag tct tac ggt ggg cac cca tgg cgc cca gcc cac ctc cac ttg cgc 787
 Glu Ser Tyr Gly Gly His Pro Trp Arg Pro Ala His Leu His Leu Arg
 215 220 225
 gtt tcc cac ccg ggc tac cgc acc atc acc acc cag ctt tac ttc gag 835
 Val Ser His Pro Gly Tyr Arg Thr Ile Thr Thr Gln Leu Tyr Phe Glu
 230 235 240 245
 ggt ggc gag tgg gtc gaa aac gac gtt gca acc gct gtg aag cca gaa 883
 Gly Gly Glu Trp Val Glu Asn Asp Val Ala Thr Ala Val Lys Pro Glu
 250 255 260
 ctg gtc ctg cac cct gag act ggc gag gat ggt aac cac gtt cac tac 931
 Leu Val Leu His Pro Glu Thr Gly Glu Asp Gly Asn His Val His Tyr
 265 270 275
 cca ttc gtc ctg gat aag gaa gac tagtttttct acctagctag cat 978
 Pro Phe Val Leu Asp Lys Glu Asp
 280 285

<210> 400

<211> 285

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 400

Met Thr Ser Ala Glu Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly
 1 5 10 15
 Asn Lys Ala Thr Asp Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr
 20 25 30
 Ser Lys Glu Arg Ala Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile
 35 40 45
 Ala Gln Val Ala His Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val
 50 55 60
 Leu Lys Gln Trp Met Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu
 65 70 75 80
 Trp Leu Asp Val Phe Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn
 85 90 95
 Arg His Asp Tyr Thr Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr
 100 105 110
 Val Glu Asn Ser Pro Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg
 115 120 125
 Asp Lys Asp Arg Ala Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr
 130 135 140
 Asp Leu Asp Gly Asn Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His

145		150		155		160
Ala Asp Glu Asp Gly Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu						
	165			170		175
Trp Asn Leu Arg Gly Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys						
	180		185			190
Ile Lys Thr Leu Gln Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro						
	195		200		205	
Thr Gly Trp Phe Ile Glu Ser Tyr Gly Gly His Pro Trp Arg Pro Ala						
	210		215		220	
His Leu His Leu Arg Val Ser His Pro Gly Tyr Arg Thr Ile Thr Thr						
	225		230		235	240
Gln Leu Tyr Phe Glu Gly Gly Glu Trp Val Glu Asn Asp Val Ala Thr						
	245			250		255
Ala Val Lys Pro Glu Leu Val Leu His Pro Glu Thr Gly Glu Asp Gly						
	260		265			270
Asn His Val His Tyr Pro Phe Val Leu Asp Lys Glu Asp						
	275		280			285
<210>	401					
<211>	780					
<212>	DNA					
<213>	Corynebacterium glutamicum					
<220>						
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<222>	(101)..(757)					
<223>	RXN02530					
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accccttcca aaccttgagt cccgtgatac aattgttgat atg tca aca aat tat	115					
		Met Ser Thr Asn Tyr				
		1 5				
gaa gca atc atc att gga gca ggt cag gct gga ctc gcg gcg gcg cat	163					
Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly Leu Ala Ala Ala His						
	10		15		20	
gaa ctt tcc cgc cgc ggt ttc act ccc gga aaa gat ttt ctc gtc ctc	211					
Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys Asp Phe Leu Val Leu						
	25		30		35	
gat tcc aac gac ggg ccc ggt ggc gcc tgg cgg cat agg tgg gat tca	259					
Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg His Arg Trp Asp Ser						
	40		45		50	
ctc aca tta ggt aaa gcc cac gga atc gcc gat ctc cca ggg ctt ccc	307					
Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp Leu Pro Gly Leu Pro						
	55		60		65	
atg aat cgc ccc gat ccg aaa act ccg gct tcc aca ttg qtt qct qgt	355					

Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser Thr Leu Val Ala Gly
 70 75 80 85

tat tac ggc gct tac gag aac gag ttc tcc ttc gca gtt gtg cgc cca 403
 Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe Ala Val Val Arg Pro
 90 95 100

gtc aaa gtc tca cga gtt gag ccc act tcc gag gat cct tcg agc cca 451
 Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu Asp Pro Ser Ser Pro
 105 110 115

ttg cgc gtg agc agc gac gat ggt cga gag tgg att acc cgc atg gtt 499
 Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp Ile Thr Arg Met Val
 120 125 130

ctt aat gca aca ggt acg tgg aca aac cct tat gtt ccg tac att cct 547
 Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr Val Pro Tyr Ile Pro
 135 140 145

ggc atc gat aaa ttc cag ggc aag cag ctc cac acc gtt aat tac cgc 595
 Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His Thr Val Asn Tyr Arg
 150 155 160 165

aag gcc gag gat ttc aaa ggt aag aaa gtc ctg gtc gtc ggc ggt ggt 643
 Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
 170 175 180

ttg agt gct gtg caa ttt ctg ctg gag ttg gaa ggc ttg gcg gaa acc 691
 Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu Gly Leu Ala Glu Thr
 185 190 195

acc tgg gcg acg cgt cgt ccg cga act tac gca gcg cga gtt cga cgc 739
 Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala Ala Arg Val Arg Arg
 200 205 210

cgg ctg ggg cat tgc ggt tgagcgcgcc gtccgcgaac gca 780
 Arg Leu Gly His Cys Gly
 215

<210> 402

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

Met Ser Thr Asn Tyr Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly
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Leu Ala Ala Ala His Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys
 20 25 30

Asp Phe Leu Val Leu Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg
 35 40 45

His Arg Trp Asp Ser Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp
 50 55 60

Leu Pro Gly Leu Pro Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser
 65 70 75 80

ccg gaa ggt cag ttg atg cca att cca gag ggt tac agc ttt gtg gaa 355
 Pro Glu Gly Gln Leu Met Pro Ile Pro Glu Gly Tyr Ser Phe Val Glu
 70 75 80 85

 gcg gcc tcg atc gtg gag gtt gcg tgc acg gtg tgg tcg aat atc ggc 403
 Ala Ala Ser Ile Val Glu Val Ala Cys Thr Val Trp Ser Asn Ile Gly
 90 95 100

 atg ctg gcg ggc ttg cag aag gag gat act ttc ctt att cat ggt ggc 451
 Met Leu Ala Gly Leu Gln Lys Glu Asp Thr Phe Leu Ile His Gly Gly
 105 110 115

 gcg ggc ggt atc gga acg ttt gcc att cag atg ggc aag gct ctg ggt 499
 Ala Gly Gly Ile Gly Thr Phe Ala Ile Gln Met Gly Lys Ala Leu Gly
 120 125 130

 gtg acg gtt gcg gtg act gcc ggt tca act gaa aag tta aaa acc tgt 547
 Val Thr Val Ala Val Thr Ala Gly Ser Thr Glu Lys Leu Lys Thr Cys
 135 140 145

 aag aac tta ggg gcc gat atc ctc atc aat tac aag gag gaa gat ttc 595
 Lys Asn Leu Gly Ala Asp Ile Leu Ile Asn Tyr Lys Glu Glu Asp Phe
 150 155 160 165

 gcc gag gtt ttg aag aac aag gcg gat gtc att ctc gat att att ggt 643
 Ala Glu Val Leu Lys Asn Lys Ala Asp Val Ile Leu Asp Ile Ile Gly
 170 175 180

 gcg aag tat ttg tca cag aat gtg aag gcg atg gcc aag gac gcg cac 691
 Ala Lys Tyr Leu Ser Gln Asn Val Lys Ala Met Ala Lys Asp Ala His
 185 190 195

 atg gta gtc atc ggg atg cag ggt ggc gtg aaa ggg gag ctg aat ttg 739
 Met Val Val Ile Gly Met Gln Gly Gly Val Lys Gly Glu Leu Asn Leu
 200 205 210

 ggt cat ctt ttg gcc aag cga ggc acg att tct gcc act gcg ctg cgt 787
 Gly His Leu Leu Ala Lys Arg Gly Thr Ile Ser Ala Thr Ala Leu Arg
 215 220 225

 ggt cgc gat gag gcg gat aag gct cgg att gtc agc agc act gtc gaa 835
 Gly Arg Asp Glu Ala Asp Lys Ala Arg Ile Val Ser Ser Thr Val Glu
 230 235 240 245

 aat att tgg ccg ctg ctg caa tcg aag gaa att acc cct cac atc gac 883
 Asn Ile Trp Pro Leu Leu Gln Ser Lys Glu Ile Thr Pro His Ile Asp
 250 255 260

 cac acc ttg ccg cta gcc gaa gca gcc gcc gcc ttg cag aaa att caa 931
 His Thr Leu Pro Leu Ala Glu Ala Ala Ala Leu Gln Lys Ile Gln
 265 270 275

 gac ggc acc atc acc ggc aag ctc gtg ctt gcg gtt taggcaagcg 977
 Asp Gly Thr Ile Thr Gly Lys Leu Val Leu Ala Val
 280 285

 atgccagcac cct 990

<210> 404

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

Val Leu Val Lys Val Lys Pro Ala Gly Val Asn Arg Ala Asp Leu Leu
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 Gln Thr Gln Gly Asn Tyr Pro Val Pro Ala Gly Ala Ser Glu Ile Leu
 20 25 30
 Gly Leu Glu Cys Ala Gly Val Ile Val Asn Ala Gly Asp Thr Gly Gln
 35 40 45
 Thr Val Gly Gln Glu Val Ala Cys Leu Leu Thr Gly Gly Gly Tyr Ala
 50 55 60
 Gln Tyr Val Ala Val Pro Glu Gly Gln Leu Met Pro Ile Pro Glu Gly
 65 70 75 80
 Tyr Ser Phe Val Glu Ala Ala Ser Ile Val Glu Val Ala Cys Thr Val
 85 90 95
 Trp Ser Asn Ile Gly Met Leu Ala Gly Leu Gln Lys Glu Asp Thr Phe
 100 105 110
 Leu Ile His Gly Gly Ala Gly Gly Ile Gly Thr Phe Ala Ile Gln Met
 115 120 125
 Gly Lys Ala Leu Gly Val Thr Val Ala Val Thr Ala Gly Ser Thr Glu
 130 135 140
 Lys Leu Lys Thr Cys Lys Asn Leu Gly Ala Asp Ile Leu Ile Asn Tyr
 145 150 155 160
 Lys Glu Glu Asp Phe Ala Glu Val Leu Lys Asn Lys Ala Asp Val Ile
 165 170 175
 Leu Asp Ile Ile Gly Ala Lys Tyr Leu Ser Gln Asn Val Lys Ala Met
 180 185 190
 Ala Lys Asp Ala His Met Val Val Ile Gly Met Gln Gly Gly Val Lys
 195 200 205
 Gly Glu Leu Asn Leu Gly His Leu Leu Ala Lys Arg Gly Thr Ile Ser
 210 215 220
 Ala Thr Ala Leu Arg Gly Arg Asp Glu Ala Asp Lys Ala Arg Ile Val
 225 230 235 240
 Ser Ser Thr Val Glu Asn Ile Trp Pro Leu Leu Gln Ser Lys Glu Ile
 245 250 255
 Thr Pro His Ile Asp His Thr Leu Pro Leu Ala Glu Ala Ala Ala Ala
 260 265 270
 Leu Gln Lys Ile Gln Asp Gly Thr Ile Thr Gly Lys Leu Val Leu Ala
 275 285
 Val

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<210> 405
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1075)
<223> RXN01619
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tagcgaaccc attttctatt gcgatgagag gaacaccacc atg cgc gca atc act	115
Met Arg Ala Ile Thr	5
cac aac act ttc ggc gac ccc gcc gac gtc cta cag att acc gag aag	163
His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu Gln Ile Thr Glu Lys	20
gaa att ccc act ccc ggc cca ggt cag gtt cgt att caa gtg acg ctg	211
Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg Ile Gln Val Thr Leu	35
gca acc atc cac aac cat gat ttg tgg acc gtg aag ggc tct tac ggc	259
Ala Thr Ile His Asn His Asp Leu Trp Thr Val Lys Gly Ser Tyr Gly	50
ttc gtc cca gat ctg ccg gcc gcc gca ggc acc gag gca gtc ggc atc	307
Phe Val Pro Asp Leu Pro Ala Ala Gly Thr Glu Ala Val Gly Ile	65
gtc gac gcc ctg ggc gag ggc gtc gaa ggt ttg cag gtc ggt cag cgt	355
Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu Gln Val Gly Gln Arg	85
gtt gcg tcc ggc acc agc ttt ggc atc tgg gcg gag tac gcg ctt gtc	403
Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala Glu Tyr Ala Leu Val	100
gac gcc tcc ggc ctc att ccc gta cca gaa cag ctc tcc gac gaa agc	451
Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln Leu Ser Asp Glu Ser	115
gca gct cag ctc gtc gca atg cct ttc agc gcc atc agc ctt ctt gat	499
Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala Ile Ser Leu Leu Asp	130
ttc ctg gat atg aaa cca ggg gag tgg ctg atc caa aac tcc gca aac	547
Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile Gln Asn Ser Ala Asn	145
ggg gcc gtc ggc cgc atg ctc gca cag ctg gca gaa tcc cgc ggc atc	595
Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala Glu Ser Arg Gly Ile	165
cat gtc gtt ggt ctc gtc cgc cgt gac gcc ggt gtc caa gaa ctc gct	643
His Val Val Gly Leu Val Arg Arg Asp Ala Gly Val Gln Glu Leu Ala	180

gct caa aac atc agc ggc gtc gtt tcc act gag acc cca ggc tgg gaa 691
 Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu Thr Pro Gly Trp Glu
 185 190 195
 aag cag gtc gaa gac atc acc ggt ggc gca agc atc gcc gtc gca ctt 739
 Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser Ile Ala Val Ala Leu
 200 205 210
 gat tcc gtc ggt gga tcc tcc gca gct gac ctg gtg aaa ctg ctt ggc 787
 Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu Val Lys Leu Leu Gly
 215 220 225
 gaa ggc ggc acc ctc gtc tcc ttc ggc gcc atg ggc aac cca atc atg 835
 Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met Gly Asn Pro Ile Met
 230 235 240 245
 gaa atc cca tcc ggc ccc gtc atc ttc aag cac atc acc gtc aag ggc 883
 Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His Ile Thr Val Lys Gly
 250 255 260
 ttc tgg gga agc aaa gtc agc cgc gaa atg cca gca gag aag aaa acc 931
 Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro Ala Glu Lys Lys Thr
 265 270 275
 cag ttg ttc ggc gag ctc att gcg cgc ata ctt gat gga aca ttg acc 979
 Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu Asp Gly Thr Leu Thr
 280 285 290
 ctt cca gtt gat tcc acc ttt gat gcc gct gac atc gtc tcg gcc gtg 1027
 Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp Ile Val Ser Ala Val
 295 300 305
 cgc gcc tcc agc gag cct ggc cgt gcc gga aaa gtg ctc att cgt ttc 1075
 Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys Val Leu Ile Arg Phe
 310 315 320 325
 taaacgttta aggcccatta gac 1098

<210> 406

<211> 325

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 406

Met Arg Ala Ile Thr His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu
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 Gln Ile Thr Glu Lys Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg
 20 25 30
 Ile Gln Val Thr Leu Ala Thr Ile His Asn His Asp Leu Trp Thr Val
 35 40 45
 Lys Gly Ser Tyr Gly Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr
 50 55 60
 Glu Ala Val Gly Ile Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu
 65 70 75 80

Gln Val Gly Gln Arg Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala
 85 90 95
 Glu Tyr Ala Leu Val Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln
 100 105 110
 Leu Ser Asp Glu Ser Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala
 115 120 125
 Ile Ser Leu Leu Asp Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile
 130 135 140
 Gln Asn Ser Ala Asn Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala
 145 150 155 160
 Glu Ser Arg Gly Ile His Val Val Gly Leu Val Arg Arg Asp Ala Gly
 165 170 175
 Val Gln Glu Leu Ala Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu
 180 185 190
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 Asp Gly Thr Leu Thr Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp
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<213> *Corynebacterium glutamicum*

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<223> RXN01842

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Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly Tyr Ala Glu Asp Thr	
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Ile Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn
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Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala
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Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu
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Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His
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 <223> RXN01993

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 Tyr Glu Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys
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 Pro Leu Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala
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 180 185 190

Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg Trp Met
 195 200 205
 His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met Asn Asp Lys
 210 215 220
 Phe Pro Gly Phe Glu Gly Lys Val Asp Arg Trp Gln Ile Ile His Tyr
 225 230 235 240
 Tyr Tyr Pro Ser Thr Ile Cys Ile Asp Val Gly Val Ala Lys Ala Gly
 245 250 255
 Thr Gly Ala Gln Glu Gly Asp Arg Ser Gln Gly Val Asn Gly Tyr Val
 260 265 270
 Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Ser Ser His Tyr Phe Trp
 275 280 285
 Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr Thr Gln
 290 295 300
 Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp Met Leu
 305 310 315 320
 Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu Phe Tyr
 325 330 335
 Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile Leu Glu
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 <223> RXN00658

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 Val Arg His Asp Glu
 1 5
 cac tac cca gct gcg gca aac ctc att gct ttc gat aag gga tgg tcc 163
 His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe Asp Lys Gly Trp Ser
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 acc ctc atc gcc cct cag ctg gaa gat cca gag gcg gag gag ttc acc 211
 Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu Ala Glu Glu Phe Thr

25	30	35	
gcc gga ttc ctc acc gaa tac cag gac aat ctg atc act gcg ggc atg			259
Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu Ile Thr Ala Gly Met			
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gag cac cag gcg ctc gcg agc ggc ttc ccg gtg ggg cgt cgc ttc aag			307
Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val Gly Arg Arg Phe Lys			
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tcc gat att gct tta cga cgc tgc gat gcg gtg acc acc cac atc ggc			355
Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val Thr Thr His Ile Gly			
70	75	80	85
cac gaa cac tcc gcc gat ggt cac tgg agg atc tac gta ttc gct ggc			403
His Glu His Ser Ala Asp Gly His Trp Arg Ile Tyr Val Phe Ala Gly			
90	95	100	
caa gcc acc cca caa gat tcc gag tct gca ctg aac aag tgg gcg cag			451
Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu Asn Lys Trp Ala Gln			
105	110	115	
tgg atg gag gaa agc gaa gac tca cca ctc aac cgc ttc acc cca gaa			499
Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn Arg Phe Thr Pro Glu			
120	125	130	
gcc ggc gac cgc aac gca gtc ttc gat atc aag gct acc tac cag cag			547
Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys Ala Thr Tyr Gln Gln			
135	140	145	
cat tac cac tcc ttc gac ctg ttc gat gcg cca gag gtc ttc ttc cca			595
His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro Glu Val Phe Phe Pro			
150	155	160	165
cga gtt gga cca tac aag ctg caa aac ctc gaa aac gtt tgg acc gca			643
Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu Asn Val Trp Thr Ala			
170	175	180	
ctg gat tcc caa gac atc ttt gag tcc cgt ggc atc agt cgc gat ggc			691
Leu Asp Ser Gln Asp Ile Phe Glu Ser Arg Gly Ile Ser Arg Asp Gly			
185	190	195	
gca att gtt gtc gtt cgc cca gac cag tac gtc gca gca gtc ctc cca			739
Ala Ile Val Val Val Arg Pro Asp Gln Tyr Val Ala Ala Val Leu Pro			
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ctc gaa gac acc gca gca ctg gct gag ttc ttc aat ggc aat ctg ctt			787
Leu Glu Asp Thr Ala Ala Leu Ala Glu Phe Phe Asn Gly Asn Leu Leu			
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Glu Pro			
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<210> 414

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

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 35 40 45
 Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val
 50 55 60
 Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val
 65 70 75 80
 Thr Thr His Ile Gly His Glu His Ser Ala Asp Gly His Trp Arg Ile
 85 90 95
 Tyr Val Phe Ala Gly Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu
 100 105 110
 Asn Lys Trp Ala Gln Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn
 115 120 125
 Arg Phe Thr Pro Glu Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys
 130 135 140
 Ala Thr Tyr Gln Gln His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro
 145 150 155 160
 Glu Val Phe Phe Pro Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu
 165 170 175
 Asn Val Trp Thr Ala Leu Asp Ser Gln Asp Ile Phe Glu Ser Arg Gly
 180 185 190
 Ile Ser Arg Asp Gly Ala Ile Val Val Val Arg Pro Asp Gln Tyr Val
 195 200 205
 Ala Ala Val Leu Pro Leu Glu Asp Thr Ala Ala Leu Ala Glu Phe Phe
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 Asn Gly Asn Leu Leu Glu Pro
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<210> 415

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<212> DNA

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<222> (101)..(985)

<223> RXN00178

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 Met Thr Ile Ser Ala

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Phe	Asp	Ser	Cys	Glu	Asn	Pro	Arg	Leu	Lys	Leu	Val	Met	Lys	Ser	Leu				
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Thr	Val	His	Leu	His	Asp	Phe	Ile	Arg	Asp	Val	Arg	Leu	Thr	Glu	Glu				
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Glu	Trp	Asn	Tyr	Ala	Ile	Asp	Phe	Leu	Thr	Lys	Val	Gly	His	Ile	Thr				
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Ser	Met	Gln	Thr	Ile	Ala	Val	Asn	Asn	Glu	Ala	Tyr	Glu	Asp	Ala	Thr				
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gaa	gca	aca	gtc	ttt	ggc	ccc	ttc	ttt	gtc	gat	gat	gcg	cca	ctg	gtc	451			
Glu	Ala	Thr	Val	Phe	Gly	Pro	Phe	Phe	Val	Asp	Asp	Ala	Pro	Leu	Val				
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caa	aac	gga	gat	gac	att	gcc	ttt	ggc	gca	gtc	ggc	cag	ccg	gca	tgg	499			
Gln	Asn	Gly	Asp	Asp	Ile	Ala	Phe	Gly	Ala	Val	Gly	Gln	Pro	Ala	Trp				
		120				125						130							
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Val	Glu	Gly	Thr	Val	Lys	Asp	Thr	Glu	Gly	Asn	Pro	Ile	Pro	Asn	Ala				
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cgc	att	gaa	gta	tgg	gaa	tgc	gat	gaa	gat	gga	ctt	tat	gat	gtg	caa	595			
Arg	Ile	Glu	Val	Trp	Glu	Cys	Asp	Glu	Asp	Gly	Leu	Tyr	Asp	Val	Gln				
	150				155					160					165				
tac	gcc	gat	gag	cgc	agt	gct	gga	cgc	gca	cac	ctg	tat	tca	gat	gaa	643			
Tyr	Ala	Asp	Glu	Arg	Ser	Ala	Gly	Arg	Ala	His	Leu	Tyr	Ser	Asp	Glu				
				170				175						180					
aac	ggc	gaa	tac	cac	ttc	tgg	gga	cta	act	ccc	gtg	cca	tat	ccc	atc	691			
Asn	Gly	Glu	Tyr	His	Phe	Trp	Gly	Leu	Thr	Pro	Val	Pro	Tyr	Pro	Ile				
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cca	cac	gat	ggt	cca	gta	gga	caa	atg	ctc	caa	gca	gtt	ggt	cgt	tcc	739			
Pro	His	Asp	Gly	Pro	Val	Gly	Gln	Met	Leu	Gln	Ala	Val	Gly	Arg	Ser				
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ccc	gtt	cgt	tgc	gcg	cac	cta	cac	ttc	atg	gtg	act	gcg	cca	gag	aag	787			
Pro	Val	Arg	Cys	Ala	His	Leu	His	Phe	Met	Val	Thr	Ala	Pro	Glu	Lys				
		215				220					225								
cga	acc	ttg	gta	acc	cat	atc	ttc	gtt	gag	ggc	gat	ccg	cag	cta	gag	835			
Arg	Thr	Leu	Val	Thr	His	Ile	Phe	Val	Glu	Gly	Asp	Pro	Gln	Leu	Glu				
	230				235				240						245				

atc ggc gat tcc gtg ttt ggc gtg aag gac tca ctg att aag aaa ttc 883
 Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe
 250 255 260

gtt gag caa cct gca gga acc gca act cca gat ggt cgc gat gtg ggt 931
 Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp Gly Arg Asp Val Gly
 265 270 275

gat caa acc tgg gca cgc aca cgt ttt gat att gtg ctc gcc ccc ggc 979
 Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly
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 Asn Val
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<210> 416
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 <213> Corynebacterium glutamicum

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 35 40 45

Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
 50 55 60

Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
 65 70 75 80

Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
 85 90 95

Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp
 100 105 110

Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val
 115 120 125

Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn
 130 135 140

Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly
 145 150 155 160

Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His
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Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro
 180 185 190

Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln

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Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe Met Val			
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Thr Ala Pro Glu Lys Arg Thr Leu Val Thr His Ile Phe Val Glu Gly			
225	230	235	240
Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser			
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Leu Ile Lys Lys Phe Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp			
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Gly Arg Asp Val Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile			
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Val Leu Ala Pro Gly Asn Val			
290	295		
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			Met Ile Asp Thr Gly
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aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac 163			
Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn			
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gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc 211			
Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val			
	25	30	35
cac atc ggt ttg acc ctt gaa ggt gcg gag cat ctc gtg gag cca ggt 259			
His Ile Gly Leu Thr Leu Glu Gly Ala Glu His Leu Val Glu Pro Gly			
	40	45	50
tcg gaa ggc gcg gtg tcc ttt act gtt tcc gca act gat ggc aac ggc 307			
Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala Thr Asp Gly Asn Gly			
	55	60	65
gac ccc atc gcg gat gcc atg ttt gaa ctg tgg cag gcc gat cca gag 355			
Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp Gln Ala Asp Pro Glu			
	70	75	80
ggc atc cac aac tct gat ttg gat cca aac cgc aca gca cca gca acc 403			
Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg Thr Ala Pro Ala Thr			
	90	95	100

gca gat ggc ttc cgc ggg ctt ggt cgc gcg atg gca aac gcg cag ggt 451
 Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met Ala Asn Ala Gln Gly
 105 110 115

gag gca acg ttc acc act ttg gtt ccg gga gca ttc gca gat gag gca 499
 Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala Phe Ala Asp Glu Ala
 120 125 130

cca cac ttc aag gtt ggt gtg ttc gcc cgt ggc atg ctg gag cgt ctg 547
 Pro His Phe Lys Val Gly Val Phe Ala Arg Gly Met Leu Glu Arg Leu
 135 140 145

tac act cgc gca tac ctg cca gac gcc gat ttg agc acc gac cca gtt 595
 Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu Ser Thr Asp Pro Val
 150 155 160 165

ttg gct gtg gtc cca gct gat cga cgt gac ctc ctg gtg gct caa aag 643
 Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu Leu Val Ala Gln Lys
 170 175 180

acc gat gat gga ttc cgc ttc gac atc act gtc cag gct gaa gac aat 691
 Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val Gln Ala Glu Asp Asn
 185 190 195

gaa acc cca ttt ttt gga ctc taaattgacc cgatctttat act 735
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<210> 418

<211> 204

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 418

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Val Gly Pro Tyr Val His Ile Gly Leu Thr Leu Glu Gly Ala Glu His
 35 40 45

Leu Val Glu Pro Gly Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala
 50 55 60

Thr Asp Gly Asn Gly Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp
 65 70 75 80

Gln Ala Asp Pro Glu Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg
 85 90 95

Thr Ala Pro Ala Thr Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met
 100 105 110

Ala Asn Ala Gln Gly Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala
 115 120 125

Phe Ala Asp Glu Ala Pro His Phe Lys Val Gly Val Phe Ala Arg Gly

130 135 140

Met Leu Glu Arg Leu Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu
 145 150 155 160

Ser Thr Asp Pro Val Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu
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Leu Val Ala Gln Lys Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val
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Gln Ala Glu Asp Asn Glu Thr Pro Phe Phe Gly Leu
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 <212> DNA
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 <222> (101)..(1561)
 <223> RXN01653

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 Met Ala Thr Ala Glu
 1 5
 aac aca aca cag gag aat cgg aaa atc ctg ttc aac gca ttt gat atg 163
 Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe Asn Ala Phe Asp Met
 10 15 20
 aac tgc gtt gcg cat cag tcc cca gga ctg tgg aca cac ccg aag gat 211
 Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp Thr His Pro Lys Asp
 25 30 35
 aag gcg cga gac tac aac act ctt gat tac tgg gtg cac ctt gcc aag 259
 Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp Val His Leu Ala Lys
 40 45 50
 act ttg gag aag ggc ctt ttc gac ggc ctt ttc atc gca gat gtg ctt 307
 Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe Ile Ala Asp Val Leu
 55 60 65
 gga act tac gat gtt tat ggt tct agt aat gaa gcg gcg ttg agc agt 355
 Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu Ala Ala Leu Ser Ser
 70 75 80 85
 ggt gcg cag gtg cct gtc aat gat ccg atc ctt ctt gtt tct gcg atg 403
 Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu Leu Val Ser Ala Met
 90 95 100
 gcc tat gcc aca aag aac ctc ggg ttt ggc att act gca ggt act gcc 451
 Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile Thr Ala Gly Thr Ala
 105 110 115
 tat gag cac ccg tat cct ttt gcg cgg cgt ctg gcc aca ctt gat cac 499

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Leu	Thr	Asn	Gly	Arg	Val	Gly	Trp	Asn	Val	Val	Thr	Gly	Tyr	Leu	Pro		
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tct	gct	gct	caa	aac	atg	ggg	gac	acc	gat	cag	ctg	cca	cat	gat	gag	595	
Ser	Ala	Ala	Gln	Asn	Met	Gly	Asp	Thr	Asp	Gln	Leu	Pro	His	Asp	Glu		
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			170						175					180			
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Glu	Gly	Ser	Trp	Glu	Asp	Asp	Ala	Val	Gln	Asn	Asn	Thr	Glu	Thr	Ser		
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Val	Phe	Thr	Asp	Ser	Ser	Lys	Val	His	Ala	Ile	Asn	His	His	Gly	Lys		
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Tyr	Phe	Asp	Val	Pro	Gly	Ile	Ala	Ile	Thr	Glu	Pro	Ser	Val	Gln	Arg		
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Thr	Pro	Val	Ile	Tyr	Gln	Ala	Gly	Ala	Ser	Pro	Arg	Gly	Leu	Lys	Phe		
	230				235					240					245		
gct	ggg	gag	aat	gca	gaa	gca	gtg	ttt	atc	aat	tcc	agc	acc	gtg	gag	883	
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Gly	Arg	Asp	Pro	His	Ala	Val	Lys	Ile	Phe	Ala	Met	Gln	Thr	Ile	Ile		
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Arg	Tyr	Ile	Asp	Pro	Val	Gly	Gly	Leu	Thr	Leu	Met	Ser	Gly	Trp	Thr		
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ggc	gcg	gat	ctg	tcg	cag	tat	gac	ctg	gat	gaa	ccg	atc	acc	aat	att	1123	
Gly	Ala	Asp	Leu	Ser	Gln	Tyr	Asp	Leu	Asp	Glu	Pro	Ile	Thr	Asn	Ile		
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gag	tca	aac	gct	att	cag	tcc	act	gca	gcc	acc	att	agc	aac	ggc	acc	1171	
Glu	Ser	Asn	Ala	Ile	Gln	Ser	Thr	Ala	Ala	Thr	Ile	Ser	Asn	Gly	Thr		
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ggg	gaa	ggg	gcg	tgg	acg	gta	cgc	aaa	ctg	ggg	gag	gca	acc	ggc	atc	1219	
Gly	Glu	Gly	Ala	Trp	Thr	Val	Arg	Lys	Leu	Gly	Glu	Ala	Thr	Gly	Ile		

360	365	370	
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gaa ctt gca cgc atc cag gat ctc agc gat gtt gat ggt ttc aac ctt Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val Asp Gly Phe Asn Leu 390 395 400 405			1315
gct tat gcc atc acc cca gga act ttt gaa gat gtc gtg gac ttt gtg Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp Val Val Asp Phe Val 410 415 420			1363
gtg cct gag ctg caa aaa ctt agc cgc tac aag acg gaa tac gcg ccg Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys Thr Glu Tyr Ala Pro 425 430 435			1411
ggt tcc ttg cgc aac aaa ttg ctc ggt aaa ggt gat cgc ctg gac gat Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly Asp Arg Leu Asp Asp 440 445 450			1459
acc cac cgc ggc gca agc tac cgc cta ggc gct cgg aac tcc acc gcc Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala Arg Asn Ser Thr Ala 455 460 465			1507
act att gat ctc agt tcc ata tcc gcc caa cta gtt tcc cag gga gcc Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu Val Ser Gln Gly Ala 470 475 480 485			1555
cac tca tgatctcacc gcaaacaatc atc His Ser			1584

<210> 420

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met	Ala	Thr	Ala	Glu	Asn	Thr	Thr	Gln	Glu	Asn	Arg	Lys	Ile	Leu	Phe
1				5					10					15	

Asn	Ala	Phe	Asp	Met	Asn	Cys	Val	Ala	His	Gln	Ser	Pro	Gly	Leu	Trp
			20					25						30	

Thr	His	Pro	Lys	Asp	Lys	Ala	Arg	Asp	Tyr	Asn	Thr	Leu	Asp	Tyr	Trp
		35					40					45			

Val	His	Leu	Ala	Lys	Thr	Leu	Glu	Lys	Gly	Leu	Phe	Asp	Gly	Leu	Phe
	50					55					60				

Ile	Ala	Asp	Val	Leu	Gly	Thr	Tyr	Asp	Val	Tyr	Gly	Ser	Ser	Asn	Glu
65					70					75					80

Ala	Ala	Leu	Ser	Ser	Gly	Ala	Gln	Val	Pro	Val	Asn	Asp	Pro	Ile	Leu
				85					90					95	

Leu	Val	Ser	Ala	Met	Ala	Tyr	Ala	Thr	Lys	Asn	Leu	Gly	Phe	Gly	Ile
			100					105						110	

Thr Ala Gly Thr Ala Tyr Glu His Pro Tyr Pro Phe Ala Arg Arg Leu
 115 120 125
 Ala Thr Leu Asp His Leu Thr Asn Gly Arg Val Gly Trp Asn Val Val
 130 135 140
 Thr Gly Tyr Leu Pro Ser Ala Ala Gln Asn Met Gly Asp Thr Asp Gln
 145 150 155 160
 Leu Pro His Asp Glu Arg Tyr Asp Lys Ala Asp Glu Tyr Leu Glu Val
 165 170 175
 Ile Tyr Lys Leu Leu Glu Gly Ser Trp Glu Asp Asp Ala Val Gln Asn
 180 185 190
 Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His Ala Ile
 195 200 205
 Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile Thr Glu
 210 215 220
 Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala Ser Pro
 225 230 235 240
 Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe Ile Asn
 245 250 255
 Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile Arg Ala
 260 265 270
 Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile Phe Ala
 275 280 285
 Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln Ala Lys
 290 295 300
 Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu Thr Leu
 305 310 315 320
 Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu Asp Glu
 325 330 335
 Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala Ala Thr
 340 345 350
 Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys Leu Gly
 355 360 365
 Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly
 370 375 380
 Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val
 385 390 395 400
 Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp
 405 410 415
 Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys
 420 425 430

Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly
 435 440 445

Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala
 450 455 460

Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu
 465 470 475 480

Val Ser Gln Gly Ala His Ser
 485

<210> 421

<211> 702

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(679)

<223> RXN02053

<400> 421

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ctaccatgac tctgtttcca acacataaaa aggataaaaa atg tca ctt tca gtc 115
 Met Ser Leu Ser Val
 1 5

gtc gag gcg att acc aac cgc cgc gcc acc cgc aaa tac acc gat gaa 163
 Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg Lys Tyr Thr Asp Glu
 10 15 20

gct cct acc cct gag ctg atc gac aaa atc gtt gac ctt gcc ctg gag 211
 Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val Asp Leu Ala Leu Glu
 25 30 35

gca ccc agt gcg ttc aat gcg cag caa cgt gaa att gtt gtg att act 259
 Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu Ile Val Val Ile Thr
 40 45 50

gat ccc gca cag aag cag aag ctt tac gag gcc tcc cat cag aaa caa 307
 Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala Ser His Gln Lys Gln
 55 60 65

ttc ctc acc gca cct gta act ttc att gcg gtt gcc cgc gtg gaa aac 355
 Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val Ala Arg Val Glu Asn
 70 75 80 85

gag cct gag gat ttg gaa gag att ctt ggt acg gaa agg gct gaa cgt 403
 Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr Glu Arg Ala Glu Arg
 90 95 100

gtc gcg gga ttc atc aac ggt cgc agc att cag cag gca cgc gaa gca 451
 Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln Gln Ala Arg Glu Ala
 105 110 115

acg ttg agg gat gcc agc ctc gcg gcg gct ttt cta att ctg gct gcc 499
 Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe Leu Ile Leu Ala Ala
 120 125 130

cag gcg gag ggt ttg agt acc agc ccg act act ggt tgg gat gag gaa 547
 Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr Gly Trp Asp Glu Glu
 135 140 145
 aaa gtg aag gaa gca atc ggt ctc ggc ggg cgt gag gat cgt gca atc 595
 Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg Glu Asp Arg Ala Ile
 150 155 160 165
 gcc ctt gtt att gct acc gga ttc cct aat gaa cag ccg gag cac cct 643
 Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu Gln Pro Glu His Pro
 170 175 180
 ggt cgt ttg cag aat agg cgc atc gac aac agc tac taactctgcc 689
 Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser Tyr
 185 190
 agctcgcccg gac 702

<210> 422

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Met Ser Leu Ser Val Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg
 1 5 10 15
 Lys Tyr Thr Asp Glu Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val
 20 25 30
 Asp Leu Ala Leu Glu Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu
 35 40 45
 Ile Val Val Ile Thr Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala
 50 55 60
 Ser His Gln Lys Gln Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val
 65 70 75 80
 Ala Arg Val Glu Asn Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr
 85 90 95
 Glu Arg Ala Glu Arg Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln
 100 105 110
 Gln Ala Arg Glu Ala Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe
 115 120 125
 Leu Ile Leu Ala Ala Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr
 130 135 140
 Gly Trp Asp Glu Glu Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg
 145 150 155 160
 Glu Asp Arg Ala Ile Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu
 165 170 175
 Gln Pro Glu His Pro Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser
 180 185 190

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<210> 423
<211> 1191
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1168)  
<223> RXN00177
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558

gct tct ggt ctc aat ggt ttg gct cac tgc att gat tct ttg tgg gga 643
 Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile Asp Ser Leu Trp Gly
 170 175 180

ccg aag gcg gat ccc atc aat gcg gct atg gct gct gag gga att cga 691
 Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala Ala Glu Gly Ile Arg
 185 190 195

gca ctt tct gct ggc ctt ccc aag att gtg gca gat gct cag gac gta 739
 Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala Asp Ala Gln Asp Val
 200 205 210

gat ggt cgc gat gaa gcg ctc tac ggt gcc tac ctg gct gcg gtg tct 787
 Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr Leu Ala Ala Val Ser
 215 220 225

ttt gcc tct gct ggc tct ggt ctc cac cac aag atc tgc cac gtg ttg 835
 Phe Ala Ser Ala Gly Ser Gly Leu His His Lys Ile Cys His Val Leu
 230 235 240 245

ggt gga act ttt aac ctt cca cac gcg caa acc cat gca aca gta ctg 883
 Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr His Ala Thr Val Leu
 250 255 260

cct tat gtt ctt gcc ttc aac gcg cca tat gcg cca cag gca gaa caa 931
 Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala Pro Gln Ala Glu Gln
 265 270 275

cgc gca gcg gca gct ttc ggt tct gcg aca gca ctt gaa gga ttg caa 979
 Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu Gln
 280 285 290

cag ctg cgt gcc caa gtg gga gca cca cag cga cta tcc gat tac gga 1027
 Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr Gly
 295 300 305

ttc acc gca gca gga atc cca gag gca gtg gaa atc atc ttg gag aaa 1075
 Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu Lys
 310 315 320 325

gta ccg gcg aat aat cca cgg acg gtc aca gaa gaa aac ctc act gcg 1123
 Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr Ala
 330 335 340

ctg ctt acc aca gcg ctc aac ggc gac gat cca gca act ttg aat 1168
 Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
 345 350 355

taaggagacc aacatgacta ttt 1191

<210> 424

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Ser Leu Gln Phe Asp His Glu Thr Leu Gly Gln Arg Val Leu Phe
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Gly Ser Gly Glu Ala Ala Gln Asn Leu Ala Ala Glu Ile Ser Arg Leu
 20 25 30
 Asp Ala Lys Asn Val Met Val Val Ala Gly Asp Phe Glu Leu Pro Met
 35 40 45
 Ala Arg Gln Val Ala Ala Asp Ile Asp Val Lys Val Trp His Ser Asn
 50 55 60
 Val Val Met His Val Pro Ile Glu Thr Ala Glu Glu Ala Arg Ser Val
 65 70 75 80
 Ala Lys Glu Asn Asp Ile Asp Val Val Val Cys Val Gly Gly Gly Ser
 85 90 95
 Thr Thr Gly Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile
 100 105 110
 Ile Ala Val Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp
 115 120 125
 Gly Leu Thr Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Asn Lys Val
 130 135 140
 Leu Pro Val Thr Val Ile Tyr Asp Ser Ala Leu Thr Met Ser Leu Pro
 145 150 155 160
 Val Glu Met Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile
 165 170 175
 Asp Ser Leu Trp Gly Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala
 180 185 190
 Ala Glu Gly Ile Arg Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala
 195 200 205
 Asp Ala Gln Asp Val Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr
 210 215 220
 Leu Ala Ala Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His His Lys
 225 230 235 240
 Ile Cys His Val Leu Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr
 245 250 255
 His Ala Thr Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala
 260 265 270
 Pro Gln Ala Glu Gln Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala
 275 280 285
 Leu Glu Gly Leu Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg
 290 295 300
 Leu Ser Asp Tyr Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu
 305 310 315 320
 Ile Ile Leu Glu Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu
 325 330 335
 Glu Asn Leu Thr Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro

340

345

350

Ala Thr Leu Asn
355

<210> 425

<211> 960

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(937)

<223> RXC00963

<400> 425

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acctgcacg tacttttact ccggaaggaa tctagaactt atg cgt ctt gca aca 115
                                         Met Arg Leu Ala Thr
                                         1 5

atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac 163
Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
                        10 15 20

acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag 211
Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln
                        25 30 35

gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg 259
Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
                        40 45 50

acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag 307
Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
                        55 60 65

att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc 355
Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
                        70 75 80 85

cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg 403
Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
                        90 95 100

ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag 451
Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
                        105 110 115

gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca 499
Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
                        120 125 130

cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct ggc tac gca 547
Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala Gly Tyr Ala
                        135 140 145

gtg atg aac gat tac acc acc cgc gat ttc cag tac gca gca cct gca 595
Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln Tyr Ala Ala Pro Ala

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150	155	160	165	
aag act cca cag tgg cac cag ggc aag tct ttg gaa aag tcc gct ggc				643
Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu Glu Lys Ser Ala Gly				
170		175	180	
ttc ggg cct tgg atg act acc cca gat tct ttt gag ttc ggc ggc gag				691
Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe Glu Phe Gly Gly Glu				
185		190	195	
ctg gca acc tac ctc gag ggc gag aag gta cag tcc acc cct acc aat				739
Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln Ser Thr Pro Thr Asn				
200		205	210	
gac ctg gtc ttt agc cca gaa aag ctc atc gaa tac atc acc cac atc				787
Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu Tyr Ile Thr His Ile				
215		220	225	
tac cca ttg gat gct ggc gac gtc att gtc acc ggt acc cca ggc ggc				835
Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr Gly Thr Pro Gly Gly				
230		235	240	245
ggt ggc cac gca cgt aac cca cag cgc tac atc ggt gac ggc gaa acc				883
Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile Gly Asp Gly Glu Thr				
250		255	260	
gta aag gtt gag att gcg ggc ctc ggc ttc att gaa aac aag acg gtg				931
Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile Glu Asn Lys Thr Val				
265		270	275	
ttt gaa taaatgacaa ctttccacga tct				960
Phe Glu				

<210> 426

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
1 5 10 15

Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
20 25 30

Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
35 40 45

Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
50 55 60

Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
65 70 75 80

Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
85 90 95

Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro
100 105 110

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
 115 120 125
 Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
 130 135 140
 Ile Ala Gly Tyr Ala Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln
 145 150 155 160
 Tyr Ala Ala Pro Ala Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu
 165 170 175
 Glu Lys Ser Ala Gly Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe
 180 185 190
 Glu Phe Gly Gly Glu Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln
 195 200 205
 Ser Thr Pro Thr Asn Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu
 210 215 220
 Tyr Ile Thr His Ile Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr
 225 230 235 240
 Gly Thr Pro Gly Gly Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile
 245 250 255
 Gly Asp Gly Glu Thr Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile
 260 265 270
 Glu Asn Lys Thr Val Phe Glu
 275

<210> 427
 <211> 1101
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1078)
 <223> RXN00299

<400> 427
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 atccatttcc gtctaatacgc taattgacgag gagtctttgc atg tct atc cca ctt 115
 Met Ser Ile Pro Leu
 1 5
 tca ctg att gat ttt gcc acc att ttt gag ggc gaa agg cct ggt gac 163
 Ser Leu Ile Asp Phe Ala Thr Ile Phe Glu Gly Glu Arg Pro Gly Asp
 10 15 20
 agc ttc aaa cga tca gtg gca ttg gcg caa aaa gct gaa ggt tta ggc 211
 Ser Phe Lys Arg Ser Val Ala Leu Ala Gln Lys Ala Glu Gly Leu Gly
 25 30 35
 ttc aag cgc att tgg tac gca gag cat cac aac atg gag agc att tct 259

Phe	Lys	Arg	Ile	Trp	Tyr	Ala	Glu	His	His	Asn	Met	Glu	Ser	Ile	Ser		
	40						45					50					
tca	gct	gct	cct	gca	gtg	ctt	att	tct	cac	atc	ggg	gcg	aac	acc	aag	307	
Ser	Ala	Ala	Pro	Ala	Val	Leu	Ile	Ser	His	Ile	Gly	Ala	Asn	Thr	Lys		
	55					60					65						
act	att	cgt	ctg	ggg	gcc	ggc	ggc	gtc	atg	ctg	ccc	aac	cac	tcc	cca	355	
Thr	Ile	Arg	Leu	Gly	Ala	Gly	Gly	Val	Met	Leu	Pro	Asn	His	Ser	Pro		
70					75					80					85		
tat	gtc	atc	gct	gag	cag	ttc	ggc	acc	ttg	gcg	gag	ttg	tac	cca	gac	403	
Tyr	Val	Ile	Ala	Glu	Gln	Phe	Gly	Thr	Leu	Ala	Glu	Leu	Tyr	Pro	Asp		
				90					95					100			
cgc	atc	gac	ctc	ggc	ctg	ggc	cgt	gcc	cct	ggc	acg	gac	atg	aat	acc	451	
Arg	Ile	Asp	Leu	Gly	Leu	Gly	Arg	Ala	Pro	Gly	Thr	Asp	Met	Asn	Thr		
			105					110					115				
ttg	cgc	gct	tta	cga	cgc	gac	cct	cag	tcc	gcc	gag	aac	ttc	ccg	tcc	499	
Leu	Arg	Ala	Leu	Arg	Arg	Asp	Pro	Gln	Ser	Ala	Glu	Asn	Phe	Pro	Ser		
	120						125					130					
gac	gtt	gtc	gag	ctg	aac	tct	tac	ctc	acc	ggc	cgt	tcc	cgt	ctc	cca	547	
Asp	Val	Val	Glu	Leu	Asn	Ser	Tyr	Leu	Thr	Gly	Arg	Ser	Arg	Leu	Pro		
	135					140					145						
ggg	gtt	aac	gca	att	cca	ggc	aag	ggc	acc	aac	gta	ccg	ctg	tac	atc	595	
Gly	Val	Asn	Ala	Ile	Pro	Gly	Lys	Gly	Thr	Asn	Val	Pro	Leu	Tyr	Ile		
150					155					160					165		
ttg	ggg	tca	tcc	ctc	ttt	ggg	gca	caa	ttg	gca	gca	cag	ttg	ggg	atg	643	
Leu	Gly	Ser	Ser	Leu	Phe	Gly	Ala	Gln	Leu	Ala	Ala	Gln	Leu	Gly	Met		
				170					175					180			
cct	tat	tcc	ttc	gca	tcc	cac	ttc	gca	cca	act	cac	ctt	gag	cac	gcg	691	
Pro	Tyr	Ser	Phe	Ala	Ser	His	Phe	Ala	Pro	Thr	His	Leu	Glu	His	Ala		
			185					190					195				
gtg	caa	acc	tac	cgg	gat	aac	tac	cag	cct	tca	gag	cag	cat	cct	gag	739	
Val	Gln	Thr	Tyr	Arg	Asp	Asn	Tyr	Gln	Pro	Ser	Glu	Gln	His	Pro	Glu		
	200						205					210					
cct	tat	gtc	att	gcg	gcc	gtc	aat	gtc	acc	gca	tct	gat	tcc	act	gaa	787	
Pro	Tyr	Val	Ile	Ala	Ala	Val	Asn	Val	Thr	Ala	Ser	Asp	Ser	Thr	Glu		
	215					220				225							
caa	gcc	cac	gat	gat	ttc	tac	aag	gta	gcg	cgt	gca	cgc	gtg	aag	aac	835	
Gln	Ala	His	Asp	Asp	Phe	Tyr	Lys	Val	Ala	Arg	Ala	Arg	Val	Lys	Asn		
230					235					240					245		
atg	gca	ttg	cgt	ggc	cga	caa	gtt	act	gat	gag	caa	ctt	gat	gaa	ctc	883	
Met	Ala	Leu	Arg	Gly	Arg	Gln	Val	Thr	Asp	Glu	Gln	Leu	Asp	Glu	Leu		
				250					255					260			
atg	gat	tca	cca	gct	gct	cgc	caa	att	gtc	gac	atg	ctt	cac	tac	acc	931	
Met	Asp	Ser	Pro	Ala	Ala	Arg	Gln	Ile	Val	Asp	Met	Leu	His	Tyr	Thr		
			265					270					275				
gct	ata	ggc	act	gga	tcc	gaa	gtt	aaa	gaa	tac	cta	gac	ggt	ttt	gta	979	
Ala	Ile	Gly	Thr	Gly	Ser	Glu	Val	Lys	Glu	Tyr	Leu	Asp	Gly	Phe	Val		

280	285	290	
aag acg gca cag gct gat gaa ctg atg atc tcc ctg caa tcc ccc aac			1027
Lys Thr Ala Gln Ala Asp Glu Leu Met Ile Ser Leu Gln Ser Pro Asn			
295	300	305	
act gaa gca acc acg cgc aat atg gaa att ctt gcg gat gcg tgg att			1075
Thr Glu Ala Thr Thr Arg Asn Met Glu Ile Leu Ala Asp Ala Trp Ile			
310	315	320	325
aat tagtaccgat gggccggtag aca			1101
Asn			

<210> 428
 <211> 326
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 428
 Met Ser Ile Pro Leu Ser Leu Ile Asp Phe Ala Thr Ile Phe Glu Gly
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 Glu Arg Pro Gly Asp Ser Phe Lys Arg Ser Val Ala Leu Ala Gln Lys
 20 25 30
 Ala Glu Gly Leu Gly Phe Lys Arg Ile Trp Tyr Ala Glu His His Asn
 35 40 45
 Met Glu Ser Ile Ser Ser Ala Ala Pro Ala Val Leu Ile Ser His Ile
 50 55 60
 Gly Ala Asn Thr Lys Thr Ile Arg Leu Gly Ala Gly Gly Val Met Leu
 65 70 75 80
 Pro Asn His Ser Pro Tyr Val Ile Ala Glu Gln Phe Gly Thr Leu Ala
 85 90 95
 Glu Leu Tyr Pro Asp Arg Ile Asp Leu Gly Leu Gly Arg Ala Pro Gly
 100 105 110
 Thr Asp Met Asn Thr Leu Arg Ala Leu Arg Arg Asp Pro Gln Ser Ala
 115 120 125
 Glu Asn Phe Pro Ser Asp Val Val Glu Leu Asn Ser Tyr Leu Thr Gly
 130 135 140
 Arg Ser Arg Leu Pro Gly Val Asn Ala Ile Pro Gly Lys Gly Thr Asn
 145 150 155 160
 Val Pro Leu Tyr Ile Leu Gly Ser Ser Leu Phe Gly Ala Gln Leu Ala
 165 170 175
 Ala Gln Leu Gly Met Pro Tyr Ser Phe Ala Ser His Phe Ala Pro Thr
 180 185 190
 His Leu Glu His Ala Val Gln Thr Tyr Arg Asp Asn Tyr Gln Pro Ser
 195 200 205
 Glu Gln His Pro Glu Pro Tyr Val Ile Ala Ala Val Asn Val Thr Ala

210 215 220
 Ser Asp Ser Thr Glu Gln Ala His Asp Asp Phe Tyr Lys Val Ala Arg
 225 230 235 240
 Ala Arg Val Lys Asn Met Ala Leu Arg Gly Arg Gln Val Thr Asp Glu
 245 250 255
 Gln Leu Asp Glu Leu Met Asp Ser Pro Ala Ala Arg Gln Ile Val Asp
 260 265 270
 Met Leu His Tyr Thr Ala Ile Gly Thr Gly Ser Glu Val Lys Glu Tyr
 275 280 285
 Leu Asp Gly Phe Val Lys Thr Ala Gln Ala Asp Glu Leu Met Ile Ser
 290 295 300
 Leu Gln Ser Pro Asn Thr Glu Ala Thr Thr Arg Asn Met Glu Ile Leu
 305 310 315 320
 Ala Asp Ala Trp Ile Asn
 325

<210> 429

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (18)..(761)

<223> FRXA00299

<400> 429

gggtgccggc ggcggtcatg ctg ccc aac cac tcc cca tat gtc atc gct gag 53

Met Leu Pro Asn His Ser Pro Tyr Val Ile Ala Glu

1 5 10

cag ttc ggc acc ttg gcg gag ttg tac cca gac cgc atc gac ctc ggc 101

Gln Phe Gly Thr Leu Ala Glu Leu Tyr Pro Asp Arg Ile Asp Leu Gly

15 20 25

atg ggc cgt gcc cct ggc acg gac atg aat acc ttg cgc gct tta cga 149

Met Gly Arg Ala Pro Gly Thr Asp Met Asn Thr Leu Arg Ala Leu Arg

30 35 40

cgc gac cct cag tcc gcc gag aac ttc ccg tcc gac gtt gtc gag ctg 197

Arg Asp Pro Gln Ser Ala Glu Asn Phe Pro Ser Asp Val Val Glu Leu

45 50 55 60

aac tct tac ctc acc ggc cgt tcc cgt ctc cca ggg gtt aac gca att 245

Asn Ser Tyr Leu Thr Gly Arg Ser Arg Leu Pro Gly Val Asn Ala Ile

65 70 75

cca ggc aag ggc acc aac gta ccg ctg tac atc ttg ggt tca tcc ctc 293

Pro Gly Lys Gly Thr Asn Val Pro Leu Tyr Ile Leu Gly Ser Ser Leu

80 85 90

ttt ggt gca caa ttg gca gca cag ttg ggt atg cct tat tcc ttc gca 341

Phe Gly Ala Gln Leu Ala Ala Gln Leu Gly Met Pro Tyr Ser Phe Ala

95	100	105	
tcc cac ttc gca cca act cac ctt gag cac gcg gtg caa acc tac cgg			389
Ser His Phe Ala Pro Thr	His Leu Glu His	Ala Val Gln Thr Tyr Arg	
110	115	120	
gat aac tac cag cct tca gag cag cat cct gag cct tat gtc att gcg			437
Asp Asn Tyr Gln Pro Ser	Glu Gln His Pro	Glu Pro Tyr Val Ile Ala	
125	130	135 140	
gcc gtc aat gtc acc gca tct gat tcc act gaa caa gcc cac gat gat			485
Ala Val Asn Val Thr Ala Ser Asp Ser	Thr Thr Glu Gln Ala His	Asp Asp	
	145	150 155	
ttc tac aag gta gcg cgt gca cgc gtg aag aac atg gca ttg cgt ggc			533
Phe Tyr Lys Val Ala Arg	Ala Arg Val Lys Asn Met	Ala Leu Arg Gly	
160	165	170	
cga caa gtt act gat gag caa ctt gat gaa ctc atg gat tca cca gct			581
Arg Gln Val Thr Asp Glu Gln	Leu Asp Glu Leu Met Asp	Ser Pro Ala	
175	180	185	
gct cgc caa att gtc gac atg ctt cac tac acc gct ata ggc act gga			629
Ala Arg Gln Ile Val Asp	Met Leu His Tyr Thr	Ala Ile Gly Thr Gly	
190	195	200	
tcc gaa gtt aaa gaa tac cta gac ggt ttt gta aag acg gca cag gct			677
Ser Glu Val Lys Glu Tyr	Leu Asp Gly Phe	Val Lys Thr Ala Gln Ala	
205	210	215 220	
gat gaa ctg atg atc tcc ctg caa tcc ccc aac act gaa gca acc acg			725
Asp Glu Leu Met Ile Ser	Leu Gln Ser Pro Asn Thr	Glu Ala Thr Thr	
225	230	235	
cgc aat atg gaa att ctt gcg gat gcg tgg att aat tagtaccgat			771
Arg Asn Met Glu Ile Leu	Ala Asp Ala Trp Ile Asn		
240	245		
gggccggtag aca			784
<210> 430			
<211> 248			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 430			
Met Leu Pro Asn His Ser Pro Tyr Val	Ile Ala Glu Gln Phe Gly Thr		
1	5	10	15
Leu Ala Glu Leu Tyr Pro Asp Arg Ile Asp Leu Gly Met Gly Arg Ala			
20	25	30	
Pro Gly Thr Asp Met Asn Thr Leu Arg Ala Leu Arg Arg Asp Pro Gln			
35	40	45	
Ser Ala Glu Asn Phe Pro Ser Asp Val Val Glu Leu Asn Ser Tyr Leu			
50	55	60	
Thr Gly Arg Ser Arg Leu Pro Gly Val Asn Ala Ile Pro Gly Lys Gly			
65	70	75	80

Thr	Asn	Val	Pro	Leu 85	Tyr	Ile	Leu	Gly	Ser 90	Ser	Leu	Phe	Gly	Ala	Gln 95
Leu	Ala	Ala	Gln 100	Leu	Gly	Met	Pro	Tyr 105	Ser	Phe	Ala	Ser	His 110	Phe	Ala
Pro	Thr	His 115	Leu	Glu	His	Ala	Val 120	Gln	Thr	Tyr	Arg	Asp 125	Asn	Tyr	Gln
Pro	Ser 130	Glu	Gln	His	Pro	Glu 135	Pro	Tyr	Val	Ile	Ala 140	Ala	Val	Asn	Val
Thr 145	Ala	Ser	Asp	Ser	Thr 150	Glu	Gln	Ala	His 155	Asp	Asp	Phe	Tyr	Lys	Val 160
Ala	Arg	Ala	Arg	Val 165	Lys	Asn	Met	Ala	Leu 170	Arg	Gly	Arg	Gln	Val 175	Thr
Asp	Glu	Gln 180	Leu	Asp	Glu	Leu	Met	Asp 185	Ser	Pro	Ala	Ala	Arg 190	Gln	Ile
Val	Asp 195	Met	Leu	His	Tyr	Thr	Ala 200	Ile	Gly	Thr	Gly	Ser 205	Glu	Val	Lys
Glu 210	Tyr	Leu	Asp	Gly	Phe	Val 215	Lys	Thr	Ala	Gln 220	Ala	Asp	Glu	Leu	Met
Ile 225	Ser	Leu	Gln	Ser	Pro 230	Asn	Thr	Glu	Ala	Thr 235	Thr	Arg	Asn	Met	Glu 240
Ile	Leu	Ala	Asp	Ala 245	Trp	Ile	Asn								

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<210> 431
<211> 825
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(802)  
<223> RXA00332
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gttacgccag ccctgcgaca ccaccatcta gggttagagt atg gcc ttc aac aaa 115
                                         Met Ala Phe Asn Lys
                                         1                               5

gcg tac gat gca ctt cgc gcc cct caa atc acc ctc gga ctc atg aca 163
Ala Tyr Asp Ala Leu Arg Ala Pro Gln Ile Thr Leu Gly Leu Met Thr
                        10                               15                               20

cca aac ggc cct gaa cta ggg cgc agt gaa atg gtt cca acc gaa aat 211
Pro Asn Gly Pro Glu Leu Gly Arg Ser Glu Met Val Pro Thr Glu Asn
                        25                               30                               35

agc atc gaa cta gcc ata caa gca gaa gct caa gga ttc aga ggc atg 259

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Ser Ile Glu Leu Ala Ile Gln Ala Glu Ala Gln Gly Phe Arg Gly Met
40 45 50

tgg gtt cga gac gtt cca ctc gca gtt cct caa gga atc act gtt acc 307
Trp Val Arg Asp Val Pro Leu Ala Val Pro Gln Gly Ile Thr Val Thr
55 60 65

gat aaa cag gct acg tat tta gat gat cca ttc tta atg ctc ggt gcg 355
Asp Lys Gln Ala Thr Tyr Leu Asp Asp Pro Phe Leu Met Leu Gly Ala
70 75 80 85

atg gcc tct gtg acc tct aca atc gcg ctg ggc act gca gcg acc gtg 403
Met Ala Ser Val Thr Ser Thr Ile Ala Leu Gly Thr Ala Ala Thr Val
90 95 100

ctt cca ctc aga cat ccg cta cat gtg gcg aaa tcc gcg ctc acc ctt 451
Leu Pro Leu Arg His Pro Leu His Val Ala Lys Ser Ala Leu Thr Leu
105 110 115

gat cga ctc agc cac gga cgt ttc gtt tta ggc atc ggc tct ggc gac 499
Asp Arg Leu Ser His Gly Arg Phe Val Leu Gly Ile Gly Ser Gly Asp
120 125 130

agg cct gaa gaa ttc gag att ttt ggc aaa agc tta gac aat cga cgc 547
Arg Pro Glu Glu Phe Glu Ile Phe Gly Lys Ser Leu Asp Asn Arg Arg
135 140 145

gct gat att cag tct ggg tgg gca att ttg cgt gca gct ttg tcg ccg 595
Ala Asp Ile Gln Ser Gly Trp Ala Ile Leu Arg Ala Ala Leu Ser Pro
150 155 160 165

gat cct gcg atg cgg gcc gac ctt gaa ttt gcg cca acc acg cca cct 643
Asp Pro Ala Met Arg Ala Asp Leu Glu Phe Ala Pro Thr Thr Pro Pro
170 175 180

gaa gct cag atc ccc atg atc gct gta ggt tct gcc cga caa aca gtg 691
Glu Ala Gln Ile Pro Met Ile Ala Val Gly Ser Ala Arg Gln Thr Val
185 190 195

caa tgg atc gcc cga aac gcc gac gga tgg gca acc tac tac cgc ccc 739
Gln Trp Ile Ala Arg Asn Ala Asp Gly Trp Ala Thr Tyr Tyr Arg Pro
200 205 210

gct gaa gct caa gtc gga cgc ctc gat ctc tgg gac aaa gcc cgt ggt 787
Ala Glu Ala Gln Val Gly Arg Leu Asp Leu Trp Asp Lys Ala Arg Gly
215 220 225

ggc acc cgc cct tgt tgatttcctc catggggctc aac 825
Gly Thr Arg Pro Cys
230

<210> 432

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Ala Phe Asn Lys Ala Tyr Asp Ala Leu Arg Ala Pro Gln Ile Thr
1 5 10 15

Leu Gly Leu Met Thr Pro Asn Gly Pro Glu Leu Gly Arg Ser Glu Met
 20 25 30
 Val Pro Thr Glu Asn Ser Ile Glu Leu Ala Ile Gln Ala Glu Ala Gln
 35 40 45
 Gly Phe Arg Gly Met Trp Val Arg Asp Val Pro Leu Ala Val Pro Gln
 50 55 60
 Gly Ile Thr Val Thr Asp Lys Gln Ala Thr Tyr Leu Asp Asp Pro Phe
 65 70 75 80
 Leu Met Leu Gly Ala Met Ala Ser Val Thr Ser Thr Ile Ala Leu Gly
 85 90 95
 Thr Ala Ala Thr Val Leu Pro Leu Arg His Pro Leu His Val Ala Lys
 100 105 110
 Ser Ala Leu Thr Leu Asp Arg Leu Ser His Gly Arg Phe Val Leu Gly
 115 120 125
 Ile Gly Ser Gly Asp Arg Pro Glu Glu Phe Glu Ile Phe Gly Lys Ser
 130 135 140
 Leu Asp Asn Arg Arg Ala Asp Ile Gln Ser Gly Trp Ala Ile Leu Arg
 145 150 155 160
 Ala Ala Leu Ser Pro Asp Pro Ala Met Arg Ala Asp Leu Glu Phe Ala
 165 170 175
 Pro Thr Thr Pro Pro Glu Ala Gln Ile Pro Met Ile Ala Val Gly Ser
 180 185 190
 Ala Arg Gln Thr Val Gln Trp Ile Ala Arg Asn Ala Asp Gly Trp Ala
 195 200 205
 Thr Tyr Tyr Arg Pro Ala Glu Ala Gln Val Gly Arg Leu Asp Leu Trp
 210 215 220
 Asp Lys Ala Arg Gly Gly Thr Arg Pro Cys
 225 230

<210> 433

<211> 842

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(819)

<223> RXA01838

<400> 433

cag cac ctc tcc ggc ggc cgt gtt gac ctt atg atg ggc cgt ggc aac 48
 Gln His Leu Ser Gly Gly Arg Val Asp Leu Met Met Gly Arg Gly Asn
 1 5 10 15
 acc gga ccc gtt tac cca tgg ttt ggc aaa gac atc cac caa ggc atc 96
 Thr Gly Pro Val Tyr Pro Trp Phe Gly Lys Asp Ile His Gln Gly Ile
 20 25 30

cca cta gcg att gaa aac tac cac ctc ctg cgc cgc ctc tgg cgc gaa	144
Pro Leu Ala Ile Glu Asn Tyr His Leu Leu Arg Arg Leu Trp Arg Glu	
35 40 45	
gac gta gtc aac tgg cag ggc aaa ttc cgc aca ccg ttg cag gga tac	192
Asp Val Val Asn Trp Gln Gly Lys Phe Arg Thr Pro Leu Gln Gly Tyr	
50 55 60	
acc tct acc cca gca cca tta gac ggc gtt gca cca ttc gtc tgg cac	240
Thr Ser Thr Pro Ala Pro Leu Asp Gly Val Ala Pro Phe Val Trp His	
65 70 75 80	
ggc tcc atc cgc tcc acc gaa atc gca gag caa gca gcc ttc tat ggc	288
Gly Ser Ile Arg Ser Thr Glu Ile Ala Glu Gln Ala Ala Phe Tyr Gly	
85 90 95	
gac ggc ttc ttc cac aac aac atc ttc tgg aac aaa gag cac acc gcc	336
Asp Gly Phe Phe His Asn Asn Ile Phe Trp Asn Lys Glu His Thr Ala	
100 105 110	
caa atg gtc aac ctc tac cgc cag cgt ttc gaa cac tac gga cac ggc	384
Gln Met Val Asn Leu Tyr Arg Gln Arg Phe Glu His Tyr Gly His Gly	
115 120 125	
caa gca gac cag gcc atc gtg gga ctc ggt ggc caa gtc ttc atc ggc	432
Gln Ala Asp Gln Ala Ile Val Gly Leu Gly Gly Gln Val Phe Ile Gly	
130 135 140	
gat tct gaa gaa gaa gca aag aag acc ttc cgc ccc tac ttc gac aac	480
Asp Ser Glu Glu Glu Ala Lys Lys Thr Phe Arg Pro Tyr Phe Asp Asn	
145 150 155 160	
gcc cct gtc tac gga cac gga cca tca ctt gaa gat ttc tcc cgc ctg	528
Ala Pro Val Tyr Gly His Gly Pro Ser Leu Glu Asp Phe Ser Arg Leu	
165 170 175	
acc cca cta acc gtc ggt acc gct gag caa gtt atc gaa cgc acc atg	576
Thr Pro Leu Thr Val Gly Thr Ala Glu Gln Val Ile Glu Arg Thr Met	
180 185 190	
gaa ttc gcc gac tgg gta ggc gat tac cag cgc cag ctc ttc ctc atc	624
Glu Phe Ala Asp Trp Val Gly Asp Tyr Gln Arg Gln Leu Phe Leu Ile	
195 200 205	
gac cac gcc ggc ctg cca cta gaa atg gtc ctt gat cag atc gaa cgc	672
Asp His Ala Gly Leu Pro Leu Glu Met Val Leu Asp Gln Ile Glu Arg	
210 215 220	
ctc ggc cac gat gtc gtc cca gag gta cgc cgc cgc atg gag gag cgt	720
Leu Gly His Asp Val Val Pro Glu Val Arg Arg Arg Met Glu Glu Arg	
225 230 235 240	
cgc cca gac cac gtt ccc tcc aac cca cca acc cac cag agc ctg aag	768
Arg Pro Asp His Val Pro Ser Asn Pro Pro Thr His Gln Ser Leu Lys	
245 250 255	
gcc aac cga aac agc cct tac ttt cag atc aac cct ggt cag cca act	816
Ala Asn Arg Asn Ser Pro Tyr Phe Gln Ile Asn Pro Gly Gln Pro Thr	
260 265 270	

gag tagtttttct gaaactaagg aga
Glu

842

<210> 434

<211> 273

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 434

Gln His Leu Ser Gly Gly Arg Val Asp Leu Met Met Gly Arg Gly Asn
1 5 10 15

Thr Gly Pro Val Tyr Pro Trp Phe Gly Lys Asp Ile His Gln Gly Ile
20 25 30

Pro Leu Ala Ile Glu Asn Tyr His Leu Leu Arg Arg Leu Trp Arg Glu
35 40 45

Asp Val Val Asn Trp Gln Gly Lys Phe Arg Thr Pro Leu Gln Gly Tyr
50 55 60

Thr Ser Thr Pro Ala Pro Leu Asp Gly Val Ala Pro Phe Val Trp His
65 70 75 80

Gly Ser Ile Arg Ser Thr Glu Ile Ala Glu Gln Ala Ala Phe Tyr Gly
85 90 95

Asp Gly Phe Phe His Asn Asn Ile Phe Trp Asn Lys Glu His Thr Ala
100 105 110

Gln Met Val Asn Leu Tyr Arg Gln Arg Phe Glu His Tyr Gly His Gly
115 120 125

Gln Ala Asp Gln Ala Ile Val Gly Leu Gly Gly Gln Val Phe Ile Gly
130 135 140

Asp Ser Glu Glu Glu Ala Lys Lys Thr Phe Arg Pro Tyr Phe Asp Asn
145 150 155 160

Ala Pro Val Tyr Gly His Gly Pro Ser Leu Glu Asp Phe Ser Arg Leu
165 170 175

Thr Pro Leu Thr Val Gly Thr Ala Glu Gln Val Ile Glu Arg Thr Met
180 185 190

Glu Phe Ala Asp Trp Val Gly Asp Tyr Gln Arg Gln Leu Phe Leu Ile
195 200 205

Asp His Ala Gly Leu Pro Leu Glu Met Val Leu Asp Gln Ile Glu Arg
210 215 220

Leu Gly His Asp Val Val Pro Glu Val Arg Arg Arg Met Glu Glu Arg
225 230 235 240

Arg Pro Asp His Val Pro Ser Asn Pro Pro Thr His Gln Ser Leu Lys
245 250 255

Ala Asn Arg Asn Ser Pro Tyr Phe Gln Ile Asn Pro Gly Gln Pro Thr
260 265 270

Glu

<210> 435

<211> 1167

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA02643

<400> 435

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tgagaacacc taaaaacctt gcggaatac caccaacccc atattgttga tatatctaca 60

aactctttta ataagtctga tcaacaacgt gaggaagca atg aaa aac gtc tcc 115
                Met Lys Asn Val Ser
                        1                5

ttc ggc ctc gac acc ttc ggc gac aac gcc atc gac ctg cag ggc aac 163
Phe Gly Leu Asp Thr Phe Gly Asp Asn Ala Ile Asp Leu Gln Gly Asn
                10                15                20

ccg gtc tcc cct gca caa aca ctt cga aac atc att gat gaa gcc aag 211
Pro Val Ser Pro Ala Gln Thr Leu Arg Asn Ile Ile Asp Glu Ala Lys
                25                30                35

atg gca gac aaa gtc ggg gtg gat atc atc ggc atc gga gag cac cac 259
Met Ala Asp Lys Val Gly Val Asp Ile Ile Gly Ile Gly Glu His His
                40                45                50

cgt gag gaa tac tca gtt tct gca cct gac atc gtc atg aca gct atc 307
Arg Glu Glu Tyr Ser Val Ser Ala Pro Asp Ile Val Met Thr Ala Ile
                55                60                65

ctc gca tcc act gag cga ctc aaa gtc acc tct tcc gtg act gtg ctg 355
Leu Ala Ser Thr Glu Arg Leu Lys Val Thr Ser Ser Val Thr Val Leu
                70                75                80                85

tcc tct gat gat cct gtt cgc ctg ttt gag cgt tat tcc acc atg aat 403
Ser Ser Asp Asp Pro Val Arg Leu Phe Glu Arg Tyr Ser Thr Met Asn
                90                95                100

gca ctg tcc aac ggt cgc gcc gaa atc acc ttg gga cgc ggt tcc ttc 451
Ala Leu Ser Asn Gly Arg Ala Glu Ile Thr Leu Gly Arg Gly Ser Phe
                105                110                115

att gag tct ttc cca ttg ttt ggt ttt gat ctt cag gac tac gag cag 499
Ile Glu Ser Phe Pro Leu Phe Gly Phe Asp Leu Gln Asp Tyr Glu Gln
                120                125                130

ctg ttt agt gaa cgc ctt gat ttg ttc gcg aag att ctt gag gcc gac 547
Leu Phe Ser Glu Arg Leu Asp Leu Phe Ala Lys Ile Leu Glu Ala Asp
                135                140                145

agc cgt ggt cag ggc gtg acc tgg cat ggt gag acc cgc tcg gcg ttg 595
Ser Arg Gly Gln Gly Val Thr Trp His Gly Glu Thr Arg Ser Ala Leu
                150                155                160                165

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gaa aac cag atg ctt tac cca cca act gag aat ggc att cac gct tgg 643
 Glu Asn Gln Met Leu Tyr Pro Pro Thr Glu Asn Gly Ile His Ala Trp
 170 175 180

gtt gca gtg ggt ggc agc cca gaa tca gtc gtg cgc gct gct aag tat 691
 Val Ala Val Gly Gly Ser Pro Glu Ser Val Val Arg Ala Ala Lys Tyr
 185 190 195

cgt ttc ccg ttg atg ctt gcc atc atc ggc ggt gct cct gag cgt ttc 739
 Arg Phe Pro Leu Met Leu Ala Ile Ile Gly Gly Ala Pro Glu Arg Phe
 200 205 210

cgc ccg tat gtg gat ctg tac aag cgt gcc aac gaa cag ttc ggg cag 787
 Arg Pro Tyr Val Asp Leu Tyr Lys Arg Ala Asn Glu Gln Phe Gly Gln
 215 220 225

cct caa aag ccc att ggt gtg cac tcc cct gga ctc att gcg gca act 835
 Pro Gln Lys Pro Ile Gly Val His Ser Pro Gly Leu Ile Ala Ala Thr
 230 235 240 245

gat gag gaa gcc cgt gag cta gca ctt aat gat tgg ttg gaa ctc caa 883
 Asp Glu Glu Ala Arg Glu Leu Ala Leu Asn Asp Trp Leu Glu Leu Gln
 250 255 260

cgc aag atc ggt gct gaa cgc ggt tgg gct cct gcg gat gca atg cag 931
 Arg Lys Ile Gly Ala Glu Arg Gly Trp Ala Pro Ala Asp Ala Met Gln
 265 270 275

ttt gaa cgc gaa atc gat cac ggt tcc tta tac atc ggt tcc cct gag 979
 Phe Glu Arg Glu Ile Asp His Gly Ser Leu Tyr Ile Gly Ser Pro Glu
 280 285 290

acg gtc gca aag aag atc gcc aaa acc att tca gtg ctt gat ctt gat 1027
 Thr Val Ala Lys Lys Ile Ala Lys Thr Ile Ser Val Leu Asp Leu Asp
 295 300 305

cgc ttt acc ctc aaa tac gcc agt ggc cag acc cct cat gag tac ttg 1075
 Arg Phe Thr Leu Lys Tyr Ala Ser Gly Gln Thr Pro His Glu Tyr Leu
 310 315 320 325

ctg aag tcc att gag ttg tat ggc act gag gtt att ccg ctg gtg aag 1123
 Leu Lys Ser Ile Glu Leu Tyr Gly Thr Glu Val Ile Pro Leu Val Lys
 330 335 340

gac atc ttg acc aag cag gct taagaaggctc ttaggacatt ccc 1167
 Asp Ile Leu Thr Lys Gln Ala
 345

<210> 436

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 436

Met Lys Asn Val Ser Phe Gly Leu Asp Thr Phe Gly Asp Asn Ala Ile
 1 5 10 15

Asp Leu Gln Gly Asn Pro Val Ser Pro Ala Gln Thr Leu Arg Asn Ile
 20 25 30

Ile Asp Glu Ala Lys Met Ala Asp Lys Val Gly Val Asp Ile Ile Gly
 35 40 45
 Ile Gly Glu His His Arg Glu Tyr Ser Val Ser Ala Pro Asp Ile
 50 55 60
 Val Met Thr Ala Ile Leu Ala Ser Thr Glu Arg Leu Lys Val Thr Ser
 65 70 75 80
 Ser Val Thr Val Leu Ser Ser Asp Asp Pro Val Arg Leu Phe Glu Arg
 85 90 95
 Tyr Ser Thr Met Asn Ala Leu Ser Asn Gly Arg Ala Glu Ile Thr Leu
 100 105 110
 Gly Arg Gly Ser Phe Ile Glu Ser Phe Pro Leu Phe Gly Phe Asp Leu
 115 120 125
 Gln Asp Tyr Glu Gln Leu Phe Ser Glu Arg Leu Asp Leu Phe Ala Lys
 130 135 140
 Ile Leu Glu Ala Asp Ser Arg Gly Gln Gly Val Thr Trp His Gly Glu
 145 150 155 160
 Thr Arg Ser Ala Leu Glu Asn Gln Met Leu Tyr Pro Pro Thr Glu Asn
 165 170 175
 Gly Ile His Ala Trp Val Ala Val Gly Gly Ser Pro Glu Ser Val Val
 180 185 190
 Arg Ala Ala Lys Tyr Arg Phe Pro Leu Met Leu Ala Ile Ile Gly Gly
 195 200 205
 Ala Pro Glu Arg Phe Arg Pro Tyr Val Asp Leu Tyr Lys Arg Ala Asn
 210 215 220
 Glu Gln Phe Gly Gln Pro Gln Lys Pro Ile Gly Val His Ser Pro Gly
 225 230 235 240
 Leu Ile Ala Ala Thr Asp Glu Glu Ala Arg Glu Leu Ala Leu Asn Asp
 245 250 255
 Trp Leu Glu Leu Gln Arg Lys Ile Gly Ala Glu Arg Gly Trp Ala Pro
 260 265 270
 Ala Asp Ala Met Gln Phe Glu Arg Glu Ile Asp His Gly Ser Leu Tyr
 275 280 285
 Ile Gly Ser Pro Glu Thr Val Ala Lys Lys Ile Ala Lys Thr Ile Ser
 290 295 300
 Val Leu Asp Leu Asp Arg Phe Thr Leu Lys Tyr Ala Ser Gly Gln Thr
 305 310 315 320
 Pro His Glu Tyr Leu Leu Lys Ser Ile Glu Leu Tyr Gly Thr Glu Val
 325 330 335
 Ile Pro Leu Val Lys Asp Ile Leu Thr Lys Gln Ala
 340 345

<210> 437
 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(703)
 <223> RXA01933

<400> 437

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ctagaagcct taggcaagaa atttggttga gttttcgatc tctacgacgc gtcattctcaa 60

ttccacctag gcttggaatgc aggttagaaa ggagccttcg atg tct aag act cgt 115
                                     Met Ser Lys Thr Arg
                                     1      5

act ttt ctg ttt gat ctt tat ggt gtt ctc atc aag gag cat ggt gcg 163
Thr Phe Leu Phe Asp Leu Tyr Gly Val Leu Ile Lys Glu His Gly Ala
          10          15          20

gcg cag ttt gag cgg gtt gcg cgt gcg gtg ggg gag ccg tcc aag aac 211
Ala Gln Phe Glu Arg Val Ala Arg Ala Val Gly Glu Pro Ser Lys Asn
          25          30          35

gac aag ctg cat gag gtt tat gag tcg ctt cgt ctg gat ctg gat gcc 259
Asp Lys Leu His Glu Val Tyr Glu Ser Leu Arg Leu Asp Leu Asp Ala
          40          45          50

ggc cgc gtg agt gag gtg aat tat tgg aat cag atc aaa cta ttg gtg 307
Gly Arg Val Ser Glu Val Asn Tyr Trp Asn Gln Ile Lys Leu Leu Val
          55          60          65

ggt ttg gag ttt ttg gat atc cag gag gtc atc gcg gct gac tac agg 355
Gly Leu Glu Phe Leu Asp Ile Gln Glu Val Ile Ala Ala Asp Tyr Arg
          70          75          80          85

ggc ctt tat gag cgt gat cag gac atg gtt gat tat gtg ttg tcg ttg 403
Gly Leu Tyr Glu Arg Asp Gln Asp Met Val Asp Tyr Val Leu Ser Leu
          90          95          100

aag gcg aaa ggc cac cgc atc gga att ttg tcg aat att ccg gag ggg 451
Lys Ala Lys Gly His Arg Ile Gly Ile Leu Ser Asn Ile Pro Glu Gly
          105          110          115

ttg gcc aag ctg ttg aag gag cac aat tcg gag tgg ctt gat cag ctt 499
Leu Ala Lys Leu Leu Lys Glu His Asn Ser Glu Trp Leu Asp Gln Leu
          120          125          130

gat gcg gtg act ttg tcg tgc gat att ggc gcg gcg aag ccg gag ccg 547
Asp Ala Val Thr Leu Ser Cys Asp Ile Gly Ala Ala Lys Pro Glu Pro
          135          140          145

aag tct ttc cat gtg gca ctt gag gcc ctt ggt gaa aaa gct gag gat 595
Lys Ser Phe His Val Ala Leu Glu Ala Leu Gly Glu Lys Ala Glu Asp
          150          155          160          165

gtg acc ttt att gat gat cgc gtg cgt aac att gag gca gcg cgc gaa 643
Val Thr Phe Ile Asp Asp Arg Val Arg Asn Ile Glu Ala Ala Arg Glu
          170          175          180

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gaa ggt ctc agc aca att cac ttc act ggc tta gat tcc tta aaa gaa 691
 Glu Gly Leu Ser Thr Ile His Phe Thr Gly Leu Asp Ser Leu Lys Glu
 185 190 195

agc att cag gaa tgacacctca accactgatt ttg 726
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<210> 438

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

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Lys Glu His Gly Ala Ala Gln Phe Glu Arg Val Ala Arg Ala Val Gly
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Glu Pro Ser Lys Asn Asp Lys Leu His Glu Val Tyr Glu Ser Leu Arg
 35 40 45

Leu Asp Leu Asp Ala Gly Arg Val Ser Glu Val Asn Tyr Trp Asn Gln
 50 55 60

Ile Lys Leu Leu Val Gly Leu Glu Phe Leu Asp Ile Gln Glu Val Ile
 65 70 75 80

Ala Ala Asp Tyr Arg Gly Leu Tyr Glu Arg Asp Gln Asp Met Val Asp
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Tyr Val Leu Ser Leu Lys Ala Lys Gly His Arg Ile Gly Ile Leu Ser
 100 105 110

Asn Ile Pro Glu Gly Leu Ala Lys Leu Leu Lys Glu His Asn Ser Glu
 115 120 125

Trp Leu Asp Gln Leu Asp Ala Val Thr Leu Ser Cys Asp Ile Gly Ala
 130 135 140

Ala Lys Pro Glu Pro Lys Ser Phe His Val Ala Leu Glu Ala Leu Gly
 145 150 155 160

Glu Lys Ala Glu Asp Val Thr Phe Ile Asp Asp Arg Val Arg Asn Ile
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<210> 439

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                               Val Glu Gly Ser Val
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gaa aag ctg ggt tta att tcc tgg tgg gag gaa ctc gcg cgc acc gct 163
Glu Lys Leu Gly Leu Ile Ser Trp Trp Glu Glu Leu Ala Arg Thr Ala
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gag cgg ggc aag ctg gat gcg gtc ttt ttg gcc gat ggg cag gcg att 211
Glu Arg Gly Lys Leu Asp Ala Val Phe Leu Ala Asp Gly Gln Ala Ile
                25                30                35

aat ccg gtc ggt ctg gag aat ggg ccg ggc tgg ttt ttg gag ccg gtg 259
Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp Phe Leu Glu Pro Val
                40                45                50

acc gcg ttg act gcg atg gcg cgg gcg acg aac aat att ggg ttg atc 307
Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn Asn Ile Gly Leu Ile
                55                60                65

agc aca att tcc agt acg ttt tgg cag ccg ttt cat gcg gcg cgg atg 355
Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe His Ala Ala Arg Met
                70                75                80                85

atc gcc agc ttg gat cat att tcg ggt ggg cgt gct gga atc aat gtg 403
Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg Ala Gly Ile Asn Val
                90                95                100

gtg aca tcg atg acc gat gcg gag gcg cgt aac cac ggg atg gat gcg 451
Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn His Gly Met Asp Ala
                105                110                115

ttg ccg ggt cac gat gtt cgc tat gcg cgc gct gcg gaa ttt att gaa 499
Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala Ala Glu Phe Ile Glu
                120                125                130

acc atc act gcg ctg tgg gat tct tgg cct gcg gaa agt ttg gtg atg 547
Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala Glu Ser Leu Val Met
                135                140                145

gat cgt gct gga aaa ttt gcg gac tcc tcg ctc att aaa tct atc gat 595
Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu Ile Lys Ser Ile Asp
                150                155                160                165

cat gat ggt gag ttc ttc caa gtc gct ggt ccg ctg aat atc ccc agt 643
His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro Leu Asn Ile Pro Ser
                170                175                180

cct ccg cag ggt cga ccc gta ctt ttt cag gct gga tcc tca ccg caa 691
Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala Gly Ser Ser Pro Gln
                185                190                195

gga ccg gaa atc gct gcg aaa tac gcc gag gca att tac tct gtg gcg 739

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Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala Ile Tyr Ser Val Ala
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tgg gat ttg gag caa gcg caa gat tat cgc tct gat att cat gct cgt 787
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 215 220 225

gcc act gcc cag ggt cgc gag ccc atg ccg gtg ctt cct ggt ttg gtg 835
 Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val Leu Pro Gly Leu Val
 230 235 240 245

act ttt gtt ggc acg acc gtg gaa gaa gcg cgt gca aaa cag cag gct 883
 Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg Ala Lys Gln Gln Ala
 250 255 260

ctt aat gcg ttg ctg ccg gtc aaa gac tca cta aat cag ttg agt ttc 931
 Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu Asn Gln Leu Ser Phe
 265 270 275

ttt gtg ggt caa gat tgc tcg acg tgg gat ttg gat gca cct ccc cca 979
 Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu Asp Ala Pro Pro Pro
 280 285 290

cca ctg cca ccg cta gaa gag ttt tcc ggt cct aaa ggc agg tac gaa 1027
 Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro Lys Gly Arg Tyr Glu
 295 300 305

acg gtc ctg cgg 1039
 Thr Val Leu Arg
 310

<210> 440

<211> 313

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 440

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Leu Ala Arg Thr Ala Glu Arg Gly Lys Leu Asp Ala Val Phe Leu Ala
 20 25 30

Asp Gly Gln Ala Ile Asn Pro Val Gly Leu Glu Asn Gly Pro Gly Trp
 35 40 45

Phe Leu Glu Pro Val Thr Ala Leu Thr Ala Met Ala Arg Ala Thr Asn
 50 55 60

Asn Ile Gly Leu Ile Ser Thr Ile Ser Ser Thr Phe Trp Gln Pro Phe
 65 70 75 80

His Ala Ala Arg Met Ile Ala Ser Leu Asp His Ile Ser Gly Gly Arg
 85 90 95

Ala Gly Ile Asn Val Val Thr Ser Met Thr Asp Ala Glu Ala Arg Asn
 100 105 110

His Gly Met Asp Ala Leu Pro Gly His Asp Val Arg Tyr Ala Arg Ala
 115 120 125

Ala Glu Phe Ile Glu Thr Ile Thr Ala Leu Trp Asp Ser Trp Pro Ala
 130 135 140

Glu Ser Leu Val Met Asp Arg Ala Gly Lys Phe Ala Asp Ser Ser Leu
 145 150 155 160

Ile Lys Ser Ile Asp His Asp Gly Glu Phe Phe Gln Val Ala Gly Pro
 165 170 175

Leu Asn Ile Pro Ser Pro Pro Gln Gly Arg Pro Val Leu Phe Gln Ala
 180 185 190

Gly Ser Ser Pro Gln Gly Arg Glu Ile Ala Ala Lys Tyr Ala Glu Ala
 195 200 205

BGI-128CPC
 Phe Tyr Ser Val Ala Trp Asp Leu Glu Gln Ala Gln Asp Tyr Arg Ser
 210 215 220

Asp Ile His Ala Arg Ala Thr Ala Gln Gly Arg Glu Pro Met Pro Val
 225 230 235 240

Leu Pro Gly Leu Val Thr Phe Val Gly Thr Thr Val Glu Glu Ala Arg
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Ala Lys Gln Gln Ala Leu Asn Ala Leu Leu Pro Val Lys Asp Ser Leu
 260 265 270

Asn Gln Leu Ser Phe Phe Val Gly Gln Asp Cys Ser Thr Trp Asp Leu
 275 280 285

Asp Ala Pro Pro Pro Pro Leu Pro Pro Leu Glu Glu Phe Ser Gly Pro
 290 295 300

Lys Gly Arg Tyr Glu Thr Val Leu Arg
 305 310

BGI-128CPC: 315 Arg

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- (71) Applicant: BASF AKTIENGESELLSCHAFT [DE/DE]; D-67056 Ludwigshafen (DE).
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- (30) Priority Data:
- | | | |
|--------------|-----------------------------|----|
| 60/141,031 | 25 June 1999 (25.06.1999) | US |
| 199 31 636.8 | 8 July 1999 (08.07.1999) | DE |
| 199 32 125.6 | 9 July 1999 (09.07.1999) | DE |
| 199 32 126.4 | 9 July 1999 (09.07.1999) | DE |
| 199 32 127.2 | 9 July 1999 (09.07.1999) | DE |
| 199 32 128.0 | 9 July 1999 (09.07.1999) | DE |
| 199 32 129.9 | 9 July 1999 (09.07.1999) | DE |
| 199 32 226.0 | 9 July 1999 (09.07.1999) | DE |
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| 199 32 922.2 | 14 July 1999 (14.07.1999) | DE |
| 199 32 924.9 | 14 July 1999 (14.07.1999) | DE |
| 199 32 928.1 | 14 July 1999 (14.07.1999) | DE |
| 199 32 930.3 | 14 July 1999 (14.07.1999) | DE |
| 199 32 933.8 | 14 July 1999 (14.07.1999) | DE |
| 199 32 935.4 | 14 July 1999 (14.07.1999) | DE |
| 199 32 973.7 | 14 July 1999 (14.07.1999) | DE |
| 199 33 002.6 | 14 July 1999 (14.07.1999) | DE |
| 199 33 003.4 | 14 July 1999 (14.07.1999) | DE |
| 199 33 005.0 | 14 July 1999 (14.07.1999) | DE |
| 199 33 006.9 | 14 July 1999 (14.07.1999) | DE |
| 199 41 378.9 | 31 August 1999 (31.08.1999) | DE |
| 199 41 379.7 | 31 August 1999 (31.08.1999) | DE |
| 199 41 390.8 | 31 August 1999 (31.08.1999) | DE |
| 199 41 391.6 | 31 August 1999 (31.08.1999) | DE |
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN HOMEOSTASIS AND ADAPTATION

(57) Abstract: Isolated nucleic acid molecules, designated HA nucleic acid molecules, which encode novel HA proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing HA nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated HA proteins, mutated HA proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of HA genes in this organism.

WO 01/00842 A3

INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 00/00911

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/31 C12N15/52 C12N9/00 C07K14/34

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 93 09225 A (MASSACHUSETTS INST TECHNOLOGY) 13 May 1993 (1993-05-13) page 8	1,2, 8-19,22, 25-34,37
X	EIKMANN ET AL: "The phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: molecular cloning, nucleotide sequence, and expression" MOL. GEN. GENET,XX,XX, vol. 218, 1989, pages 330-339, XP002138580 page 333, column 1, paragraph 2 page 330, column 2, paragraph 2	1,2, 8-19,22, 25-34,37
X	EP 0 401 735 A (KYOWA HAKKO KOGYO KK) 12 December 1990 (1990-12-12) claims 1-4	1,2, 8-19,22, 25-34
	--- -/-	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"G" document member of the same patent family

Date of the actual completion of the international search

19 December 2000

Date of mailing of the international search report

23.03.01

Name and mailing address of the ISA

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Authorized officer

Mata-Vicente, M

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00911

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LEE J -K ET AL: "NUCLEOTIDE SEQUENCE OF THE GENE ENCODING THE CORYNEBACTERIUM GLUTAMICUM MANNOSE ENZYME II AND ANALYSES OF THE DEDUCED PROTEIN SEQUENCE" FEMS MICROBIOLOGY LETTERS,AMSTERDAM,NL, vol. 119, no. 1-2, 1994, pages 137-146, XP000960685 ISSN: 0378-1097 abstract	1,2, 8-13, 15-19, 22, 25-27, 30,31, 34,37
X	--- DATABASE EMBL/GENBANK/DDBJ [Online] EBI; 17 May 1996 (1996-05-17) "M. tuberculosis H37Rv complete genome; segment 57/162" XP002155887 Acc. No. Z73419 -----	6-13,17, 23, 25-27, 30,31, 34,37

INTERNATIONAL SEARCH REPORT

Int tional application No.
PCT/IB 00/00911

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although as far as an "in vivo" method is concerned, claim 35 is directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-38 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1 : Claims (1-38) - partially

Isolated nucleic acid molecule from *Corynebacterium glutamicum* of SEQ ID NO:1; the polypeptide thereby encoded (SEQ ID NO:2); fragments, variants and fusions thereof; expresion vectors comprising the polynucleotide of the invention or its derivatives, host cells transfected with said vectors and methods for the production of fine chemicals involving the culture of said host cells; use of the above-mentioned polynucleotide/polypeptide for diagnosis of *Corynebacterium diptheriae* infections.

2. Claims: Inventions 2-174 : Claims (1-38) - partially

Idem as subject 1, but limited to the rest of the sequence pairs (polynucleotide-polypeptide) listed in Table 1, with the exception of the F-designated ones (disclaimed).

INTERNATIONAL SEARCH REPORT

International Application No
PCT/18 00/00911

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9309225	A	13-05-1993	NONE

EP 0401735	A	12-12-1990	JP 2967996 B 25-10-1999
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			DE 69022631 D 02-11-1995
			DE 69022631 T 21-03-1996
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			US 5447857 A 05-09-1995
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